SEQUENCE LISTING

<110> Hosted, Thomas J. Wang, Tim X. Horan, Ann C.

<120> Everninomicin Biosynthetic Genes

<130> ID0983K US

<140> US 09/758,759

<141> 2001-01-11

<150> US 60/175,751 <151> 2000-01-12

<160> 204

<170> PatentIn Ver. 2.1

<210> 1

<211> 109519 <212> DNA

<213> Micromonospora carbonacea

<400> 1

ggtacccgac	cgtgtcccgg	aacaacgagt	cgagatacgg	cgagaggaac	accccccggt	60
agtccgggta	gacggtgggc	gcgaaggcgt	acgcgccttc	gacggtcagc	gggcgggcgg	120
acaccggcgg	gtcagctcgt	cacgtgtacg	cgggggacgt	acaggatcca	ctgtccgcca	180
gcccggcgga	actcctgctc	cttcgccatg	atctcgtcgg	cgtggttcca	ggcgaagagc	240
agcgcgtagt	ccaccgcgtc	gggcgtgaac	gcgtccgggg	tgcgcaccgg	gatgtgcgtg	300
ccgggggtga	gccggccctg	cttggccggc	gtcgtgtcgc	acacccagga	gaccaggtcc	360
ggaccgatgc	cgcagaagtt	cgtcacggtg	gcgctcttcg	ccgtcgcgcc	gtacgccacc	420
acccgcttgc	cctcggcctt	gagcgagttc	agcagggcga	gcaggtcggt	gcggatgccc	480
tcgacgtcgg	cggcgaacct	gtcgagccgg	ctgcggtcgg	cgacccctcg	ggcgtcctcc	540
tcgccgatca	gcgcggccac	ccgctcggcc	ggctgccgcg	cgccggcacg	ggcgatggtg	600
tagcggacct	ccccaccgtg	caccggaagg	cgttccacgt	cgacgagcgc	gaagccgaag	660
cgggccgcca	gcgcctgcac	cgaccgcgcc	gagaagaaga	agaaatgctc	gtcgtagatc	720
tggtcgaagg	acgtcttgtc	caggatgtcc	ccgaggtacg	ggtcctcgaa	gacgaagacc	780
ccgtccggtg	ccagcagcgc	gtcaacgccc	cggaggatgg	agtcgaggta	ggggatgtgg	840
cagatggtgt	tggccgcgaa	gatcacatcg	gcggggccgt	cggtctccct	gacccggcgg	900
gcggtggact	cctcgaagaa	ctcggtgacc	acccgcaccc	cgtgcccacg	ggccacatcg	960
gccaccccac	ccgacggctc	gaagcccagg	tgccgcactc	ccgcctcgtg	gacggtacgc	1020
agcatcaccc	cgtcgttgca	gccgatctcc	accacgaacg	ggtccgggcc	ggtggcctcg	1080
tgctccagca	ggtgccgcgc	ggtgtcggcg	aagtgcttct	gcatcacgga	ggagcccgac	1140
gagtggtacg	ggtagtcctg	gtggaacatc	tcctcccggg	gcacctcctc	catgagctgc	1200

accatcgtgc	agcccgcgca	gacccccacc	gccaggtgga	agaagaactc	gtccgcgagc	1260
tggtcctcgg	tgaggaaccg	gtcggagagc	ggctgccgac	ccaggtcgag	gaactgggcg	1320
gtggtgccgc	cacacgcccg	gcaggtgccg	cgccggggcg	tgccgtcggc	tgaatcggtc	1380
atcgcattcc	ttccatggat	acccctgcct	caggcagggc	ggatgtcaac	gacgtctcct	1440
tgtcgggatg	ggtcgtccag	ctctcggctg	cggcgtgccg	gccggcgact	cagagcgccg	1500
cgagcacgtc	gcgcagcgcg	tcgatcaccc	ggtcctgcgt	ctccggcggc	agcgagggat	1560
acatggggag	ggagaagatc	tcgccggcca	accgttccgt	ggtggggagg	gagccggtct	1620
ggtagccgag	cttggcgaag	ccggtcatgg	tgtgcaccgg	ccaggggtag	ctgatgttga	1680
gcgcgatgtc	ccgcgccgcc	aactgttcga	ggatgcggtc	gcgggcgggg	tggcggacca	1740
cgtagacgta	ccagacgtgt	tcgttgtcgg	tcgccgtcac	cggcagggtc	aggccgacct	1800
ggtcggcgat	gtcggccagg	ccctcctcgt	agcgccgggc	cacggcgcgg	cgcccggcga	1860
tgtagtcgtc	gagccggcac	agcttgcggc	gcaggatctc	ggcctgcacc	tcgtcgaggc	1920
ggcagttgtg	ccccggcgtc	tcgacgacgt	agtagacctg	ttccatgccg	tagtagcgca	1980
gccgccgcag	ccgctcgtcg	atcacggcgt	ccgcggtgac	cacgccgccg	ccgtcgccgt	2040
acgcgcccag	caccttcgtc	ggatagaacg	agaaggcagc	ggcgtcgccc	atcgtgccgg	2100
ccagccgtcc	gccccgacgc	gcgccgtgcg	actgcgcgca	gtcctccagg	accttgaggc	2160
cgtgttcccg	ggccacccgc	agcaccgggt	ccatgtcgac	gcactggccg	tagaggtgca	2220
ccggcagcag	cgccttcgtc	cggggggtga	ccgcctcggc	cagcagctcg	gtgtccatca	2280
ggtagtcgtc	ggcgcggacg	tccacgaaga	ccggcgtcgc	gccgaccgcg	tcgatggcga	2340
gcaccgtcgg	cgcggccgtg	ttggagacgg	tgatgacctc	gtcgcccggc	ccgacgtcga	2400
gcgcctggag	tgcgagcttg	atggcgttgg	tgccgttgtc	caccgtgacg	cagtgcggca	2460
tgtcgtgata	ggcggcgaac	tcctgctcga	agccgcgcac	gctcgcgccg	aggatgaggt	2520
tcccggactc	gaagaccgtc	tgcacggcgt	cgaggaggtc	gtcccgttcc	ttctcgtact	2580
ccggcaggta	gccccacact	cggatggtca	tcttcgccct	tctacgccga	ggtccgggag	2640
cggagcgcgc	gcacgctcat	gtagtcgttg	tcccggtcga	gtccaagtgc	ctgaccgctc	2700
aggtagtcga	cggcgtccac	gtagctgtag	ggctgcatga	acccgccggc	ccgcacgtcg	2760
cgatagagcc	gggagagtgg	gtgcccggcc	gtgtaggcga	ggccgccgac	caggctgagg	2820
cagtcgtcca	ccaccgccgg	ggccagctcg	ttgacggtca	tcttcgcgta	ctggaacggg	2880
gtcatcatcc	gtcggccgcg	ttcgtccggg	tcgccggaca	ggtcgaccga	cgccgcgtcg	2940
gcgttggtca	acgccgcgcc	gaccgtggtg	cgtagcgcgt	agagccgggt	gtccagcccg	3000
gcgaccagcg	cccgggcacc	ggcccgtggc	tegeegeege	gccccgcgca	gaaaccgacc	3060
gcgatgtccc	gggccgcctg	ggcgatgccg	gcgtagatgc	cgagcatggt	gatcgagctg	3120

accettetece eggecageae geogtecege eggeceega eeggeegee etecageage 3180 tegteggece ggacegggea ceggtegaag accaecteca gegteeeega ggeaegeatt 3240 cccaggccgt cccagttgtc cagcaccgtg agcccggggg cgtcgcggtg cacgaccggc 3300 acggcgagga acaccgagcc gtcgtcgtcg cgccgctggg cgtgcacgaa gaagtgggtc 3360 gcgatgggcg ccatgctgac cagcaccttg cggcccgaca gcagccagcc gccggcgccg 3420 teggaatgea geteggtgae eaegeegggg gegteettga gegegeegea gaeggeggee 3480 tegeceteeg ceategeeeg cageageege teegecateg egegeacegg eggegtgeeg 3540 tgctgccact cgtaggtgag ggtgaggccc cggctgagct gcacgtgcca ggccagcgcg 3600 gtggacgcgt cggcctcggc cagccgcatc agcgcggtcg ccacgtcgta cagccgggtc 3660 aaccccagge egeccagete ggegggaaeg gtggegeeca teaaccegag ettegegaae 3720 tgctcgaacg cctccaccgg gaaggtgccg gtgcggtccc ggtcggcggc ctccgcactg 3780 atteteggga teaegeegge aageaggteg accaeegtge geeeegeegg egtgagegge 3840 gegegaagat cegeegeeac ceatetetee teggteagat tagacatege etgetteegt 3900 tegegetgtg cegaacetgt egetateagg gtgegeggeg ateaceaatt getggetgat 3960 tgtccaccga cgatgctcga cagggatacc cagaataggc ggcaacggct tggcgaaacc 4020 cctgtcgtgc gccggagttc gccaagtcta gttggatcac tcgagcttcc cccgcagaag 4080 ccgtgaacca tgggccagcg gttgacgtcg ctatatattc ggccgacacg tgcggaggac 4140 tegtgaagat actgtteate geaggaeega egaagteeag eetattegge etggeeeeae 4200 tggcaatcgc cgcccggatg agcgggcacg aggtcgtgat ggcttccacg caggaggtcg 4260 taccggcgac gatgtccgtc gggctgccgg ccttcccgct ggcggcgctg accetcgccg 4320 ageteatgae cacegaeegg geeggegate egetgegeat eeeggeegag gaegeegeet 4380 tegteeett egteggeegg atgtteggee ggetggegge gateageetg gateegetge 4440 gcgacctggt cggcgggtgg cggcccgacc tgatcgtcgg cggcccgcac gcctacgccg 4500 cgccgatcct ggccaccgaa cttggggtgc cctgcgtgcg gcacctgctc accggcaacc 4560 eggtggaceg egagggeace cateeggggg tegaegagga getgeggeeg gagetggeeg 4620 egeteggeet ggeeeaggtg cegeegttee acetggeeet ggaeatette ceggeeagea 4680 eceggatega egaegteeeg eeggegeage eggtgegaee getgegetgg atteegaeea 4740 accagcagca gccggtggcg ccgtggatgc tctcgcgcgg gccgcgtcgc cgtgtcctgg 4800 teacegoegg cagtetggte accaecacee acaacttega ettectecae ggaetggeeg 4860 gcaccetgge egageaggae gtegaggteg tggtegegge geegeeggag gtgggteggg 4920 ccctgcacga cgtgccgggt gtgcggcacg ccggctggct cccgctggac gtggtgctgc 4980 eccactgtga cetgategtg caccacteeg geacgatgae egegetgaee geettgaaeg 5040 egggggtgcc ccagctgatc gtgccgcagg agagccggtt catcgagtgg gcgcgcaacc 5100

tgtcgaccct	gggcgtggcg	cagaccctcg	cgccgggcga	ggacacgccg	gaggccgtgg	5160
gcaaggtcgc	ccgcctgctg	ctggaggatc	cggtccacgc	caccagcgcc	gccgcgatcg	5220
cccgggagat	cgccgagatg	cccggcccca	cggaggtcgt	gggccagctc	accgagttcg	5280
cgacccgggg	cctgacatgc	gcgtcctcgt	gaccggcgga	gccgggttca	tcggctccca	5340
cctcaccgac	gcgctgctcg	aacgcggcga	cagcgtcacc	gtgctcgacg	acctgtccac	5400
cgggcggccc	gagcggctgc	ccgccggggt	gccgctgcac	cacgggtcga	tcaccgaccg	5460
ggccgggttg	acccggctgg	ccgagcagtg	tegeeeggag	gtcatctgcc	acctggccgc	5520
ccaggcggac	gtgcgcaact	cggtggccga	cgccacctcg	gacaccgggg	tcaacgtggt	5580
cggcaccgtc	aacgtcctgg	aggccgcccg	ggccatcgac	gcccgggtgg	tcttcgcctc	5640
cagcggcggc	gccctctacg	gggaggtcga	cgagctgccc	tcccccgagg	acgteeggee	5700
ggcgccgtgg	gcgccgtacg	gggccgccaa	gtactgcgcg	gagcagtacc	tggcgctcta	5760
caaccggctc	tacggctcga	cccacgcggc	gctgcggctc	ggcaacgtgt	acgggccacg	5820
ccaggacccg	accggcgagg	ccggggtcgt	ctcgatcttc	tgcggctgcc	tggtggccgg	5880
gcgccggccg	acggtgttcg	gcgacggcga	gcagacccgg	gactacatct	acgtggccga	5940
cgtggtggag	gcgttcctgc	tcgcggtcgg	gcacggtggc	cccggcctgt	ggaacatcgg	6000
caccgggacc	tccaccagca	tccgcaaact	actggacctg	gtcggccgca	ccgccgggcg	6060
cgtcccggac	ccccgcttcg	agccaccccg	cctgggcgag	ctgaagcact	ccgcgctgga	6120
ggtgacccgc	geggeeeggg	agctgcgctg	ggcggcccga	acgaggctcg	ccgacggcat	6180
cgcgaaggtc	tacaagtggg	tcgaggcgga	cgaaccggtc	cggggggagc	gatgacccgc	6240
gaggggtcaa	cgccgccggt	tagggtcgcc	accatcacgg	tcggcaccaa	cgagatccgt	6300
tggctggacc	gcgcgctcgg	ctcgctgctc	gccagcgaca	cgaccggctt	cgagctgacg	6360
gtcttctacg	tggacaacgc	ctcggccgac	ggcagcgtgg	cgcacgtcat	gtcggcgttt	6420
cccggcgtcc	gggtcatccg	aaacccccgc	aatctcggct	tcaccggcgc	gaacaacgtc	6480
ggcatgcggg	cggccctggc	ggagggcttc	gaccacatct	tcctggtcaa	cccggacacc	6540
tggacaccgc	cggggctggt	ccgcgggctg	gtcgagttcg	cgcagcggtg	gccgcagtac	6600
ggcgtcatcg	gcccgttgca	gtaccgctac	gacccggcgt	cgaccgagtt	gaccgacttc	6660
aacgactgga	cgcaggtcgc	cctctacctg	ggcgagcagc	acaccttcgc	cggcgacctg	6720
ctggatcatc	cctcgcacgt	caccgcgacg	gtccgcgacc	gcgcgccgcg	caccctggag	6780
cacgcgtacg	tgcagggctc	ggcgctgttc	gtccgggccg	ccgtgctacg	cgaggtcggc	6840
ctgctcgacg	aggtgttcca	cacctactac	gaggaggtcg	acctgtgccg	gegggeeegg	6900
tgggcgggct	ggcgggtggc	gctcctactc	gacctcggca	tccagcacaa	aggcggcggt	6960
ggcaccgccg	cgagcgcgta	cagccggata	cacatgcgcc	gcaaccgcta	ctactatctg	7020

	ctgaccgatg	tggactggcc	cccggccaag	gccgcccggc	tegeegeeeg	ctggctgttc	7080
	tccgacgtcc	gtgggcgggg	cgtgacgggt	cggacgagcg	cgggcgtcgg	ggcgcgggag	7140
	accttcgtgg	cgctcgggtg	gctggcccgc	caggccccgg	tgatccggga	acgtcgtcgg	7200
	cggcaccggc	tgctgcgggc	acgagggacg	ggcgtggacc	gcgcccgaga	gcggaaggaa	7260
	accgtgcggg	gatgagcagg	ccacggattc	tcgtcgcggg	caacttccac	tggcaggccg	7320
	ggttcagcca	gaccgtcgcc	gcgtacgtgc	gggcggcccg	ggaggccgac	tgcgaggtgc	7380
	ggctctgcgg	cccgctgtcc	cgggtcgacg	ccgagacggc	ccggcacctg	ccggtcgagc	7440
	cggacctccg	ctggggcacc	cacctggtga	tcatgttcga	ggccaagcag	ttcctcaccg	7500
	aggcgcaact	ggacctcgtc	gaggcgttcc	cccgacagcg	ccgggccatc	gtcgacttcg	7560
	acgggcactg	gggtgccgag	gagggcgggg	acggcgacag	cgcgtcgggc	cggtactccg	7620
	cggagagttg	gcggcggttg	tactcgaccc	tgagcgacct	gatcctgcaa	ccccggctgg	7680
	gtccgctccc	ggccggcgcc	cggttcttca	agtgcttcgg	cctggcagcg	ccggtgcggc	7740
	acccgctgga	actgggcacc	ggcgcgcagt	cgcgcccgta	cgacctccag	tacatcggca	7800
	gcaactggtg	gcggtgggag	ccgatgaccg	agatggtcga	ggccgcggcg	gcggcccggc	7860
	cgccgctgcg	ccggctgcgg	gtgtgcggac	gctggtggga	cggcggcagt	tgcgcgggct	7920
	tcgaggaggc	gacgctcagc	gagccgggct	ggctgcgggc	gcgcggcgtc	gaggtgcatc	7980
	cgcccgtgcc	gttcggccac	gtggtcgagc	agatgggccg	gtcgctgatc	tcaccggtcc	8040
	tggtgcggcc	gctggtcacc	agcaccggcc	tgttgacccc	ccggatgttc	gagacgctgg	8100
	cctcgggcag	cctgcccgtg	ctcccggtcg	ccgcgaagtt	cctcgcgccg	gtctacggcg	8160
	acgaggcgga	acacctgatg	ctcggcgacg	acccggccgg	aacgctgagc	cggctctcgg	8220
	ccgagcacga	acggtacgga	cgactggtcg	gtgagattca	ggaccggctc	cgcgtcgagt	8280
	acggctaccc	tcgcgtcctg	cgggacctgc	tcgatctgct	ggcctgagga	atgaggagca	8340
	gatgaccccc	ctgcggatcg	cgatggtcaa	cataccgttc	cggttgccga	gcgacgagcg	8400
	gcagtggatc	acggtcccgc	cgcaggggta	cggcgggatc	cagtggatcg	tggccaacaa	8460
	gatcaagggc	ctgctcgaac	tcgggcacga	ggtgttcctg	ctcggtgccc	cgggcagtcc	8520
	gcgtacgcat	ccacgcctga	ccgtggtgcc	ggcgggcgag	cccgaggaca	tccgggcatg	8580
	gttgaagtcc	gctccggtgg	acgtcgtcaa	cgactacagc	tgcggcaagg	tggatccgat	8640
	cgagctgccc	ccgggggtcg	gcctggtggc	ctcgcaccac	atgaccaccc	gcccgtccta	8700
	tccggccggc	tgcgtgtacg	cctcgaaggc	gcagcgggag	cagtgcggcg	gcggcgcgga	8760
	cgcccggtc	atcccgatcg	gggtggatcc	gtcgctctac	cgccccggcg	accgcaagga	8820
•	cgacttcctg	ctcttcatgg	gccggatctc	cccgttcaag	ggcgcgctgg	aggeggeege	8880
	gttcgcccgg	gccgccggcc	gccggctact	gatggccggt	ccggcctggg	agccggagta	8940
	cctcgaccgg	atcatgggcg	agtacggcga	ccacgtcacc	ctcgtcggcg	aggtgggggg	9000

ggccagcggc accccggtgg teggaccgag caacggctge etggcggag tegtgccge 91. cgtcggcgag gtggtggct teggaccgg ettegacgag eggaggccc gagcggtgct 92. gtcccgactg ccgtcgcccg cccaggcgcg gaaggccgcg atccggtgct gggggaccgc gagcggtgct 92. ggagatcgcc eggcgctacg aggcggtga ccggacgtgg etggccggcg egcacggtg 93. ggagatcgcc cggcggcgc gcacggtgg egcacgtcg egacgtagg gggtgccgc egacgggag 94. accggcggtg teggacgtcc gaccggcg egccggca ggcaggtgg egacggtag 94. accagggcgc ggctggtcc gaccaggcg egccggcag gtcatgaca ecaggacgta 95. ccagggcgc ggctggtcc gtctcgttcgg gcggcgtag teggacgag ggaagtgtg 96. catgaccgc tegccggcc gcagcggca ggcagcgtg teggacgag gaagtcgtg 96. catgaccgc tegccggcc gacgggaca ggcagcgtg teggtggag gcaccccgc 97. catgaccgc tegccggcc gacgggaca ggcagcgtg teggtggag gcaccccgc 97. ccatgaccgc tegccggcc gacgggaca ggcagcgtg teggtggag gacacccgcc 97. ccggtgcagg eccggaagt actgagaca gccgtgaga accgtggag gacacccgcc 97. ccggtgcagg eccggaagt actgagaca gccgtgaga accgtgcgc egtcagagg 97. ggtccagatg ggtgcccgt aggaggaca gccggagac accgtgcgc egtcagagg 97. ccacggagtg ggtgcgccg agcggagaca gccggagac accgtgcgc ggaagtcgag 97. ccacggagtg ggtgcgccg agcgagaca ggcgatggc eggacgcg agaagtcgag 97. ggtctcaca aactccggca ggaagggac etgaggac eggaggac eggaggacgag 97. ggcggcggtcg tegcacggc ggaagggac eggaggac eggaggacg gacggaggag 10.0 cgcggcgatg tegcacggc ggcgatgtc eggaggac eggaggacg gacggacgg 10.0 cgcggcgatg tegcacggc ggcgatgtc eggaggacg acctcgggag gacggcgga 10.0 cgcggcgatg tegcacggc eggagatgc eggagacgag acctcggga gacggacgg 10.0 cgcggcgatg tegcacgg eggatacc eggatgcc acctcggag gacacacac eggacgaga gccacacaca gtcccacaga cattgacc eggatgcc acctcggag gacacacacacacacacacacacacacacacaca	tcaggaacgt	atggacctgc	tcgccacggc	ggctgccatc	ctggtgctct	cccagccggt	9060
egteggegag gtggtggget teggeaceg ettegaegag egggaggee gaggggaegt 92. gtccegactg cegtegceeg ceaaggeggg gaaggeegg atecggtget gggggaeaggt 93. ggagategee eggegetaeg aggeggtga eeggeggeg etggeeggeg eggeagggg 94. agggeeggt teggeggee getaeggeeg egeceggeea ggteagetee gggeggeagg 94. agggeeggt teggeggtee gacaeeggee egeceggeea ggteagetee ggtegteagg 94. agggeeggt teggeggtee gacaeeggee egeceggeea ggteagetee ggtegteagg 94. ceagggtege ggetggteeg tetegttegg geeggetag teggeggeae ggaagtegtg 96. ceatgaeegee tegeeeggee geaggggae ggeeggtag teeggtege egaaeetegee geeggeggae ggetggteeg gtegttegt ggtegatgg teeggtegg eatgaeegee egaaegggae ggeggaegg ggeagetgg egaaeggagg ggagteegge eggetggteeg gtegttegg gtegatggae acegteggee ggetggteeg ggaggaegg ggegggaegg ggaggaegg ggagteegg ggaggaeggaegg ggaggaeggaegg ggaggaeggae	gcccggcccg	tggggcggca	cgtggtgcga	gccgggtgcg	accgtggtgt	ccgaggcggc	9120
greccegacty cegtegeese cecaggegeg gaaggeegeg atceggege gegegetegte 933 gagagtegee eggegetaeg aggeggtgta cegegacgtg etggeegege egegetegte 933 aggegeggeg eegggeggeg getacggteg egacegtagg gggaggeegeg eggeggggg 943 aggeegggtg teggeggee gacaceggeg egeceggea ggtaagetee ggteggeag 943 agegeeggtg teggeggtee gacaceggeg egeceggeag ggtaagetee ggteggeag 943 ceagggtege ggeteggggt eggtaacete gaceggetgg etcatgaaca ceaggaegta 953 cggegggege ggeteggggt etcegttegg geeggegtag teggggeae ggaagtegtg 966 catgaacegee tegeceggee geaggggaa ggegaeggt teegtgtegt egacetegte 966 catgaacegae tegeceggee gacggggaa geeggeggtag teggtgegg geacecegee 973 cggtaacaga cettegatge ggtegtegtg gttgatgtga teggtgegga gaceceggee 973 ggtecatcaga cettegatge ggtegtegtg gttgatgtga teggtgegga gacecegge 973 ggtecagatg etcaggege gacgggaca gegegggtee atgtacgeet egtectggtg 984 ceacgggagtg ggtegeegt ageggggae ettgaggate aggtggeegt agaagtegag 994 ggtecagatg ggtgegeegt agegggggg ettgagggee eggatggeeg gaagtgegg 994 ggtetecace aacteeggea ggtattete eggeeggaeg atctggggg gacacegggg 1003 eggggggteg tegecacgge eggegatgte eeggggaeg acttegggg gegacggggg 1003 egggggggaa gteacgaagg eateggegg gacgaggg acctegggg ggaaggggggggggggggggggggggggggggg	ggccagcggc	accccggtgg	tcggcacgag	caacggctgc	ctggcggaga	tcgtgccggc	9180
ggagategee eggegetaeg aggeggtgta eeggegggg eggegggg getaeggge gegeggggg ggagegggg getaeggteg eggeggggg ggagggggggggg	cgtcggcgag	gtggtgggct	t cggc accgg	cttcgacgag	cgggaggccc	gagcggtgct	9240
etgagecgge ceggeggeg getaeggeg egacegtagg gggtgecege egacegegga 94.5 agegecggtg teggeggte gacacegeg egeceggea ggteagete ggtegggg egaceggeg egeceggea ggteagete ggetagggt eggteacete gaceggegga teeggegaa eggageggga geeggegaa ggaagteggg 96.6 caaggacgge ggetaggee egaceggea ggeggaeggaa teegggegaa gaagtegge 97.6 catgacege tegeceggee gacggggaa ggegaeggt teegtgegt egacetegte 96.6 cgteateaga cettegatge ggtegtetg gttgatgtga tggtgeggga geacecegee 97.7 ceggtggaag ceeggeaggt actgagaca geeggtgaa acegtegee egteagagg ggtecagagg eceggagga actgagagaa geegggggaag acegtgggaag geacecegee 97.7 ggtecagatg etcaggeeg gacgggacaa geeggggtee atgtaeggee egteagggg 97.6 ggtecagatg etcaggeeg gacgggagaa geegggggee atgtaeggee eggegggggggggg	gtcccgactg	ccgtcgcccg	cccaggcgcg	gaaggccgcg	atccggtgct	gggggcacgt	9300
agegecegsty teggeggte gacaceggeg egeceggea gyteagetee gytegtegag 946 ceagggtege gyetegggyt egyteacete gacegyetgg eteatgaaca ecaggaegga 956 catgacegee tegeceggee geagegggaa gyegaeggta teegtgegg egacetegte 966 catgacegee tegeceggee gacggggaa gyegaeggty teegtgeggaa gacaceeggee 976 cgteatcaga cettegatge gytegtegt gytgatgya tggtgeggga gacaceegge 976 cggtgaggg eceggaggt actggagaac geegetggac accgtegee egteagagg 976 gytecagatg eteagageeg gacggagaca geegetggac acgtegeet egteagaggg 976 gytecagatg eteagageeg gacgggaca geegetggac acgtegeet egteagaggg 976 gytecagatg gytgegeeg ageeggggg ettgaggate gegtggeeg agaagteggg 996 ceacggagtg gytgegeeg ageeggggg ettgaggate gegtggeeg agaagtegga 996 teegteeteg gygatgtega ggaaagegga gycgatggee eggeategge eggaatgege 996 gytetecace aacteeggea gytattete eggeeggaeg atetgeggga gacgggagg 1000 eggegggteg tegecaegge eggegatgte eeggtagteg eggatgegg gegaegggg 1000 eggaggegteg tegecaegge eggegatgte eeggtagteg eggstgegg gegaegggg 1000 eggagggaga gyteacgaag eateggeeg gaagecagga accteggegt egteggegg 1000 eggageggaga gyteacgaag eateggeeg gaagecagg acctegggg eggaeggag 1000 eggaccaaca gyteceacagg eattyace acctetegga atageetge eggaataaa 1020 egaaccaaca gyteceacagg eattyace acctetegga atageetge eggaataaa 1020 egaaccaaca gyteceacagg eggataceg eteeggagg gyaaataggg attegaaca 1020 egaaccaaca gyteceacagg eggataceg eggeteteg attgteeatt eateecegtg 1030 egagactege eggegetge eagaacggaa eggegeteteg attgteeatt eateecegtg 1030 egagactege etegatgtee tegatgtegg tggggggttt gygatgaeeg gyaacaggee 1040 egtegegetg gacgtegge gygtegteta etaagaegag eegteegge tggeetteet 1050 egagacace ttegacegee teegageae egageggae eegagegge gaacetgget 1060 ecaateggag geegeegge tgagetgge egageggeg eagaeegge egageaegge 200 ecaateggag geegeegge tgagetgge egageggeggae eacaceggee gaacetgget 1060 ecaateggag geegeegge tgagetgge egageggeggae eacaceggee gaacetgge 1060 ecaateggag geegeegge tgagetgge egageggeggae eacaceggee gaacetgge 1060 ecaateggag geegeegge tgagetgge egagegggae eacaceggagae taceeggagaetggeeggagaetggeeggagaetggeeggagaetggeeggagaetggeegg	ggagatcgcc	cggcgctacg	aggcggtgta	ccgcgacgtg	ctggccggcg	cgcgctggtc	9360
ccagggtcgc ggctcggggt cggtcacctc gaccggctgg ctcatgacac ccaggacgta 950 cgcgcggcgc ggctggtccg tctcgttcgg gccggcgtag tgcggcgcac ggaagtcgtg 960 catgaccgcc tcgcccggcc gcagcgggca ggcgacgctg tccgttcgt cgacctcgtc 960 cgtcatcaga ccttcgatgc ggtcgtcgtg gttgatgtga tggggggga gcaccccgcc 970 ccggtgcagg cccggcaggt actggagaca gccgctggac accggtcgcc cgtcagacgg cccggcaggt actggagaca gccgctggac accggcgct cgtcagaggg 970 ggtccagatg ctcaggcgc gacgggacca gcgcgggtcc atgtacgcct cgtcgagcgg 970 ggtccagatg ctcaggccg agcgggacca gcgcgggtcc atgtacgcc cgtcctggtg 980 ccacggaggtg ggtgcgct agcgcgggg cttgaggac gcgtggccgt agaagtcgag 990 ggtctccacc actccggca ggaaagcgga ggcgatggcc cggcatcgg cgaagtggcc 990 ggtctccacc actccggca ggtatttctc cggccggacg atctgcggga gacgggcagg 1000 accgggggtcg tcgccacggc cggcgatgtc ccggtagtcg ccggtgggg gcgacggtg 1000 atcggggaag agccggtcg aggcggccg gacggccg gacgcaggg acctcggggaag agccggtcgt aggcggccg gacgcaggg gacgacggg acctcgggaag agccgggaag gcacacaca gccccacaca gcccacacaca	ctgagccggc	ccgggcggcg	gctacggtcg	cgaccgtagg	gggtgcccgc	cgcacgcgga	9420
cacgacage gactagatec geagegaca gacagacata tecategaca gacactecte catacacaca cettegaca gacagacaca gacacacacacacacacacacaca	agcgccggtg	tcggcggtcc	gacaccggcg	cgcccggcca	ggtcagctcc	ggtcgtgcag	9480
catgaccgcc tegeceggec geagegggaa ggegacgetg teegtgtegt egacetegte 960 cgtcatcaga cettegatg ggtegtegtg gttgatgtga tggtgeggga gcaccecgcc 970 ceggtgeagg eceggeaggt actggagaca geegetggac acegtegeet egtegagegg 970 ggtecagatg eteaggecg gaegggaca geeggggtec atgtacgeet egteegggg 970 ggtecagatg eteaggecg gaegggaca geeggggtec atgtacgeet egteetggg 980 ceaegggatg ggtgegeet ageggggggg ettgaggate geggtggeegt agaagtegag 990 ggteteecace aacteeggea ggaaagegga ggegatggee eggeggggg eggagggggggggg	ccagggtcgc	ggctcggggt	cggtcacctc	gaccggctgg	ctcatgaaca	ccaggacgta	9540
cgtcatcaga ccttcgatgc ggtcgtcgtg gttgatgtga tggtgcggga gcaccccgcc 973 ccggtgcagg cccggcaggt actggagaca gccgctggac accgtcgcct cgtcgagcgg 974 ggtccagatg ctcaggccgc gacgggacca gcgcgggtcc atgtacgcct cgtcctggtg 984 ccacggagtg ggtgcgccgt agcgggggg cttgaggatc gcgtggccgt agaagtcgag 994 ttcgtcctcg gggatgtcga ggaaagcgga ggcgatggcc cggcatcgcg cgaagtgcgc 994 ggtctccacc aactccggca ggtattctc cggccggacg atctgcgga gacgggcagg 1003 cgcggggtcg tcgccacggc cggcgatgtc ccggtagtcg cggggtcgg gcgacggtg 1004 atcggcgaaa agccggtcgt aggcggcccg gagccaggcg acctcggcgg cgacgcgtg 1004 ctgcgggaga gtcaccacacg catctgcgcg gtaagcctc agccgacgt cgacgactc 1024 cgcaccaaca gtccccacgg ccatttgacc acctctcgga atagcctgc cgcgaataaa 1024 cgaaccaaca gtccccacgg cgggataccg ctcccgagcg ggaaataggg atcgacaca ccatacggta ggaacagcg ggcgataccg ctcccgagcg ggaaatagg atcgactag 1033 tattcggtcc gcgccgctgc cagaacggca cgcgctctcg attgtccatt catccccgtg 1034 cgagactcgc ctcgatgtcc tcgatgtcg tggggggttt gggatgaccg ggcacagcgc 1044 cgtcgcgctg gacgtcggc gggtcgtcta ctacgacgag ccgtcgagc tggcctggct 1056 ccaggacacc ttcgaccgc tccaggccac cgacccgacg ctcgacctg gtgcgtttct 1056 ggagcacgtc gacgggttct accactacgg cgagggcgac ccaaccggcc ggacctggct 1066 ccactcggag gccgcgcgc ttgagctgtc gcgggtccg gaccacggc aggccaggaactccacggagatt cccggtgcc ttcgcgggt caccaggcc gcacaccggc gagggaactccaccggagagatt cccggtgccg ttcgcgggt caccaggccg gcacaccggc gcacaccggc ttcgagaatt cccggtgcc ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1066 ccactcggag gccgccgcgc ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1074 gatcgtcgc aaccagccc ccgagtgcc ggacggtccg ggacgtaccg gcacagggaac tacccgtcgt 1074 gatcgtcgc gagggtccc tcgagtgcc ggacggtcgg gccagggaac tacccgtcgt 1074 gatcgtcgc gagggtccc tcgagtgcc ggacggtcg gccagggaac tacccggcc 1066 ccaggagatt cccggtgcc tcgacgcgc ggacgggc gccagggcacaccggc aaccaggcc aaccaggcc gaggcacaccaccaccaccaccaccaccaccaccaccacc	cgcgcggcgc	ggctggtccg	tctcgttcgg	gccggcgtag	tgcggcgcac	ggaagtcgtg	9600
ccggtgcagg cccggcaggt actggagaca gccgctggac accgtcgct cgtcgagcgg 9778 ggtccagatg ctcaggccg gacggacca gcgcgggtcc atgtacgcct cgtcctggtg 9878 ccacggagtg ggtgcgccg agcggggcg cttgaggatc gcgtggccgt agaagtcgag 9998 ttcgtcctcg gggatgtcga ggaaagcgga ggcgatggcc cggcatcgcg cgaagtgcgc 9998 ggtctccacc aactccggca ggtatttctc cggccggacg atctgcggg gacgggcagg 1002 cgcggcgtcg tcgccacggc cggcgatgtc ccggtagtcg ccggtgtcgg gcgacgcgtg 1002 atcggcgaag agccggtcgt aggcgacgc gagccaggcg acctcgggg gcgacgcgtg 1002 ctgcgggaga gtcacgaagc catcgcgccg gaacgcagcg acctcggcgt cgtcggcgag 1002 ctgcaggaga gtcaccacgg catttgacc acctctcgga atagcctc cgcgaataaa 1024 cgaaccaaca gtccccacgg ccatttgacc acctctcgga atagcctgt cgcgaataaa 1024 cgaaccaaca gtccccacgg cagaacggca ctcccgagcg ggaaatagg attcgactag 1033 tattcggtcc gcgccgtgc cagaacggca cgcgctctcg attgtccatt catccccgtg 1034 cgaagactcgc ctcgatgtcc tcgatgtcg tggggggttt gggatgaccg ggcacagcgc 1044 cgtcgcgctg gacgtcggc gggtcgtca ctacgacgag ccgttcgag tggcctggct 1056 ccaaggacacc ttcgaccgc tccaaggcca cgacccgacg ctcgacctgc gtgcgtttct 1056 ccaaggacacc ttcgaccgc tgagctggtc gcgggtcgg cagtcctgg ggcactggct 1066 ccaaggagatt cccggtgccg ttgagctggt gcgggtccgg cagtcctgg gcgagttgc ccaaggagatt cccggtgccg ttcgcgcggt caccaggcg gccaagccc 1046 ccaaggagatt cccggtgccg ttcgccggt caccaggct gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgccg ttcgccggt caccaggctg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgccg ttcgccgggt caccaggctg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgccg ttcgccgggt caccaggctg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgcc ttcgccgggt caccaggctg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgcc tccgagtgcc ggacgtactg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgcc tccgagtgcc ggacgtactg gccagggaac tacccgtcgt 1066 ccaaggagatt cccggtgcc tccgagtgcc ggacgtactg gccagggaac tacccggccc 1066 ccaaggagatt cccggtgcc tccgagtgcc ccgagggca agccaggcca agccagcca 1086 ggtctgccgg gaggtgccc ccgagtgcc ccgggggcgggagggggggggg	catgaccgcc	tcgcccggcc	gcagcgggca	ggcgacgctg	tccgtgtcgt	cgacctcgtc	9660
ggtccagatg ctcaggccgc gacgggacca gcgcgggtcc atgacgcc cgtcctggtg 986 ccacggagtg ggtgcgcct agcgcggcgg cttgaggatc gcgtggccgt agaagtcgag 996 ttcgtcctcg gggatgtcga ggaaagcgaa ggcgatggcc cggcatcgcg cgaagtgcgc 996 ggtctccacc aactccggca ggtatttctc cggccggacg atctgcggga gacgggcagg 100 gcgcggctcg tcgccacggc cggcgatgtc ccggtagtcg ccggtgtcgg gcgacgcgtg 100 gcgcggaag agccgggaag acctcggga gacggcggg 100 gcgcggaag agccggaag acctcggcga gacggcggg 100 gcgcggaag gcacgagga ggcaaggaag agccggaag acctcggcga gacgaggaag cggcggaag gcacgagga gacgggaag acctcgggaag agccacgaag agccggaag gacacgaag 100 gcgcggaag gtcacgaag catcggccg gaagcctcc agccgacggt cgacgacctc 102 gcgcaccaaca gtccccacgg ccatttgacc acctctcgga atagcctgc cgcgaataaa 102 gcacacaaca gtccccacgg ggcgataccg ctcccgagcg ggaaataggg attcgactag 103 gcgagactcgc gcgcgctgc cagaacggc cggcgctctcg attgccatt catcccgtg 103 gcgagactcgc gcgcgctg gacgtcggc ggggggggtt gggagagacgg ggcacagcgc 104 gcgcgcgctg gacgtcggcg gggtcgtcta ctacgacgag ccgttcgagc tggcctggct 106 ggaggacacgc gacgggttct accactacgg cgagggggac ccaaccggcc ggacctggct 106 ggaggacacgtc gaggggttct accactacgg cgagggcgac ccaaccggcc ggacctggct 106 gcaggagaat ccgggggggggac cacacgggc ggagggggac ccaaccggcc ggacctggct 106 gcaggagaat cccgggggggggggggggac cacacgggc ggaggggggaccagggggggg	cgtcatcaga	ccttcgatgc	ggtcgtcgtg	gttgatgtga	tggtgcggga	gcaccccgcc	9720
ccacqgaqtq ggtqcqcqt agcqcqqqq cttqaqqatc gcqtqqcqt agaaqtcqaq 990000000000000000000000000000000000	ccggtgcagg	cccggcaggt	actggagaca	gccgctggac	accgtcgcct	cgtcgagcgg	9780
ttegteeteg gggatgtega ggaaagegga ggegatggee eggeategeg egaagtgeee ggteteeaee aacteeggea ggtatttete eggeeggaeg atetgeggga gaegggeagg 1002 egeggegteg tegeeaegge eggegatgte eeggtagteg eeggtgtegg gegaeggetg 1002 ateggeggaag ageeggtegt aggeggeeg gageeaggeg aceteggegt egteggegag 1002 etgegggaag ageeggtegt aggeggeeg gageeaggeg aceteggegt egteggegag 1002 etgeggggaag gteacgaage eateggeeg gtaageetee ageegaeggt egaegaeete 1022 eegaaceaaea gteeceaegg eeattgaee acetetegga atageetgte egegaataaa 1022 eeataceggta ggaacagege ggegataeeg etecegageg ggaaataggg attegaetag 1032 eegagaeetee etegatgtee eagaaeggea eggegeteteg attgteeatt eateeeegtg 1032 eegagaeeteg etegatgtee tegatgtegg tggggggttt gggatgaeeg ggeaeaggee 1044 eegaeggeetg gaegteggeg gggtegteta etaegaegag eegttegage tggeettget 1056 eeaggaeaege etegaeegge ggaeetgget 1056 eeaggaeaege gageggtee eeagaeggee eeaaeeggee ggaeetgget 1056 eeaggaeaegte gageggtet taeeaetaegg egagggegae eeaaeeggee ggaeetgget 1056 eeaggagatt eeegggege tgagetggte gegggteegg eagteetggg gegagetgge 1066 eeaggagatt eeeggtgee ttegeeggt eageetgge gegagetgge 1066 eeaggagaatt eeeggtgeeg ttegegeggt eaceagggetg geeagggaae taeeeggeeg 1066 eeaggagaatt eeeggtgeeg ttegegeggt eaceaggetg geeagggaae taeeeggee 1066 eeaggaggatte eeeggtgee ttegeegggt eageeggtgg geeaggeegg aggteegee 1066 eeaggaggatte eeeggtgee ttegegeggt eaceaggetg geeaggeegg aggteegee 1066 eeaggaggatte eeeggtgee ttegegeggt eaceaggetg geeagggae aggteageea 1066 eeaggaggatte eeeggtgee ttegegeggt eaceaggeegg geeaggege aggteageea 1066 eeaggaggagtee aaceageee eegggggeggggggggggggggggggg	ggtccagatg	ctcaggccgc	gacgggacca	gcgcgggtcc	atgtacgcct	cgtcctggtg	9840
ggtetecace aacteeggea ggtattete eggeeggaeg atetgeggga gaegggeagg 1000 egeggegteg tegecacegge eggegatgte eeggtagteg eeggtgtegg gegaegegtg 1000 ateggegaag ageeggtegt aggeeggeeg gageeaggeg aceteeggegt egteeggegag 1010 eeggeggaag gteacegaag eatetgegeg gageeaggeg aceteeggegt egteeggegag 1010 eeggeggaag gteacegaag eatetgegeeg gtaageetee ageegaeggt egaegaeete 1020 eegaaceaaca gteeceacegg eeatttgaee acetetegga atageetgte eggegaataaa 1020 eeataceggaa ggaacaageg ggegataeeg etecegageg ggaaataagg attegaetag 1030 eegagaeetee eegaageege eagaacegge eegaeggegggggggggg	ccacggagtg	ggtgcgccgt	agcgcggcgg	cttgaggatc	gcgtggccgt	agaagtcgag	9900
cgcggcgtcg tegecacgge eggcgatgte eeggtagteg eeggtgtegg gegacgegtg 1000 ateggegaag agecggtcgt aggeggeceg gagccaggeg aceteggegt egteggegaag 1010 eeggeggaag gtcacgaage eateggegeg gtaageetee agecgacggt eggcgaacete 1020 eegaccaaca gtccccacgg eeatttgace acetetegga atageetgte egegaataaa 1020 eeatteeggta ggaacagege ggcgataceg etcecgageg ggaaataggg attegactag 1030 eegagaceteg eegagacege eagaacggea eggegeteteg attgteeatt eateceegtg 1030 eegagaceteg etcegaegeg ggaagtgaeeg ggeacagege 1040 eegtegegetg gaegteegeg gggtegteta etacgaegag eegttegage tggeettget 1050 eegagacace etcegaegeg eggagegeteg eegagegegegegegegegegegegegegegegegeg	ttcgtcctcg	gggatgtcga	ggaaagcgga	ggcgatggcc	cggcatcgcg	cgaagtgcgc	9960
ateggegaag ageeggtegt aggeggeeg gageeaggeg aceteggegt egteggeggg 1014 etgegggaag gteacgaage categegeeg gtaageetee ageegaeggt egaegaeete 1026 egeaceaaca gteeceaegg ceatttgace acetetegga atageetgte egegaataaa 1026 eeatteegga ggaacagge ggegataeeg eteecegageg ggaaataagg attegaetag 1032 etatteggte gegeegetge eagaacggea egegeteteg attgteeatt eateecegtg 1038 egagaetege etegatgtee tegatgtegg tggggggttt gggatgaeeg ggeacagege 1044 egeteggetg gaegteggeg gggtegteta etacgaegag eegttegage tggeetgget 1056 eeaggaeaee ttegaeege teeaggeeae egaeeegaeg etegaeetge gtgeettet 1056 eeaggeaege gageggttet aceaetaegg egagggegae eeaaeeggee ggaeetgget 1066 eeaaeteggag geegeegee tgagetggte gegggteegg eagteetggg gegagetgge 1066 eeaggagatt eeeggtgeeg ttegeeggt eaceaggeeg geeagggaae taceegtegt 1076 gategtege aaceageee eegagtgee ggaegtaetg geeagggaae taceegtegt 1076 gategteege aaceageeee eegagtgee ggaegtaetg geeagggaae taceegtegt 1076 gategteege aaceageeee eegagtgee ggaegtaetg geeagggaae aggteageea 1086 ggtetgeegg gaggteetee tegaeteet egteggggt geeaggeeg aggteageea 1086 ggtetgeegg gaggteetee tegaeteet egteggggt geeaageeeg aceeggeeet 1086 ggtetgeegg gaggteetee tegaeteete egteggggt geeaageeeg aceeggeeet 1086 ggtetgeegg gaggteetee tegaeteete egteggggt geeaageeeg aceeggeeete 1086 ggtetgeegg gaggteetee tegaeteeteeteeteeteeteeteeteeteeteeteeteete	ggtctccacc	aactccggca	ggtatttctc	cggccggacg	atctgcggga	gacgggcagg	10020
ctgegggaga gteacgaage categegeeg gtaageetee ageegaeggt egaegaeete 1026 egeaccaaca gteeceaegg ceatttgace acetetegga atageetgte egegaataaa 1026 eeataeeggta ggaacagege ggegataeeg eteecegageg ggaaataggg attegaetag 1038 tatteggtee gegeegetge eagaaeggea egegeteteg attgteeatt eateecegtg 1038 egagaetege etegatgtee tegatgtegg tggggggttt gggatgaeeg ggeacagege 1046 egtegegetg gaegteggeg gggtegteta etaegaegag eegteegge tggeettgget 1056 eeaggaeaee ttegaeege teeaggeeae egaeeegaeg etegaeetge gtgeettget 1056 eeaggeaeete gageggttet aceaeetaegg egagegegae eeaaeeggee ggaeetgget 1056 eeaggaeaegte gageggttet aceaeetaegg egagggegae eeaaeeggee ggaeetgget 1066 eeaggagaett eeeggtgeeg ttegeeggt eaceaggetg geeagggaae taeeegtegt 1076 gategtegee aaceaggeeg ttegegggt eaceaggetg geeagggaae taeeegtegt 1076 gategtegee aaceaggeee eegagtgee ggaeettgee aceaeggeeg ggaegteegg aggteegee 1086 ggtetgeegg gaggtgeee tegaeetee egaegggggggggg	cgcggcgtcg	tcgccacggc	cggcgatgtc	ccggtagtcg	ccggtgtcgg	gcgacgcgtg	10080
cgcaccaaca gtccccacgg ccatttgacc acctctcgga atagcctgtc cgcgaataaa 1026 ccatacggta ggaacagcgc ggcgataccg ctcccgagcg ggaaataggg attcgactag 1032 tattcggtcc gcgccgctgc cagaacggca cgcgctctcg attgtccatt catccccgtg 1032 cgagactcgc ctcgatgtcc tcgatgtcgg tggggggttt gggatgaccg ggcacagcgc 1042 cgtcgcgctg gacgtcggcg gggtcgtcta ctacgacgag ccgttcgagc tggcctggct 1056 ccaggacacc ttcgaccgcc tccaggccac cgacccgacg ctcgacctgc gtgcgttct 1056 ggagcacgtc gagcggttct accactacgg cgaggggcgac ccaaccggcc ggacctggct 1066 ccactcggag gccgccgcc tgagctggtc gcgggtccgg cagtcctggg gcgagctggc 1068 ccaggagatt cccggtgccg ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1076 gatcgtcgc aaccagccc ccgagtgcc ggacgtactg gccagggaac tacccgtcgt 1076 gatcgtcgc aaccagccc ccgagtgcc ggacgtactg gccagggaac tacccgtcgt 1076 ggtctgccg gaggtgccc accaggctg gccagggaac tacccgtcgt 1076 ggtctgccg gaggtgccc accaggctg gccagggaac tacccgtcgt 1076 ggtctgccg gaggtgccc ccgagtgcc ggacgtactg gccagggaac acccggccc 1086 ggtctgccg gaggtgccc accaggctg gccaagccc acccggccc 1086 ggtctgccg gaggtgccc tcgactccct cgtcggggtg gccaagcccg acccggccct 1086 ggtctgccgg gaggtgccc tcgactccct cgtcggggtg gccaagcccg acccggccct 1086 ggtctgccg gaggtgccc tcgactccct cgtcggggtg gccaagccc acccggccct 1086 ggtctgccg gaggtgcccg gaggtgccc tcgactccct cgtcgggtg gccaagcccg acccggccct 1086 ggtctgccg gaggtgcccg gaggtgccc tcgactccct cgtcggggtg gccaagcccg acccggccc acccggccct 1086 ggtctgccg gaggtgcccg gaggtgcccg acccggccc acccgccc acccggccc acccgccc acccgcc	atcggcgaag	agccggtcgt	aggcggcccg	gagccaggcg	acctcggcgt	cgtcggcgag	10140
ccatacggta ggaacagcgc ggcgataccg ctcccgagcg ggaaataggg attcgactag 1032 tattcggtcc gcgccgctgc cagaacggca cgcgctctcg attgtccatt catccccgtg 1032 cgagactcgc ctcgatgtcc tcgatgtcgg tggggggttt gggatgaccg ggcacagcgc 1042 cgtcgcgctg gacgtcggcg gggtcgtcta ctacgacgag ccgttcgagc tggcctggct 1056 ccaggacacc ttcgaccgcc tccaggccac cgacccgacg ctcgacctgc gtgcgtttct 1056 ggagcacgtc gagcggttct accactacgg cgagggcgac ccaaccggcc ggacctggct 1066 ccactcggag gccgccgcc tgagctggtc gcgggtccgg cagtcctggg gcgagctggc 1068 ccaggagatt cccggtgccg ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1068 gatcgtcgc aaccagccc ccgagtgcc ggacgtactg gccagggaac tacccgtcgt 1068 gatcgtcgc aaccagccc ccgagtgcg ggacgtactg gccagggaac tacccgtcgt 1068 ggtctgccg gaggtgccg gaggtgccg ggacgtagc aggtcagcca 1088 ggtctgccgg gaggtgccg gaggtgccg gaggtcccg acccggccct 1088 ggtctgccgg gaggtgccc tcgactccct cgtcgggtg gccaagcccg acccggccct 1088 ggtctgccgg gaggtgctcc tcgactccct cgtcgggtg gccaagcccg acccggccct 1088 ggtctgccgg gaggtgccc tcgactccct cgtcgggtg gccaagcccg acccggccct 1088 ggtctgccg gaggtgccc tcgactccct cgtcggggtg gccaagcccg acccggccct 1088 ggccaagcccg gaggtgccc	ctgcgggaga	gtcacgaagc	catcgcgccg	gtaagcctcc	agccgacggt	cgacgacctc	10200
tatteggtee gegeegetge cagaacggca egegeteteg attgteeatt cateceegtg 1038 egagactege etegatgtee tegatgtegg tggggggttt gggatgaceg ggcacagege 1044 eggegegetg gacgteggeg gggtegteta etacgacgag cegttegage tgggeetgget 1056 ecaggacace ttegacegee tecaggecae egaceegacg etegacetge gtgegtttet 1056 egagegeaegte gageggtet accaetaegg egagggegae ecaaceggee ggaeetgget 1068 ecaeteggag geegeegege tgagetggte gegggteegg eagteetggg gegagetgge 1068 ecaggagatt eceggtege ttegegeggt eaccaggetg geeagggaae taccegtegt 1078 gategtegee aaccageee eegagtege ggaeegtaetg geeagggaae taccegtegt 1088 ggtetgeegg gaggtgetee tegacteeet egtegggtg geeaageeeg acceggeet 1088 ggtetgeegg gaggtgetee tegacteeet egtegggtg geeaageeeg acceggeet 1088 ggtetgeegg gaggtgetee tegacteeet egteggggtg geeaageeeg acceggeeet 1088 ggtetgeegg	cgcaccaaca	gtccccacgg	ccatttgacc	acctctcgga	atagcctgtc	cgcgaataaa	10260
cgagactege etegatgtee tegatgtegg tggggggttt gggatgaceg ggcacagege 1044 cgtegegetg gacgteggeg gggtegteta etacgacgag cegttegage tggeetgget 1056 ccaggacace ttegacegee tecaggecae egaceegaeg etegacetge gtgegttet 1056 ggageaegte gageggtet accaetaegg egagggegae ecaaceggee ggaeetgget 1066 ccaeteggag geegeegee tgagetggte gegggteegg eagteetggg gegagetgge 1066 ecaggaggt eeegggggggae eagteetggg gegagetgge 1066 ggategteege aaceageeeg eegaggggggae eagteetggg gegagetgge 1066 ggategteege aaceageee eegagtgeeg ggaeegtaetg geegggtaeeg aggteageea 1086 ggtetgeegg gaggtgetee tegacteeet egteggggtg geeaageeeg acceggeeet 1086 ggtetgeeggeeggeeggeeggeeggeegggggggggg	ccatacggta	ggaacagcgc	ggcgataccg	ctcccgagcg	ggaaataggg	attcgactag	10320
cgtcgcgctg gacgtcggcg gggtcgtcta ctacgacgag ccgttcgagc tggcctggct 1050 ccaggacacc ttcgaccgcc tccaggccac cgacccgacg ctcgacctgc gtgcgtttct 1050 ggagcacgtc gagcggttct accactacgg cgagggcgac ccaaccggcc ggacctggct 1060 ccactcggag gccgccgcgc tgagctggtc gcgggtccgg cagtcctggg gcgagctggc 1060 ccaggagatt cccggtgccg ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1070 gatcgtcgc aaccagccc ccgagtgcg ggacgtactg gccaggtggc aggtcagcca 1080 ggtctgccgg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1080 ggtctgccg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1080 ggtcgccg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1080 ggtcgccg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1080 ggtcgccgccc gagggtgccc tcgactcccc gccgactccc gagggtgccc tcgactcccc gaggggtgccc tcgactcccc gagggggggggg	tattcggtcc	gcgccgctgc	cagaacggca	cgcgctctcg	attgtccatt	catccccgtg	10380
ccaggacace ttegacegee tecaggecae egaceegaeg etegacetge gtgegtttet 1056 ggageaegte gageggttet accaetaegg egagggegae ecaaceggee ggaeetgget 1068 ecaeteggag geegeegege tgagetggte gegggteegg eagteetggg gegagetgge 1068 ecaggaggtt eceggtgeeg ttegegggt eaccaggetg geeagggaae taccegtegt 1076 gategtegee aaccageece eegagtgege ggaegtaetg geeeggtgge aggteageea 1086 ggtetgeegg gaggtgetee tegacteeet egteggggtg geeaageeeg acceggeet 1086	cgagactcgc	ctcgatgtcc	tcgatgtcgg	tggggggttt	gggatgaccg	ggcacagcgc	10440
ggagcacgtc gagcggttct accactacgg cgaggggac ccaaccggcc ggacctggct 1062 ccactcggag gccgccgcc tgagctggtc gcgggtccgg cagtcctggg gcgagctggc 1068 ccaggagatt cccggtgccg ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1074 gatcgtcgcc aaccagccc ccgagtgcgc ggacgtactg gcccggtggc aggtcagcca 1086 ggtctgccgg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1086	cgtcgcgctg	gacgtcggcg	gggtcgtcta	ctacgacgag	ccgttcgagc	tggcctggct	10500
ccacteggag geegeegee tgagetggte gegggteegg eagteetggg gegagetgge 1068 ccaggagatt eeeggtgeeg ttegeeggt caccaggetg geeagggaac taccegtegt 1074 gategtegee aaccageece eegagtgege ggaegtaetg geeeggtgge aggteageea 1086 ggtetgeegg gaggtgetee tegacteeet egteggggtg geeaageeeg acceggeeet 1086	ccaggacacc	ttcgaccgcc	tccaggccac	cgacccgacg	ctcgacctgc	gtgcgtttct	10560
ccaggagatt cccggtgccg ttcgcgggt caccaggctg gccagggaac tacccgtcgt 1074 gatcgtcgcc aaccagcccc ccgagtgcgc ggacgtactg gcccggtggc aggtcagcca 1086 ggtctgccgg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1086	ggagcacgtc	gagcggttct	accactacgg	cgagggcgac	ccaaccggcc	ggacctggct	10620
gategtegee aaccageece eegagtgege ggacgtactg geeeggtgge aggteageea 1080 ggtetgeegg gaggtgetee tegacteeet egteggggtg geeaageeeg acceggeeet 1080	ccactcggag	gccgccgcgc	tgagctggtc	gcgggtccgg	cagtcctggg	gcgagctggc	10680
ggtctgccgg gaggtgctcc tcgactccct cgtcggggtg gccaagcccg acccggccct 1086	ccaggagatt	cccggtgccg	ttcgcgcggt	caccaggctg	gccagggaac	tacccgtcgt	10740
	gatcgtcgcc	aaccagcccc	ccgagtgcgc	ggacgtactg	gcccggtggc	aggtcagcca	10800
getegggete geeetgegge ggetggegat eeegeeegee gagttgetgg tggtgggeaa 1092	ggtctgccgg	gaggtgctcc	tcgactccct	cgtcggggtg	gccaagcccg	acccggccct	10860
	gctcgggctc	gccctgcggc	ggctggcgat	cccgcccgcc	gagttgctgg	tggtgggcaa	10920

ccggacggat	cacgacgtcc	tgcccgcgct	cgggctcggt	tgcccggtgg	cgttcgtgct	10980
gcccgatccg	gcgtaccgcc	ggccgccggg	cgtccatccg	gacctggtcc	gggtctacac	11040
ggagctgagg	gcgttccgca	ccggctcccc	gcccgcggac	gcccgggtca	ccaccgtggc	11100
gtccctggcg	gccctggccg	actctcccct	gacgagtgcc	accccgcgtt	cgaacgccgg	11160
caccggcgga	ctttgacgaa	ggagtgcagt	tgcgacgccc	cgcagcggtg	gtcggcgcca	11220
ccggcttcat	cggctcacgc	ctcgtctccc	gcctggccga	ggccgggcat	ccggtggcgc	11280
gcttcagccg	tgccgcccca	cccgtcgtcg	acggccggcc	cgcgccgggg	ctccgcgagg	11340
cgcaggtcgt	ctacttcctc	gccgcccggc	tgagcccggc	gctggcggag	cagcaaccgg	11400
aacgggtcgt	ccgggaacgc	gagttgttgc	tggacgtgct	aagtgcgctg	gcgggggtgg	11460
accaccggcc	ggtgttcgtc	ctggccagct	cgggcggggc	ggtgtacacg	ccgacggtgt	11520
ggccgcccta	ccacgagcgg	tcggccaccg	ggcccgcctc	ggcgtacggc	cgggcgaagc	11580
tgcggctgga	acaggagctg	ctgcgccaca	ccgaccgggt	gcagccggtg	gtgacccggc	11640
tgagcaacgt	ctacggtccg	gggcagcggc	cgacccccgg	gtacggtgtc	ctgtcacact	11700
ggctggaggc	caccgtgcgc	ggagagccga	tccggctctt	cggcgatccg	gccgtggtgc	11760
gggactacgt	acacgtcgac	gacgtcaccg	cgatcatgga	ggtcatcgcg	cagcgggccg	11820
gtgacggcga	ccgggaccgg	ctgcccacgg	tcgtgaacgt	cggctcgggc	ctgcccacct	11880
ccctcgccga	gttgctccag	acgatgtcca	cggtggccgg	tcgtgagctg	gaggtcatcc	11940
gggacgtccg	ccggcagttc	gaccatcggg	gcaactggct	cgacaccacc	ctcgcccggg	12000
agaccctggg	ctggcaggcg	cggatcagcc	tccccgacgg	cgtccgccag	tgctgggagg	12060
ccgtcctcac	ccgggcgggc	ggcccggggg	gttccccggc	ccgaccgtca	gcccggctcg	12120
ggagagcgtc	tcgggggcgg	gaaccgccgc	aaccgcgccc	ttcgcagcag	ttcgtggctc	12180
aacccggcgg	cggtcgccgc	ggtgtagccg	agggccagtg	gcagggcgag	ccgggattcc	12240
ggggccgtac	ggtgccggtc	ccattccttg	cgcaggccgg	cccgtgcctg	gttccgtccg	12300
gcctcgcacc	gcccctgcca	gtacgcccgc	cgcagcaggt	accggggggt	cagccggccc	12360
gggtcgatgt	catgggtgac	cgcgtggtcc	gggagcagtt	gctcgcgggc	gccggcggcc	12420
ttcatggcgc	tgatgaagga	ggtgtcctcc	cctgactgga	ggttgccccc	ggtacggctg	12480
agggccaggt	cgaaatccaa	cccgtgggcg	tgcgcgaacg	cggagtccac	ccccatgcac	12540
gcgccccaga	tcttgatgtt	tccctggtca	cggtgccagc	cgaccaggtg	gaactggccg	12600
gaggtgacgt	accacggcag	acgcagcgcg	gggcgggcca	gccgggtgcc	gaccacgtgc	12660
gcgccgtcgc	gcaggctctt	gcggacggcg	tcgacggcag	cggcgtcgag	ccgcacgtcg	12720
tcgtcgacga	acatcagatg	gtggtgcggc	cagcgggcga	gcatcgcgtt	gcgggaggcc	12780
gacaggccat	tggtggcacc	gaggatgcgc	atggtgccgc	cggcggcccg	gacctcctcg	12840
gcgacctcct	ccgcctcggc	cgtgacgggc	cggtccagca	ggacgtagta	ctcgtcgccg	12900

gagagetggg ceatgttgtg egegaggtgt tteetgaegt tetecaceeg gaaegegeag 12960 ategecacea ceategggtg gteggaegga tegeggetga ceaeagagge gttgttegge 13020 ategtecete gacatgageg ttgtggggee ggeggggaga ggeggeeeae eggategege 13080 teegeggeag egtgeegegg eeceggeege eecaeggaca ggtggegeac egeagegegg 13140 egggeegtee ggtgagegge egggggegga geteaggeeg ettegteett getgaeggte 13200 ggcggccagg tgcccgccgc gaggatgccc atcgcgtacg ccttcgcgat cagggccggc 13260 cggttgggca ctcgcaggtt ctgcaacagc ttgctgacgt ggtactcgac gccctgacgg 13320 ctgaggtaga ccttgttggc gatatgcacc gtccgttcgc ctgcggcgat gctttcgatg 13380 atgegeget ceagategga cagtgagaac ttgagattea caaegeeece ttgattgtgg 13440 atctgttggc tcgtacgcgg ccagacgtca tcgcccggac accccctga ggtgccggtg 13500 gacgagtggt cgcttccgct ggaagaccgt cagcggcgga aggccgggtg cccgccactc 13560 gtcgtcctgc gcttgcggag ctgtctcagt gtgcggcgat gcccccggca cgtagcccgc 13620 ctgacgggcc tgtcggcttg ggctccaact tcggcaaccc atcggttcgc gctgcacaga 13680 accageggag gaacattgag tttegaagee ettegetaet gtegategae atcaetggeg 13740 aaatgaaacc gaccggattc gagccgatag ttacggaaag tgacaatcgg ctggccctgt 13800 13860 cgctcgcgct gaactcacca atacgccaaa agcgtagccg gcccactgcg gagcgtccac cccccgagga tatcgccagg cttccatgca gaactggcag gatctttcat ctcagccgca 13920 13980 cctggcgaca aaacccctgc tcaagaccat gagtaagcag gcgcgggaaa tccatgcagt gacatgtgtc actttagaca acccagctcc agccaggccc accaccctga caaaaggggc 14040 14100 ggaatcgcga ccagagcgac accagcacat tcctagggga ttccttagtc tggcgagcgt cgatccccca cccgtcaatc aattgcccga acaaattgcc cacccgtcaa gatcaaccac 14160 teegeacegt gageaggeeg acegteegge aatgegaacg acgaegteea eecegteeeg 14220 14280 gtagcctcac cgccgctggg ggggcacggg cccggacacc gtccggcgtc gtgatcagcg ggtcgctcgc cggctgtcgc cccgcgcggg gaccggcatc gcgcgcgggg ccggcacgaa 14340 14400 gateteegge gacetgteag eeetgeaage ggaceggeat egegegeggg geeggaacea ecegaeggtt eagegeeggg acegateggg aageegaete geggeetegt eecagageee 14460 gcccaccgca tcccgcagcg atcgtcgggg ccgccacccg agcaggtcac gcgcgggccc 14520 egggtegacg egggeecagt egacgacete cacegageeg ggeegateeg geaactecae 14580 cacctcggtc ggcaccccgc tcacctcgat caacatctcc acgagggagc ggaccggaac 14640 ggcctccccc cgccccacgc cgatcacccg cccggtgacg gactcccgcg tggccgacac 14700 14760 caccgcctcg gcgacgtccc gcacgtcgac gtagtcccgg tgggcgcgca acggagacaa 14820 etccaccetg gecgaceggt egeggeeege egegtegace aggegaaega egaceegeee

caacaggctg	tcgggtggca	cgcccggacc	caccacgttc	gcgagccgca	gcaccgtcgc	14880
gtccaccgag	ccggcccgcg	tcgccgcgag	cacggcctgg	gtggcggcca	gcttcgccct	14940
gccgtacatg	ctctccggct	gggtgggcac	cgtggcaccg	gcgggagccc	cgggtggctc	15000
ctggacgcgt	tccaggaccg	agccgaggtg	caccagcctg	ggccggcaac	gggtgcgctc	15060
cagcgccgcg	gtgacactcc	acgtcgggat	cgtgcagctc	gacggcagct	cggcgtccgt	15120
caggttccac	ttgccgccgg	tggcgttgac	caccgcgtcg	ggctgctcgg	cgtcgaacac	15180
ggcggccagc	gcggcgggct	ccagggtggc	gacgtccagc	gcccgggccc	ggtacggcag	15240
ccccgccgac	gggacgcggc	gggccaacac	gaggacgtcg	tcgccccggg	cggcaagcgc	15300
ggcgctcacg	tgacgcccga	cgaagcccgt	accaccgacg	accacgacac	gccgcgcgcc	15360
catccgtacc	tcctggggat	cagtctcgtg	cgccggcggc	gtccaggcga	ccgcccggcc	15420
cctgacaggt	cacgggggcg	cgcaacaccc	tggcccggtc	gcgaacctcg	tccagcagcc	15480
gggcccgggc	gcggatcgcc	gtcacctcct	ccgccggctg	accggcggtg	acggcgcgga	15540
cgaactctcg	catcgtgttg	acgaactggt	cctcggccgg	gaaggtcagc	tcccgcgtct	15600
cgtcctgccg	ctccacccgc	accaccgggt	gccaggccgg	cggtggggtg	tacgcccggt	15660
cgacgacgat	ccggccggcg	cttccccaga	gctggtactc	gcaccggtag	gagtgctcga	15720
aaccgaaggc	gatctgtgcg	gtccgcccgt	ccggcgtaca	caacagcgcg	gcacccgaaa	15780
cgtccacgcc	gcgatcgggg	tectecegga	gggtggccgc	caccacctcc	ggctcctccg	15840
gcaggaagaa	ccgggccgcg	cccaacgggt	agacgcccag	atccagcagc	gctccgccac	15900
ccagctcggg	tcggtaacgg	atgtcgcccg	caggcagcgg	cggaaacccg	aagacgccgg	15960
agaccatccg	cagctcgccg	atctcgccgg	ccgcgaccat	ccggcgcacg	aagtggtgca	16020
ccccatgtcg	gaggaaggtg	aggttgtcca	tcaacacgag	cccacgcgac	cgggcctggg	16080
tcagcaccgc	cgcggtgtcg	accagccggg	tggtcagcgg	cttctccacc	agcacgtgtt	16140
tgcccgcggc	cagggcgcgt	tcgatccagg	tgtggtgcag	cccggtcggc	agcggaatgt	16200
agacggcatc	gatgtccggg	cggtcgagaa	cggactggta	gccctcggcg	gcggcgcacc	16260
cgaactccgc	ggcgaaggcg	cgcgccttgg	ccagttcccg	cgccgcgacc	accacgagct	16320
ccgcctccgg	gacccgcctg	atcgccggca	gggcacggcg	gcgcgcgatg	tcggcgcagc	16380
cgagaacccc	gatgcggacc	gtcatctccg	ccatcgggtc	accacaggct	gcgcaggcag	16440
gccagcaagc	tgcgggcctc	gatgttgagg	tagtagccgt	gccggagcag	ggcctccagc	16500
tggcgcaccg	tcacccagca	gaactcgtcc	ggcacctcgg	tcgggaagtc	gtcgccggcg	16560
tcgaccagga	ggtaacggtt	ctccgaccgg	tagaatcgcc	cgccctcctc	ggtgagcacg	16620
gtgtcgtaga	ggacacgctc	gggggcggct	tccagcacct	cggccaggaa	cagtggtcgg	16680
gggccgggct	ggttgtccgg	gatgcactgc	accgttgggc	ccatctccat	cgcgtcgagc	16740
agccccgcct	ggtagcgcgc	gtgcaccagc	aggtgcgcca	ctccgtcgat	ttccttgacc	16800

tegegytty cyatgogca cytagogca cogcago acaeggaa aygocggc ytegtecege 169 gegatecegt cegegyty cegecaytee ggaageete gtagoggae cegecagaag gegatecegt geoggeett ggeecegyty aacaegeta acaeggaaa cageggag gegetygg cyccoggog gaagegaag teggegygg cyccoggog gaagegaag teggetygg cyccoggog gaagaggaag teggygaag cyccoggog gaagaggaag teggygaag cyccoggog gaagaggaag tecatytya cagegygag cacegaaga atgacagaac cyaagggagaa tecatytya cagegygag cacegaaga gaagagaag tecatytya cacaggagac cacegaaga gaagagaag teggyyaaga cyccoggog cacegaaga teggyyaaga cyccoggog cacegaaga cacegaaga teggyyaaga teggyyaaga acaagagac cygyaagaaga teggyyaaga tegyyaaga tegyyaaga tegyyaaga tegyyaaga tegyyaaga teg	aggaaggga	ccacacccca	ataccacaaa	tacaacacc	actaactaca	cccaatcacc	16860
gegateccept cegeggtgtg cegecagte gegagecett gegagecett gegagecett gegagecett gegagecett gegagegage accagetega cegecggage cegegggage cegeggage cegegggage cegegggage cegegggage cegegggage cegeggage							
gleateletet geeggeett ggeeceggt aacaagelea acacegaca cagglegtgg 170 cggeeggggg cgeegeege cgagegeacg alegeegea cgeeggga cgaegggee 171 teggteteet gggeegggg glagaaggee gagggagaa algaeaggaa cgaeggggee 171 tecatgliga caggeegge glagaaggee gagggagaa algaeaggaa cgaeggggagaa 172 ceggtggtagt cgeeggeegg cacegleege legaeeggaga glagaaggaa caacealgta ceggtgggag acagggagagaa tlagaeaggaa acacaggaaa cegggaggaga cacegggggggggg							16920
eggecggggg egecgecge egagegeaeg ategecgeae eegegegga egaeggggg 171 teggteteet gggecgggg gtagaaggee gagggaagaa atgacagcae egaeggggg 171 tecatgttga ecaggeegge gtagaaggee gagggaagaa gtteggegag egggageaae 172 eggtggtagt egeeggeegg eacgteeteg tegacetgga ecaceatgtt eeggttgege 172 ttgegeagga aceaggagee etgeteegae tgeaggage eacaceatgtt eeggttgege 173 eegggeggg tgaagtagte gaggtaette gtgeegeege eacggtgeae eegggtgtag 174 ttgeteeggg tgaagtagte gaggtaette gtgeegeege eacggtgeae eegggtgtag 174 ttgeteeggg tgaagtagte gaggtaette eeggeegga eettgaaga eatgeegggg 175 acettggeet ggageagga gtaeggtgte eegtegaag eettgaaga eatgeegggg 175 atgeegatet eeggetggtt gatgategge tggteeatg egegaacegg eeggtagggg 175 atgeegatet eeggetggtt gatgategge tggteeatg egegaacegg eeggtagggg 176 gteaggage gaaceecte gateaegaag aaceggeeg tetegtgee gaggttgeeg 176 gteageggg egaacegee eegggaacea ggggeegge gaggeggge eeggtagggg 177 taggtaagge gggteegte ggegaaceag gagaggaagt eeggeeggge eggteeggg 177 tggaaacgeeg aceaegagee geegtegaae gggeeggge ggtgeggge eggteeggg 178 gteageaagg geegggaaag geegtegaae ggggeggge gggggge eggeteegg 178 gteageaagg eegggaaaag gegtgggaag aceaeteeg gggeeggge egggggee eggeteegg 178 gteageaagg eegggaaaag gegtgggaag aceaeteeg gggeeggge eggggge eggateegg 178 eggecagtte ggeggaaaag gegtgggaag aceaeteeg ggggggge eggatgggg 180 eeggecaggt eetegtegg teeegeeag geaggggg eggatgggge eggatgggg 180 eetgegggge ettegtegg teeegeeag geagetega etteggegge eggatgggg 180 eetgegggge ettegtegg teeegeeag teeegeagg gaagetega gtagteetee ggeteeteg 181 eeggeeageat eaggaceatg eecgeagg gaagetega gtagteetee ggeteeteg 181 eeggeaggagt geeegggaa ageggaetg gaategeeag etteaeggg eggatagaeg 180 eegagaaggtt geceaggega ageggaetg gaategeeag etteaeggg eggatagaeg 180 eegagaaggtt geeegggaa ageggaetg gaategeeag etteaegg eggategeegg 182 eegagagggt geeeggaa gggaaetge gaategeeg gaategeeg geateggg eggateggg eggateggg eggaaeggg eggaaeggg eggateggg eggaaeggg eggateggg e	gcgatcccgt	ccgcggtgtg	ccgccagtcc	ggcagccctc	gtagcggcac	ccgccgcacg	16980
teggteteet gggeeggge gtagaaagge gagggaagaa atgacagcae egtaeggggg 171 tecatgttga ceaggeegge cacegeegge ageggaagaa gtteggegag egggagecaa 172 eggtggtagt egeeggeegg cacegteeteg tegacetgga ceaceatgtt eeggttgegg 172 ttggegaaga accaaggagee etgeteegaa tgeaggaegg cacegatgta eeggttgege 173 eegggeggg tgaagtagte gaggtaette gtgeeggeeg cacegatgaa eegggggggegg 173 eeegggeggg tgaagtagte gaggtaette gtgeegeeg cacegatgaa eegggggttag 174 ttgeteeggg tggeetgeae egteggegaa gaetgeatga egttgatgt geeggggttag 174 ttgeteeggg tggeetgeae egteggegaa gaetgeatga egttgatgt geeggggtte 174 accttggeet ggageaggaa gtaeggtge eegtegaaga eettgaegga eatgeegagg 175 atgeegatet eeggetggt gatgategg tggtgeeatt egegeaeegg egegtaggtg 175 gtetggaegg egaaeeeee gateaegaag acceggeege tetegtgeee gaggttegeg 176 gteaeegggt egaaegeeete gaeaeagaag acceggeege tetegtgeee gaggttegeg 177 tggaaeegg gggeeegete ggegaaeaea gagaggaagt eeggeeggee egegteeggg 177 tggaaeegg gggeegete ggegaaeeae gggeegggee	gtcatctcgt	gccggccctt	ggccccggtg	aaccagctca	acaccgacac	caggtcgtgg	17040
ceatgttga caggeegte cacegoage agegegagea gttegegage egggageace 172 cggtggtagt egecggeegg cacgtecteg tegacettga ccaccatgtt egggttgege 172 ttgegeagga accaggagee etgeteega tgeaggaegt caaccatgtt egggttgege 173 ceegggeggg tgaagtagte gaggtaette gtgegegee caceggtgaa eegggtgag 174 ttgeteeggg tggeetgaac egteggega agetgeatga egttgatgtt geegggagg 174 accttggeet ggaegagga gtacggtge eggtgeatgag ettgatgtt geegggagg 175 atgeegatet egggetggt gatgategge tggtgeeatt eggeacege geeggaggg 175 atgeegatet eeggetggt gatgategge tggtgeeatt eggeacege geegtagggg 175 gtetggaegt geageceete gateagaag accegegee tetegtgee gaggttgeeg 176 gteacegggt egaacgeee eeggeaceg eggteeaggg geagegggte eacceggagg 177 taggteagae gggteegete ggegaaceag gagaggaagt eeggeeggte eacceggag 177 taggteagae gggteegete ggegaaceag gggteeggge ggtegggge eggteeggg 177 tggaacgee geegteegge geggaaceag gggegggge ggtegggge eggteeegg 177 tgeaacgeeg accaegagee geeggaeette gggeeggge ggtegggge eggteeegg 178 gteageaacg geegteegge geggaacette gggeeggge ggtegggge eggteeegg 178 gteageaacg geegtegga geeggaeette gggeeggge ggtegggge eggteeegg 178 gteageaacg geegteggg gegggaatete gggeeggge gggeggge eggteeegg 177 tggaacgaea geegtegga accaetetee eggaeggge gteegggee eggteeegg 178 gteageagae ettegtegga teeggeagaa accegteegt gteeggagae ggaggttte eagegagae 179 eggtgeggge ettegtegg teeggeagaa geageteega etteggeagae ggaggttte eagegagae 180 actegteea eaccaegtgg teeeggeaga geagetegae etteggeagae ggaggetee 181 eeagetegge gaegetgtge gtgaeceeeg tgeegaggae gtagteete ggetegteet 181 gggecageat egggagae acceggaeg ageggaegg eacgeeag teeegeega 183 gegacacett gegggtgae acceggae acceggaeg eacgeeag teeegeeag 184 acgeettgge ggeatacatg eggtaegee gaatgeeag etteacege geacegeea 183 gegacacett gegggtgae acceggae ggatgaege gatggaaceg ggteagetea teetggaeg 184 acgeettgge eggeatacatg eggeataege gatggaaceg ggteagetea teetggaeg 184 acgeettgge egggaatee gggetaegge gatggaaceg ggteagetea teetggaeg 184 acgeettgge egggaatee gggetaegge gatggaaceg ggteagete acceggaegg 184 acgeettgge egggaatee gggetaegge gaaggeegg aagaeggeg acaggge	cggccggggg	cgcccgccgc	cgagcgcacg	atcgccgcca	ccgccggcga	cgacggcgcc	17100
cggtggtagt cgccggcgg cacgtccteg tegacetgga ccaccatgtt ccggttgcgc 172 ttgcgcagga accaggagcc ctgetecgac tgcaggacgt caaccagcac ccgaceggcc 173 cccgggcggg tgaagtagtc gaggtacttc gtgccgccg cacggtgcac ccgggtgtag 174 ttgctccggg tggcctgcac cgtcggcgag agctgcatga cgttgatgtt gccgggggg 175 accttggcct ggagcaggca gtacggtgc ccgtcgacga ccttgacgag catgccgggg 175 atgccgatct ccggctggtt gatgatcggc tggtgccatt cgcgcaccgc gccgtaggtg 175 gtctggacgt gcagccctc gatcacgaag accggccgc tctcgtgccc gaggttgcg 176 gtcaccgggt cgaacgccca cccgggcaga cggtccagcg gcacgcggtc cacccggcag 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggcggac cccctggcg 177 taggtcgacc gggtccgctc ggcgaaccag gagaggagat ccggcggac cccctggcg 177 tgcaacgcc gggtccgctc ggcgaaccag gagaggagat ccggcggac cccctcggcg 177 tgcaacgcc gccgtcgcg gcggaccttc gggtcgggc ggtgcgggc cgcgtccgg 178 gtcagcaacg gcccgtcggc gcggaccttc gggtcgggc ggtgcgggc cgcgtccgg 178 gtcagcaacg gccgtcggc gcggaccttc gggtcgggc gtccgcaac aggcgcagat 179 cgctgtcgac catcatggc accatctcct cgaaggagac ggaggtttc caccacagct 178 cgctgtcgac catcatggc accatctcct cgaaggagac gtcggcgaa gcggatgacg 180 actcgtccac caccacgtgg tcccgccag tgaggccac gtgggggaag gccgctcga 181 ccagctcgcg gacgctggc gtgaccccc tgccgaagac gtaggcgaag gccgctcga 181 ccagctcgcg gacgctggc gtgaccccc tgccgaagac gaagcccaa tcccgctcgg 182 ccgagaggtt gcccaggca acccgggac cacggacca gatgcccac ggcgccca 183 gggcaacctt gcgggtaac acccggac acccggacc accggcca 183 gcgacacctt gcgggtaac acccggaac cacggacca gatgcccac gcacccac 183 gcgacacctt gcgggtaac gcgatacac gggctacgc gatggaacg ggtatcgg 184 acgccttggc cgccgtac gggctacgc gatggaacg ggtcaccac ttctggacg 184 acgccttggc cgcgccac gggctacgc gatggaacg ggtcacctc tctggacg 184 acgccttggc cgcgcgtac gggctacgc gatggaacg ggtcacctc tctggacg 184 acgccttggc cgcgcgtac gggcacccc accacgacc aacgccca accacgcc 184 acgccttggc ccggaatcc gggcacccc cacacgcc aacacgcc aacacgcc accaccgc 185 ctgcgggact gcggaatcc ccccgcacg aacacccc aaagcccc accaccac accacgcc 186 accacccac cttgccgaac acccccacacgc aacacgccc aacacgccc accacaccac accacgcac 186 accacccac ctcgcgaatcc cccccacacac	tcggtctcct	gggccgcggc	gtagaaggcc	gagggcagac	atgacagcac	cgtacgcgtg	17160
ttggggaggg tgaagtagt gaggtactt gggaggagg caacgagc caggggggg tgaagtagt gaggtactt gtggcgcgc cacggtgcac cagggtgtag 174 ttgctccggg tggcctgcac cgtcggcgag agctgcatga cgttgatgtt gccggggtcc 174 accttggcct ggagcaggca gtacggttc ccgtcgacga ccttgacgag catgccggg 175 atgccgatct caggctggtt gatgatcggc tggtgcatt cgcgcaccc gccgtagggg 175 gtctggacgt gaagcccct gatcacgaag accggccgc tctcgtgccc gaggttgccg 176 gtcaccgggt cgaacgccca cccgggcagc cggtccagcg gcacgcggtc cacccggcag 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggccggac cccctcggcg 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggccggac cccctcggcg 177 tgcaacgccg accacgagc gccgtcgac gggccgggc ggtcaggc cgcgtccgg 178 gtcagcaacg gccgtcggc gcggaccttc gggtcgggc acgaatcgc caccacagct 178 cggccagttc ggcggaaaag gcgtgggaag acccgtcgt gtccgcaac aggcgagat 179 cgctgtcgac catcatggg accatctcct cgaaggagac gagggtttc caccacagct 178 cgctgtcgac catcatggg accatctcct cgaaggagac gagggtttc cagccgagc 180 actcgtccac caccacgtg tcccgccagt tgaggccac gtaggcggaag gccgcctcga 181 ccagctcgcg gacgetgtgc gtgaccccc tgacgaggac gtagtcccc ggctccgg 182 gggccagct caccacgtgg tcccgccagt agtcgccac gaaggccca tcccgctcgg 182 ccagctcgcg gacgctgtgc gtgaccccc gacgccca gaagcccca tcccgccgca 183 gggccagct gccggtgac acctcgcac accgcaccg tgatcgcc gcacccca 183 gcgacacctt gcggggaac acctcggac cacgcaccg tcccgcacca 183 gcgacacctt gcgggtacc agcgcacc cggacccc agcaccca tcccgcacca 183 gcgacacctt gcgggtacc agcccca ggccaccc agcaccca tcccgcacca 183 acgccttggc cgccccac ggccccac agcaccca ggccaccac tcccgcacca 184 acgccttggc cgcgccac gggctaccac ggctacgcc gatcgccca tcctggacg 184 acgccttggc cgcgccac accccaccaccaccaccaccaccaccaccaccacc	tccatgttga	ccaggccgtc	cacccgcagc	agcgcgagca	gttcgcgcag	cgggagccac	17220
ttgctccggg tggcctgcac cgtcggcgag agctgcattc cgtcgacga catggtgcac ccggggttag 174 accttggcct ggagcagga gtacggtgtc ccgtcgacga ccttgacgag catgccgagg 175 atgccgatct ccggctggtt gatgatcggc tggtgccatt cgcgacgag catgccgagg 175 gtctggacgt gaacgccctc gatcacgaag acccggcgc tctcgtgccc gaggttgccg 176 gtcaccgggt cgaacgccca cccgggcagc cggtccagcg gcaccgggt cacccggggt 177 taggtcagac ggacccctc gatcacgaag acccggcgc tctcgtgccc gaggttgccg 177 taggtcagac ggaccgcca cccgggcagc cggtcaagcg gcacgcggc cccctcggcg 177 tgcaacgccg accacgagcc gccgtcgacc gggccgggc ggtgcgggc cgcgtccggg 178 gtcagcaacg gcccgtcggc gcggaccttc gggtcgggc ggtgggggc cgcgtccggg 178 gtcagcaacg gcccgtcggc gcggaccttc gggtcgggc acgaatcgct caccacagct 178 cggccagttc ggcggaaaag gcgtgggaag acccgtcgt gtccgccaac aggcgcagat 179 cgctgtcgac catcatggcg accatctct cgaaggagac gtcgcgcaac aggcgcagat 179 cgctgtcgac catcatggcg accatctct cgaaggagac gtcggcggc cggatagacg 180 actcgtccac caccacgtgg tcccgccagt tgaggcccac gtgggggaag gccgctccga 181 ccagctcgcg gacgctgtgc gtgacccccg tgccgaggac gtagcccaa tcccgctcga 181 gggccagcat caggaccat cccggacgt agcaccccg tgccgaggac gtagcccaa tcccgctcgg 182 ccgaagggtt gcccaggcga acctcggcac accggaccg gaagccccaa tcccgctcgg 182 ccgaagggtt gcccaggcga acccgggac cacgaccg gaagccccaa tcccgccca 183 ggcacacctt gcgggtaac acctcggac cacgacccg tgccacca gtagtcccc gcacgccca 183 gccggaagc ggcatacatg cccgcacgt cacgacccg tgattcgtgg ttgaacagaa 183 tgccggaaac ggcatacatg ccgtacgac cacgacccg gatgaacgg ggtcagcca 184 acgccttggc cgcgctac gggctacgc gatgaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac acctccgac gacagcccc cacgaccg gatgaacgg ggctagccg ggctgaccg 186 ctgcgggacc gcggtaacc gacagcccc cacacgacc aacacgcc accgcaccg gacacccca ctgcgaaccg ggctaaccgg 184 acgccttggc cgcgcacc ctcgcgacc gacacccc cacacaccc accacaccc tccgcacc accacaccc	cggtggtagt	cgccggccgg	cacgtcctcg	tcgacctgga	ccaccatgtt	ccggttgcgc	17280
ttgctccggg tggcctgcac cgtcggcgag agctgcatga cgttgatgtt gccgggctcc 174 accttggcct ggagcaggca gtacggtgtc cegtcgacga ccttgacgag catgccgagg 175 atgccgatct ccggctggtt gatgatcggc tggtgccatt cgcgcacege gccgtaggtg 175 gtctggacgt gcagccctc gatcacgaag aaccggccgc tctcgtgccc gaggttgccg 176 gtcaccgggt cgaacgccca cccgggcagc cggtccagcg gcagcggtc cacccggcag 177 taggtcgacc gggtccgct ggcgaaccag gagaggaagt ccggcggac cccttcggcg 177 taggacgcca accacgagcc gcgtcgacc gggccgggcc	ttgcgcagga	accaggagcc	ctgctccgac	tgcaggacgt	caaccagcac	ccgaccggcc	17340
accttggcct ggagcaggca gtacggtgtc ccgtcgacga ccttgacgag catgccgagg 175 atgccgatct ccggctggtt gatgatcggc tggtgccatt cggcaccgc gccgtaggtg 175 gtctggacgt gcagccctc gatcacgaag aaccggccgc tctcgtgccc gaggttgccg 176 gtcaccgggt cgaacgccca cccgggcagc cggtccagcg gcaccgcggtc cacccggcag 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggccggac cccctcggcg 177 tgcaaccgcg accacgagcc gccgtcgacc gggccgggcc	cccgggcggg	tgaagtagtc	gaggtacttc	gtgccgccgc	cacggtgcac	ccgggtgtag	17400
atgccgatct ceggetggtt gatgategge tggtgccatt egegeacege geegtaggtg 175 gtctggacgt geagececte gateacgaag aaceggeege tetegtgeec gaggttgeeg 176 gtcacegggt egaacgeea eeegggaace eggeteageg gaaggaag eeegteggge 177 taggtegace gggteegete ggegaaceag gagaggaag eeggetggge eggeteeggg 177 taggtegace gggteegge geegtegace gggeegggee ggtgegggee eggeteeegg 178 gtcageaacg geegtegge geggacette gggteeggge ggtgegggee eggeteeegg 178 gtcageaacg geegtegge geggacette gggteggge aegaateget eaceaegget 178 eggetageaggte ggeggaaag accepteegg geegteegge geggatgeeggeeggeeggeeggeeggeeggeeggeegge	ttgctccggg	tggcctgcac	cgtcggcgag	agctgcatga	cgttgatgtt	gccgggctcc	17460
gtctggacgt gcagccctc gatcacgaag aaccggccgc tctcgtgcc gaggttgccg 176 gtcaccgggt cgaacgcca cccgggcagc cggtccagcg gcacgcggtc cacccggcag 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggccggac cccctcggcg 177 tgcaacgccg accacgagcc gccgtcgacc gggcgggcc ggtgcgggcc cgcgtcccgg 178 gtcagcaacg gcccgtcggc gcggaccttc gggtcgggcc ggtgcgggcc cgcgtcccgg 178 cggccagttc ggcggaaaag gcctgggaag accatctcct ggagtcgggc gagaggtttc caccacagct 178 cgctgtcgac catcatggcg accatctcct cgaaggagaa gccggcgaac caccacagct 179 cgctgtcgac catcatggcg accatctcct cgaaggagac ggaggtttc cagccagac 180 actcgccaac accacagtgg tcccgcaga gcagctcgac gtgggggaa gccgctcga 181 ccagccagc gagacctca caccacgtgg tcccgcagt tgaggccacc gtgggggaag gccgctcga 181 gggccagcat caggaccatg ccccgcacgt tgaggccacc gtaggcgaag gccgctcga 182 ccgagaggtt gcccacaca accacagtg agtcgcccc gaatgccca gtgagccaag tcccgctcgg 182 ccgagaggtt gcccacaca accacagtg agcgcccca gatgagccca gtagcccaa tcccgctcgg 182 ccgagaggtt gcccacacag accacacgt gatgcccac gaagccccaa tcccgctcgg 182 ccgagaggtt gcccacacac accacagtg agcgacccc gaatgcccaa caccacagt tcccgcccaa 183 gcgacacctt gcggggaac acctcggaac acctcggaac cacgcaccag tccacacag ttaacagaa 183 tgccgagaac ggcatacatg ccgtacgac gagcacaccg gatgaaccg ggtcaaccat tccggacg 184 acccccca caccacaca ggcgcccaa accccacacaca	accttggcct	ggagcaggca	gtacggtgtc	ccgtcgacga	ccttgacgag	catgccgagg	17520
gtcaccgggt cgaacgcca cccgggcagc cggtccagcg gcacgcggtc caccggcag 177 taggtcgacc gggtccgctc ggcgaaccag gagaggaagt ccggccggac cccctcggcg 177 tgcaacgccg accacgagcc gccgtcgacc gggccgggcc	atgccgatct	ccggctggtt	gatgatcggc	tggtgccatt	cgcgcaccgc	gccgtaggtg	17580
taggtegace gggteegete ggegaaceag gagaggaagt eeggeeggee eeeeteeggg 177 tgeaacgeeg accaegagee geegtegace gggeeggee ggtgegggee eggteeeggg 178 gteageaacg geegtegge geggacette gggtegggeg acgaateget eaceaeaget 178 eggeeagtte ggeggaaaag gegtgggaag acceeteegt gteegeeaac aggegeagat 179 egetgtegae eateatggeg accateteet egaaggagae ggagggttte eageegagee 180 getggeggge ettegtegga teeggeaag geagetegae etteggegge eggatgageg 180 actegteeae eaceaegtgg teeegeeagt tgaggeeeae gtaggegaag geegeetega 181 eeagetegeg gaegetgtge gtgaceeeeg tgeegaggae gtagteetee ggetegteet 181 gggeeageat eaggaceatg eeeegeagt agtegeeege gaageeeeag teeegeeteg 182 eegagaggtt geeeaggea agegagetge gaatgeeeag etteaeege geeaegeea 183 gegacacett gegggtgaeg aactegggae eacgaeege tgattegtgg ttgaacagaa 183 tgeeggagae ggeatacatg eegtaegae eacggaeeg gatggaaegg ggteagetea teetggaegg 184 acgeettgge egegeegtae gggetaeege gatggaaegg ggteagetea teetggaegg 184 geteeegaa ettgeegaae ateteegaeg aagageeetg ataaaaggee ggetgaeegg 184 geteeegaae ettgeegaae ateteegaeg aagaegeetg ataaaaggee ggetgaeegg 185 ettgegggaet gegggaatee gaeaggeee eeaggteeg eaaggetteg ageatgeegg 186 geacaceeat geegggaatee gaeaggeee eeaaggeete ataaaaaggee ggetgaeegg 186 geacaceeat geeggtaee teegeegteg tggtggaete eacaggetteg ageatgeegg 186 geacaceeat geegggaatee gaeaggeee eeaaggeete eaaggetteg ageatgegga 186 geacaceeat geeggtaee teegeegteg tggtggaete eacaggetteg ageatgegga 186	gtctggacgt	gcagcccctc	gatcacgaag	aaccggccgc	tctcgtgccc	gaggttgccg	17640
tgcaacgccg accacgagcc gccgtcgacc gggccgggcc	gtcaccgggt	cgaacgccca	cccgggcagc	cggtccagcg	gcacgcggtc	cacccggcag	17700
gtcagcaacg gcccgtcggc gcggaccttc gggtcggcg acgaatcgct caccacagct 178 cggccagttc ggcggaaaag gcgtgggaag acccgtccgt gtccgccaac aggcgcagat 179 cgctgtcgac catcatggcg accatctcct cgaaggagac ggagggtttc cagccgagcc 180 gctggcgggc cttcgtcgga tccgcgcaga gcagctcgac ctcggcgggc cggatgagcg 180 actcgtccac caccacgtgg tcccgcagt tgaggcccac gtgggggaag gccgctcga 181 ccagctcgcg gacgctggc gtgacccccg tgccgaggac gtagtcctc ggctgtcct 181 gggccagcat caggaccat caggaccat caccacgtg agtcgcccg gaaggcccag tcccgctcgg 182 ccgagaggt gccagcat gcccagcag agcgactgc gaatgcccag tcccgccag tcccgctcgg 182 ccgagaggtt gcccaggcga agcgactgc gaatgcccag cttcaccgcc gccacgccca 183 gcgacacctt gcgggtgacg aactcgggac cacgaccgg tgattcgtgg ttgaacagaa 183 tgccggaac ggcatacatg ccgtacgac cacgaccgg tgattcgtgg ttgaacagaa 184 acgccttggc cgccgtac gggctacgcg gatggaacg ggtcagcta ttctggaccg 184 gctcccgcac cttgccgaac cttgccgaac cttgaccacg cttcaccacg ggctgaccgg 184 gctcccgcac cttgccgaac atctccgac aagacccca aagacccca ggctagccg aagacccca cacgacccg caaggctc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggccc cacagaccc cacagatccg caaggcttc accagcacg 186 gcacacccat gcgggaatcc gacaggccc cacagaccc cacagatccg caaggcttcg agcatgcgaa 186 gcacacccat gcgggaatcc gacaggccc cacagaccc cacagatccg caaggcttcg accaggaccg accggcacgt 186 gcacacccat gcgggaatcc gacaggccc cacagaccc cacagaccc cacagaccca accggcaccg accaggcaccaccac accagacccacaccaccaccaccaccaccaccaccaccac	taggtcgacc	gggtccgctc	ggcgaaccag	gagaggaagt	ccggccggac	cccctcggcg	17760
cggccagttc ggcggaaaag gcgtgggaag acccgtccgt gtccgccaac aggcgcagat 179 cgctgtcgac catcatggcg accatctcct cgaaggagac ggagggtttc cagccgagcc 180 gctggcgggc cttcgtcgga tccgccaga gcagctcgac ctcggcgggc cggatgagcg 180 actcgtccac caccacgtgg tcccgccagt tgaggcccac gtgggcgaag gccgcctcga 181 ccagctcgcg gacgctgtgc gtgacccccg tgccgaggac gtagtcctcc ggctcgtcct 181 gggccagcat caggaccatg ccccgcacgt agtcgccgc gaagccccag tcccgctcgg 182 ccgagaggtt gcccaggcga agcgagctgc gaatgcccag cttcaccgcc gccacgcca 183 gcgacacctt gcggtgacg aactcgggac cacgcacgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgac cacgcaccgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgac cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccgtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	tgcaacgccg	accacgagcc	gccgtcgacc	gggccgggcc	ggtgcgggcc	cgcgtcccgg	17820
cgctgtcgac catcatggcg accatctcct cgaaggagac ggaggtttc cagccgagcc 180 gctggcgggc cttcgtcgga tcccgcaga gcagctcgac ctcggcgggc cggatgagcg 180 actcgtccac caccacgtgg tcccgccagt tgaggcccac gtgggcgaag gccgcctcga 181 ccagctcgc gacgctggc gtgaccccc tgccgaggac gtagtcctcc ggctcgtcct 181 gggccagcat caggaccat ccccgcacgt agtcgcccgc gaagccccag tcccgctcgg 182 ccgagaggtt gcccaggcga agcgagctgc gaatgcccag cttcaccgc gccacgcca 183 gcgacacctt gcgggtgacg aactcgggac cacgcaccg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgact cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggccc ccacgatccg caaggcttc agcatgcga 186 gcacacccat gccggtagcc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186 gcacacccat gccggtacccac tccgccgtcg tggtggactg ccgccacgac accggcacgt accgcacgac accggcacgac accgccacacaccacacaccacacaca	gtcagcaacg	gcccgtcggc	gcggaccttc	gggtcgggcg	acgaatcgct	caccacagct	17880
gctggcggc cttcgtcga tccgcaga gcagctcgac ctcggcggc cggatgagcg 180 actcgtccac caccacgtgg tcccgcagt tgaggcccac gtgggcgaag gccgcctcga 181 ccagctcgcg gacgctgtc gtgacccccg tgccgaggac gtagtcctcc ggctcgtcct 181 gggccagcat caggaccatg ccccgcacgt agtcgcccg gaagccccag tcccgctcgg 182 ccgagaggtt gcccaggcga agcgagctgc gaatgcccag cttcaccgcc gccacgccca 183 gcgacacctt gcgggtgacg aactcgggac cacgcacgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgac cacggaccgg tgattcgtgg ttgaacagaa 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggaccg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggccc ccacgatccg caaggcttc agcatgcga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	cggccagttc	ggcggaaaag	gcgtgggaag	acccgtccgt	gtccgccaac	aggcgcagat	17940
actegtecae caccacgtgg tecegocagt tgaggeccae gtgggegaag geegeetega 181 ceagetegeg gaegetgtee gtgaeeeeeg tgeegaggae gtagteetee ggetegteet 181 gggeeageat caggaeeatg eccegoaegt agtegeeege gaageeeeag tecegoetegg 182 cegagaggtt geecaggega agegagetge gaatgeeeag etteaeegee geeaegeea 183 gegaeaeett gegggtgaeg aactegggae caegeaeegg tgattegtgg ttgaacagaa 183 tgeeggagae ggeataeatg eegtaegaet eaeggtagtt etgeaeeatg taatgeeega 184 acgeettgge egegeegtae gggetaeege gatggaaeeg ggteagetea ttetggaeeg 184 geteeegeae ettgeegaae ateteegaeg aagaeeetg ataaaageeg ggetgaeegg 185 etgegggaet gegggaatee gaeaggeee eeaegateeg eaaggetteg ageatgegga 186 geaeaeeeat geeggtgaee teegeegteg tggtggaetg eegeeaegae aeeggeaegt 186	cgctgtcgac	catcatggcg	accatctcct	cgaaggagac	ggagggtttc	cagccgagcc	18000
ccagctegeg gaegetgteg gtgacceeg tgeegaggae gtagteetee ggetegteet 181 gggceageat caggaceatg ceeegeacgt agtegeeege gaageeeeag teeegeteegg 182 ccgagaggtt geeeaggega agegagetge gaatgeeeag etteacegee geeaegeeea 183 gegacacett gegggtgaeg aactegggae caegeaeegg tgattegtgg ttgaacagaa 183 tgeeggagae ggeatacatg eegtaegaet eaeggtagtt etgeaeeatg taatgeeega 184 acgeettgge egegeegtae gggetaeegg gatggaaeeg ggteagetea ttetggaeegg 184 geteeegeae ettgeegaae ateteegaeg aagaegeetg ataaaaagege ggetgaeegg 185 ctgegggaet gegggaatee gaeaggeee eeaegateeg eaaggettee ageatgegga 186 geacaceeat geeggtgaee teegeegteg tggtggaetg eegeeaegae aceggeaegt 186	gctggcgggc	cttcgtcgga	tccgcgcaga	gcagctcgac	ctcggcgggc	cggatgagcg	18060
gggccagcat caggaccatg ccccgcacgt agtcgcccgc gaagccccag tcccgctcgg 182 ccgagaggtt gcccaggcga agcgagctgc gaatgcccag cttcaccgcc gccacgccca 183 gcgacacctt gcgggtgacg aactcgggac cacgcaccgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgact cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	actcgtccac	caccacgtgg	tcccgccagt	tgaggcccac	gtgggcgaag	gccgcctcga	18120
ccgagaggtt gcccaggcga agcgagctgc gaatgcccag cttcaccgcc gccacgccca 183 gcgacacctt gcgggtgacg aactcgggac cacgcaccgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgact cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	ccagctcgcg	gacgctgtgc	gtgacccccg	tgccgaggac	gtagtcctcc	ggctcgtcct	18180
gcgacacctt gcgggtgacg aactcgggac cacgcaccgg tgattcgtgg ttgaacagaa 183 tgccggagac ggcatacatg ccgtacgact cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	gggccagcat	caggaccatg	ccccgcacgt	agtcgcccgc	gaagccccag	tcccgctcgg	18240
tgccggagac ggcatacatg ccgtacgact cacggtagtt ctgcaccatg taatgcccga 184 acgccttggc cgcgccgtac gggctacgcg gatggaacgg ggtcagctca ttctggacgg 184 gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	ccgagaggtt	gcccaggcga	agcgagctgc	gaatgcccag	cttcaccgcc	gccacgccca	18300
acgeettgge egegetate gggetaegeg gatggaaegg ggteagetea ttetggaegg 184 geteeegeae ettgeegaae ateteegaeg aagaegeetg ataaaagege ggetgaeegg 185 etgegggaet gegggaatee gaeaggeeee eeacgateeg eaaggetteg ageatgegga 186 geacaeceat geeggtgaee teegeegteg tggtggaetg eegeeaegae aceggeaegt 186	gcgacacctt	gcgggtgacg	aactcgggac	cacgcaccgg	tgattcgtgg	ttgaacagaa	18360
gctcccgcac cttgccgaac atctccgacg aagacgcctg ataaaagcgc ggctgaccgg 185 ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	tgccggagac	ggcatacatg	ccgtacgact	cacggtagtt	ctgcaccatg	taatgcccga	18420
ctgcgggact gcgggaatcc gacaggcccc ccacgatccg caaggcttcg agcatgcgga 186 gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	acgccttggc	cgcgccgtac	gggctacgcg	gatggaacgg	ggtcagctca	ttctggacgg	18480
gcacacccat gccggtgacc tccgccgtcg tggtggactg ccgccacgac accggcacgt 186	gctcccgcac	cttgccgaac	atctccgacg	aagacgcctg	ataaaagcgc	ggctgaccgg	18540
	ctgcgggact	gcgggaatcc	gacaggcccc	ccacgatccg	caaggcttcg	agcatgcgga	18600
acquaracqua acquaratta tagaqatqat acquaracqua contracta concerna 100	gcacacccat	gccggtgacc	tccgccgtcg	tggtggactg	ccgccacgac	accggcacgt	18660
acgacagege geogaggttg tagacetegt eeggegeege gegttegate geogeeacea 187	acgacagcgc	gccgaggttg	tagacctcgt	ccggcgccgc	gcgttcgatc	gccgccacca	18720

ggctcgtctg	atccagaagg	tcgccgctga	tcagcttgac	cgctggatca	ggttgccgaa	18780
ggctgcggac	cgagggcgcg	gtctgcccgc	gcaccaatcc	aaatacctcg	tatccggact	18840
gaagcaggtg	ctccgcgaga	tacgtgccgt	cctggccggt	aattccagtg	atcagcgccc	18900
gccgtgtcag	ggtagtctcc	agccgtgaag	ccacctggcc	gaggcgtgac	ctcgcgccga	18960
tggcggacca	aagatccgcc	cgttcgaaat	ggggtcggat	ctcccgctac	cgcgctcacg	19020
gtacgcgaat	ctccaagcgg	attcagcgac	ccggaaagca	atatagggag	gttactagta	19080
gtactttccg	gcgggccggc	agcgacgccc	ggcccggacc	ggcaggatcg	ccccgttcgg	19140
ccggcggacc	catcccggac	accttccacc	gaagctcttc	gggatcgtcg	cccgccgatg	19200
cgaactgctt	gactccaccg	ttttgtcccc	ctaacgtcgg	cgaggctgcc	agccggcccg	19260
cgagccgggc	cgggttcacg	aaggcgccaa	cttccggtga	gagagcaggg	ctcatgtcgc	19320
agagccggcc	cgcggccgca	gcacccccag	cccgcctgcc	acgtcgccgc	gccatggtcg	19380
cgttggtcgc	ggtgatgatc	ccgatggtgc	tggccaccct	cgacaacacc	atcatcggca	19440
ccgcactgcc	caccgtggtc	ggcgagttgg	gcggcctcag	cacgctctcc	tgggtgatca	19500
cctcgtacac	gctggccacg	gccgcctcca	cgccggtctg	gggcaagctc	gccgacatgt	19560
acggcggcaa	ggtggtcttc	gtggccacgc	tggtcgtgtt	cctggccggg	tcgctgctgt	19620
ccggcatggc	gcagagcatc	acccagctga	ccgtcttccg	ggccgtgcac	gggctcggcg	19680
cgggcggcct	gatggtctgc	gcgttcgcca	tcatggtgga	ggttctcgcc	ggccctgacc	19740
tgcccaagta	ccagggcatc	atgtcggcga	ccatgggcct	gaccatggtg	gcgggcccgc	19800
tcgtcggcgg	cctgatcacc	gatgagctcg	gctggcgctg	gtgcttctac	atcaacctgc	19860
cgatcggggc	ggtcgcgctg	ctcatcgtgg	tgctgatgat	gcacctgccg	cgccgacaca	19920
ccaaggcccg	gatcgattac	gcgggtgctg	ccctgctcac	cgtggtcagt	tcgtgcgtcg	19980
tgctggtgac	cacctggggc	ggcatcacct	acccctgggc	gtctccgatg	atcctggggc	20040
tggtcgcgct	cggggtgctg	acctgcgcgc	tcttcgtggt	ggtcgagcga	cgggtggccg	20100
agccgttggt	gcccctggcc	atgttccgca	gcctgaactt	caccctgagc	accctcatcg	20160
ccttcctggt	cggcttcgcc	ctcatcgcgg	ggctgacctt	cctggccctg	ttccagcagg	20220
cggtgcaggg	tgcctccgcg	tccgactccg	gcctgttgct	gctgcccctg	ctgctgtcca	20280
tggcggcggt	caacgtggtc	gggggtcgcc	tgatgagcgg	cgggcgttcc	taccggctgc	20340
tgatgctcgc	cggtgcggcg	ctgatgaccc	tgagcctgct	gctcttcgcc	ctgatggacg	20400
tgggcaccag	ccggacggtc	accgcgatcc	ccatggtcgg	cttcggcgca	gggctggggc	20460
tgctcatgca	gaccagcctg	atggtggcgc	tgagcagcgt	ggagatgagg	aacctcgggg	20520
tggccgcctc	cacgtccacg	ctcttccgca	ccatcggtgg	ggcggtgggg	gcgtcggcga	20580
cggtctcgct	gttctccgtg	cgggtgcagt	cggcgctggc	cgatcggggg	gtcgccgacg	20640
tggctgacct	cctcggccac	tccgcgcggc	tggacgccgc	cgggctggcc	caactccccc	20700

20760 gggccgtccg tgtccacttc atgcacgcgg tggcctccgg cacccggtgg gccttcctga 20820 tgaccgtgct ggcggggctg atctgcgtcg cggcggcgtg gttcctgcgc cgggtcaccc cgttgacgtc ggcaccggtg gcacccgaac cggcgcgcga cgtcgccgcg cccgccgcca 20880 gcagcgggcg cgcgccgaac tactagcgga tttcctaggg ttcctcgtcg acggtagagc 20940 tgaattcacc ggcgacctaa cattetttte gcgatecgga atcegtecat teceetgtet 21000 ggcgatggtc gacgggccgg cccgtgccga gcggacagac acagattctc ggattggagc 21060 tegatgteca geaagateet agteateggt ggaggteegg eeggateeae ggeegeegeg 21120 ctgctcgccc gatcggggct gtcggtgacg ctcctggaaa aggagacgtt cccgcgatac 21180 cacateggeg agtegatege gteetegtge egeaceateg tegatttegt gggegetete 21240 21300 gacgaggtcg actcgcgggg ctacccgcag aagaacgggg tcctgctgcg ctggggcaac gaggactggg ccatcgactg ggccaagatc ttcggtccgg gcgtgcggtc ctggcaggtc 21360 gaccgggacg acttcgacca cgtcctgctc aacaacgccg gcaagcaggg cgccaagatc 21420 atccagggcg cggctgtcaa gcgggtgttg ttcgacggtg agcgggccac cgccgccgag 21480 tggttcgacc ccgagtcggg tgaggtccgc accatcgatt tcgactacgt ggtcgacgcg 21540 teeggeeggg eegggetgat eeegteecag eactteaage aceggegeee eacegagaeg 21600 ttcaagaacg tggccatctg gggctactgg cagggtggct cgctgctgcc gaactctccc 21660 teeggeggga teaacgteat eteeggeeee gaeggetggt aetgggteat teegetgege 21720 ggegaceggt acageategg ettegtetge caccagagee getteetgga geggegeaag 21780 gageaegeet egetggagga eatgetegee geaetggtae aggagteeee gaeegtgege 21840 ggcctgacgg cgaacgggac gtaccagccg ggcgtgcggg tggagcagga cttctcgtac 21900 atctccgaca gcttctgcgg gcccggctac ttcgcggccg gcgactccgc ctgcttcctg 21960 gacccactge tgtccaccgg cgtgcacctc gccctctaca gcggcatgct cgcctcggcg 22020 tecateetgg ecaceateea eggtgaegte acegaggagg aggegegge gttetaegag 22080 tecetetace geaacgeeta ecagegeetg tteacceteg tegeoggegt etaccageag 22140 caggccggca agagggcata cttcggcctg gccgacgcgc tggtgcacga cagcggcgaa 22200 cccgagtacg agaaggtaga cggggcccgc gccttcgccc agctcgtcgc cggcctcgcc 22260 gacctggacg acgcggcgga gggacggcac gacagcaccg cggcggcggc accggcggag 22320 caggacaact ccgtccggca gctcttcctg gccgccgagg aggcccgccg gatggccgac 22380 gcgcgcacgc cgagcgcccc ggtcagcgag gcgccgggca agctcgacag ccacgacctc 22440 ttegactegg caaceggeet ctacetggte accaeeeege gaetggggat eegeegggee 22500 aagccggccg acacgcaggc ggcggcagag cagtctgcct gaggttccac ccctggtggc 22560 ecceggeeeg gacegeege gteeggggge tgeteaacee teccaceaac ateeggeate 22620

cggtgccggc	ggctgagcag	gggcagcgcc	accgactccg	gcccgtcaca	tggacaaggt	22680
cacctctccc	gtgctgaaca	gacgacagtt	gctcgccctc	ggcagcgtgg	ccgccggagg	22740
caccgtcatg	tcacgctccc	tcagacggga	cgcgcaggcc	gcccaggcgg	caccggcgtc	22800
gcccgccaac	ccgcacgccg	ggcacgccgc	cccggtgccc	agccgggtca	gcacgaccac	22860
ggtcgcggtc	accccgttca	ccgagccgat	gcccgtcccg	ccgcggctga	ccccggtctc	22920
ccgccgcgac	ggcatcgacg	tctacgagat	ccccatccgg	ccggcgcagg	tgcagatcct	22980
gcccggcctg	ctcacgcccg	cctacaccta	cgccggttcc	ttcgtcggcc	ccaccatccg	23040
ggcccgcacg	ggccggcccg	tgcggatcac	ctacaccaac	gggctcgaca	cccacgccaa	23100
cgtgcacctg	cacggcgggc	acgtgccggc	caccagcgac	ggtcacccga	tggacctgat	23160
cccgccgggc	ggctcgaagg	tctacgacta	cccgaacctt	cagcgcggcg	cgacgctctg	23220
gtaccacgac	cacacccacg	cctacgaggc	cgaccacgtc	taccgcggac	tgcacggctt	23280
ctatctgatc	gacgacccgg	ccgagcatca	cctgcgcctg	cccgccggca	agtacgacgt	23340
gccgatcatg	ctgcgcaacg	cccagttcga	cgactccggc	gccctcgtct	tcggccaccc	23400
ggacgaccgg	gtcaccatcc	tggcgaacgg	caaggcccag	ccctacttcg	aggtggcccc	23460
gcgcaggtac	cggttccgcc	tgctcaacgc	ggcgctgaag	cacgtcttcc	ggctcaacct	23520
gggcggcgaa	ccgctcaccc	gcatcgccac	ggacggcggg	ctgctgcccg	ccccaccag	23580
tcacaccgag	ctggcgctct	cctccgggga	gcgggtcgag	attgtgatcg	acttcgccga	23640
gcacgcaggc	ggcgggccgg	tctacctcta	cgacggggac	aacccgatcc	tgcgcttcga	23700
cgtgtcgtcc	cgggcggtca	ccgaccccag	ccgggtgccg	gtcaccctgc	gcgcactgcc	23760
cccgatgggc	acgccgaccg	tggagcgcac	cgtgtcgatg	agcttcgaca	tgtcggcccg	23820
gcccccgatc	gcgctcatgg	acggcaaacc	gttcgaccct	ctccgggtgg	acgtacaggt	23880
caagcggggc	agcaccgaga	tctggaacgt	ggtcaacgcg	gataccgatc	cgttcccctt	23940
cgaccatccg	ttccacctgc	acctggtgac	gttccgggtg	ctcggccgcg	acggcgggcc	24000
gcccgcgccg	gaggacgccg	ggctcaagga	caccgtctac	gtctcgccca	aggggtctgt	24060
caagatccag	gtcaccttcg	ccacgccgta	cctcgggcag	tacgtctacc	actgccacta	24120
cctggagcac	tcgtcgctgg	ggatgatggc	ccagctggag	gttgtgccct	gagggctcag	24180
ccgtgcaggt	cgacgatcga	ggggtgggcg	ccgaacaggc	tgaccggccg	cacgtcgccc	24240
accccgaacc	cggcggcgcg	ggccaggtcg	gcctggtcgg	cgaactcgtg	cagcagcagt	24300
accgcccgcc	cgccgtcgac	cgtcacccgg	cgcagctccg	cgaagaggcg	gccggaatca	24360
ccggcgagca	cgccccgcgc	ctgcacctgc	cggtcccagg	gcggattgct	gaccacccgg	24420
tccacccgac	cggtccgcag	cggcaatcgt	ccggcgtcgg	cgaccgccca	ggtgacgcgg	24480
gcccccgacg	ccgccgagtt	ggcgacggcc	gcgccgaccg	tctccgggtc	gtggtccgag	24540
ccgaacagca	ccgcccccgg	tgccagcccg	gctgcctcca	cggggatcgt	gccggtgccg	24600

cagcacggat	cggccaccag	catcccgggg	cggatgccgg	ccagccaggc	cagcgccgcg	24660
gcgagcggcg	gatgcagggt	ccccggcgtg	gacgaccgct	tgtaggcccg	ccggtgcagc	24720
ggccggtcgg	ccacccgtac	cgccagcgtc	gcctgggtgc	cctcgacggt	gacccgcagc	24780
gacagcccgc	cctccggcgg	ggcctcgccg	ccgcggcggg	agtggtagcg	caacccgagc	24840
gcggccaccg	cgtgccgccc	cacggcgtcc	tcgatgtcgt	accggttgta	gttgcggcgg	24900
ccgaggaagg	aggcggcgac	gtccacggtc	gccggccgcc	cgggcacgcc	gcaggcggcg	24960
cgggccggca	gcaccgccgg	cagcgccgcc	gcccgggcca	gccgggtgaa	ggccgccagg	25020
tccgccttgg	tgtggccgac	gccgtcggcg	acggcgacga	gcaggaacag	gtcgtcgacg	25080
gtacgcagat	ccagcaggcg	cggctccgcg	ctggcggcgg	agaaccacac	ctcgcggtgc	25140
cggcggtgct	cgacccggcc	gaggccccgc	tcctcgatct	cctgggcggc	cacctcctcc	25200
agccctcgca	gggtccgtgc	catgaagcgc	accgtcaccg	tccgccgatc	ctctccccgc	25260
cgggtcgtcc	cgccgccgtg	ccggcggcgt	ccgcgagcct	acccaccgca	cccgccgccg	25320
ggacgcagcc	gacgccgacc	ggacccgccg	acgggggagc	cgacgccgac	cggacccgcc	25380
aagactaggt	gaacctctat	aggaattcgc	gtgccccctt	catagggtcc	gaaaggggta	25440
atggaaccgt	ccggcaccgg	acggctcgtt	ttcttccccc	aattccgtcc	gtccgacctg	25500
agccgtcgca	gggaaggcga	ggccgagcag	tcgagcagtt	gatcggtcga	tgccgcacgg	25560
gcccgtgcgc	cgaaatcgtg	gagattgcgc	agtgcgtaca	ccggatctgt	tcatcggcgc	25620
cgtcggcgcc	ttcgtcccgc	cgacggtgag	cgtcgagtgg	gcgatcgacc	gcggtcttta	25680
ctcccgcgag	caggtggagc	tgcacgagct	ggcgggcacg	gccatcgccg	gcgacctgcc	25740
cgcgccggag	atggcgctgc	gcgccgccca	acaggcggtc	aagcgctggg	gcggctcgcc	25800
gacggagttc	gacctgctgc	tctacgccag	cacctggcac	caggggcccg	acggctggcc	25860
gccgcactcc	tatctccagc	ggcacctggt	cggcggcgac	ctgctggcgt	tggagatccg	25920
gcagggctgc	aacgggatgt	tcagcgcgtt	cgagctggcc	gccagccacc	tccaggcggt	25980
acccgagcgc	accagegeee	tgctggtcgc	cgccgacaac	tacggcaccc	cgatggtcga	26040
ccgctggcgg	atgggccccg	gcttcatcgg	tggcgatgcc	ggcagcgccc	tcatcctcac	26100
caagcgaccc	ggcttcgcgc	ggctccgctc	ggtctgcacc	aagtcggtcc	cggaggccga	26160
gcggctgcac	cggggcgacg	agccgctgtt	cccccgagc	gtcctgaccg	gccgggagct	26220
gaacttcacc	gcccggatcg	accaacagtt	cgccgcccgc	agccccgcct	cgatcgccat	26280
ggcggacgtc	ggcgaccaca	tcgaggaggt	cgtggggcgc	gccctcgccg	aggcggagat	26340
cgaggtcggc	gacctcgcca	gggtcgcctt	catgaacttt	tcccgggaga	tcatggagca	26400
gcgctgcctg	gccaactggg	gcctgcccat	gagccggtcc	accttcgact	tcggtcgccg	26460
gatcgggcac	tgcggggcga	gcgacccctt	gctggccctg	gaacacctgg	ccaggacggg	26520

gggcctcggc	cccggcgatc	acctgctgac	cctcggcacc	gcgccgggcg	tggtggtgtc	26580
gtgcgcgatc	gtccaggtga	tcgagtcgcc	gacgtggcgg	gagtgacccg	ctggacacct	26640
gcggcggccc	gcccagccca	gcaaaccgac	agcaggggat	gattgtggaa	gcagagaagg	26700
accggttgcg	tccggtggcg	tccgaggcgg	tcgccgtggt	ggggatcggc	tgccggttcc	26760
cgggcgacgt	caactcgccc	gacgagttct	gggacctgct	caccgggggt	cgcaacacca	26820
ccgggacggt	gcccgaggag	cgctggagcg	cgtaccgcga	cctgggtccg	gcgttcgagt	26880
ccgcgctccg	gtcggccacc	cgggcgggca	acttcctggc	cgacatctcc	ggcttcgacg	26940
cggacttctt	cggcatctcc	ccgcgcgagg	ccgagctgat	ggacccgcag	cagcggctca	27000
tgctggaggt	gacctggcag	gcgctggagg	acgccgggat	cccgccccgc	accctggccg	27060
gcaccgacgt	cggcgtcttc	gccggcgtgt	gcacctacga	ctacggcggc	caccagttgg	27120
aggacctgcc	gcacatcgac	gcctggacgg	gcatcggcgc	cgccacctgc	gccgtcgcca	27180
accgggtctc	ccacgtgctc	gacctgcgcg	ggccgagcct	gtcgatcgac	accgcctgct	27240
cggcgtcgct	ggtcgcgttg	cacctcgccg	cgcagagcct	gcggctgggc	gagagcacgc	27300
tggccctcgc	cggcggggtc	aacctgatcg	tcacgcccgg	gcagtcgatc	accctcggct	27360
cggccggtgc	cctggcaccc	gacgggcgca	gcaagtcctt	cgacgccacc	gccgacggct	27420
acggtcgtgg	cgaggggtgc	ggcgtcctcg	tgctcaagct	gctctccgac	gcccagcggg	27480
acggggaccg	ggtgctggcc	gtgctgcggg	gcagcgccgt	caaccaggac	ggccggacca	27540
acgggatcat	ggcaccgtgc	ggccaggccc	aggagcacgt	gatggtccgc	gccctgcgct	27600
cggccggcat	cgaggccggc	agcgtcgact	acatcgaggc	gcacggcacc	ggcaccccgc	27660
tcggtgaccc	gatggaggcc	gcggcgatcg	gctcggtcta	cgggcaggac	cgcccggacg	27720
acgagccctg	cctgatcggt	tcggtcaagt	ccaacatcgg	ccacctggag	ggcgcggccg	27780
gcgtcgcagg	cgtcatcaag	gcggtcctgg	cgctgaaccg	ggccgaggtg	cccgccaccc	27840
tgctggtcac	cgaggtcaac	ccggacatcg	agtggaagcg	gctgcggctg	cgcctggtca	27900
cccgcaacca	gccctggccg	gaccggccgg	ggccgcgccg	cgccggagtc	tccggcttcg	27960
gctacggcgg	caccgtggcg	cacgtggtgc	tggaacaggc	cccgccggtc	gccgccgagc	28020
cggccccggc	gctgaccggc	gagacgctgt	tcccgatctc	cgccggctcc	gcgcactccc	28080
ttcgcgagcg	ggcccgcgcc	ctggccggga	tcgtcccgga	tgtcgacctc	gccgcgctcg	28140
ggcacaccct	ggctcggcgg	cgttcgcacc	tgacccaccg	ggcggtggcg	gtggccgccg	28200
gccgggacga	cctggtcgcg	gcgttcgcgg	cgctcgccga	cgacaggccg	cacgaccggg	28260
tgcgtaccgg	aagcccggtg	gcggagccgc	cccgcacggt	gtgggtgttc	tccgggcacg	28320
ggtcgcagtg	gacgggcatg	gggcgggaac	tgctggccac	ggagccggcc	ttcgcggacg	28380
cgatcgaccg	catcgagcag	atcttcctcg	acgagatcgg	tttctcaccc	cgccaggcga	28440
tcctcgacgg	cgactacgag	gccgtcgacc	ggacccagac	aatgatcttc	gcgatgcagc	28500

tcggcctggc	cgagatgtgg	cgagcgaggg	gagtcgagcc	ggacgcggtg	atcggccact	28560
cggtcggaga	gatcgccgcg	gcggtgaccg	ccggcatcct	gaccgtggcc	gacggcgcac	28620
ggctgatctg	ccgtcgttcc	ctgctgctgc	gcgaggtcgc	cggccagggc	gcgatggccc	28680
tggtgacgct	gcccttcgag	gaggtcgcgg	ccaggctggc	cggccgcgtc	gacgtggtcg	28740
ccgcgatcgc	ctcctcccc	tcgtcgaccg	tggtctccgg	cgacccggcc	gcgctggacg	28800
cgctggtcgc	cgagtggacc	gaggagggcc	tgggcgtacg	ccgggtcgcc	tccgacgtgg	28860
ccttccacag	cccgcacatg	gatccgctgc	tcgaccggct	gcgcgccgcc	gtcgacttca	28920
ccgcccgcgc	accccgggtg	ccgatctaca	gcacggcgct	ggccgacccg	cgggccccga	28980
tcaccgccga	cggcgagtac	tgggccgcga	atctgcgcaa	cccggtccgg	ctcgccgcag	29040
cggtggccgc	cgccgtctcc	gacggacacc	gggccttcat	cgaggtctcc	ccgcacccgg	29100
tggtgaccca	ctcgatccac	gagacgctgg	ccggaagcct	cgacgacgag	gtcttcgtcg	29160
gcggcaccct	gcgccgcgac	accccggagg	cgcaggcctt	cctgtccagc	ctgggggccg	29220
cgcactgcca	cggggtcgcg	gtcgactggg	gccgggtgca	tccgtccggg	ccgctggtca	29280
ccctgcccgg	ctacccctgg	cggcaccgga	gtcactggca	ctggccgacg	ccggccgccg	29340
ccacgggccg	gggccacgac	cccgcgtcgc	acaccctgct	cggcgcggtc	gacaacgtgg	29400
cgggcagcga	cgtgcgggtg	tggcgcaccg	cactcgacga	cgccagccgc	ccgtacccgg	29460
gcagccacgc	cctcaacggc	gtggagatcg	ttccggcggc	cgtgctggtg	gagaccctca	29520
tggctgccgc	cgggcggggc	gacggccggc	cgctgctgac	cggcttgtcg	atgcggtacc	29580
cgctgatgac	cgccgggctg	cacgaggtcc	aggtggtgcg	ggacggtgcc	gaggtgcggc	29640
tggcgtcccg	ttccgtcgac	gcggaggccg	acccgagccg	ggactggctg	atccacaccg	29700
acgccacggt	ggccgacgcc	gacgccacgg	tgctcgccgc	gcgggcgttg	gccgaccccg	29760
acgaccaccg	gatggaaccg	ggcgacccgg	gctccatcca	ccgccggctc	gccgaggtcg	29820
gggtgccgtc	gacgggattc	gactggtcgg	tggaggagct	gctctccggg	tacggcgtgc	29880
tccgcgcgcg	ggtgcgctcg	gccgactcgt	ccacctgggc	gccggtgctg	gacgccgtca	29940
tgtcggtcgc	ccccgccgtc	ttccccggcg	tgccgcagct	acgcatggtg	gtgtacgtcg	30000
acgaggtgct	gctcaccggc	gagccaccgg	aggtgacgct	gatcgaggtc	gccctcgacc	30060
cagaccggcc	cgacacggcg	aacgcgctgg	tcgcggatgc	tcagggccgg	gtcgtggcca	30120
gccttcccgg	gctgcgctac	ccggtgatcg	accagccggt	cgccccggcg	caggacagtt	30180
ccggcgaggt	ggaggaggcg	gtctccttcg	ccggcctgtc	cgacgaggaa	ctgcacgagc	30240
gggtgttcga	cgaggtgcgc	cggcagatcg	ccggggagat	gcgactcgac	gccgacgacc	30300
tgcatccccg	ccggccgctg	gccgagcagg	gcctcgactc	ggtgatgacg	gtggtgatcc	30360
ggcgacgcct	ggagaagcgc	accgggcgga	gcctctcccc	gaccgtcttc	tggcagcggc	30420

ccaccgtcgc cgccatcgcc gaccacctgg tggagctgtt gagcaccccg caggagtgag 30480 gateegegae gaeagggagg geeegtgegt teegeaeggg eeeteeetge tgtegaegga 30540 tetteaggtg geggggteag eeeggeeget ggteeacege aggggtggeg geeeacteea 30600 ggtggcggct ctcccgcagg gtctcctcgg cgttctgttc gacccgccgc atggcgacgc 30660 gcagcatcgg cggcgccatg accgaggtga cgaccgcgac cagcaccacg atggtgtatg 30720 aggeggtgtt cageacgeec aggegeagee egaceatege gatgatgate tecaeggeae 30780 cgcgcgcgtt gagcccggcg ccgagggcga cgccctccca gtggctctgc cgggccagcc 30840 gtgcacccag gtacgcgccg gtgtacttgc cgagcacggc gagcgccagg atcaccgccc 30900 eggeggegag caccteeggg teggegaggg caegeagate gacceggage eeegetegg 30960 ccaggaagat cggggcgagc acggacagca ccaccgtgcg cagcggtgcc agccgggccg 31020 geteceegtt geegggaagg eegateagga caceegeeae cagegegeeg aagategeet 31080 ccaggcccag cgcgtgcgcc cccgccgcga aggccagcac gatcaccacg gcgacggcgc 31140 tggcggcccc gccgtcgggc tgggcgttcg cccagcgcat ggcgcgccgg gtcaccggcc 31200 ggccgaccag gacggccacc gcgaggtagg ccacgággta aagcagggcg gtcaccacct 31260 gcccggcggt gagggtgctc accgccaccg acgagatgag cgacagcagg aaccaggccg 31320 cagegteete cagegaegee geageeagga tgatetgeee caegtegegg tgeageagge 31380 gcatgtcggt gagcgtcttc gcgatcaccg gcacggcgct gaccgccatc gccacgccga 31440 cgaacagcgc gaagacagtc cgctcctgcc cggccgcgag aagcgccgcc ggggccagca 31500 ggccggcggc gatgcccagg ccgaggggca ccgcgaggcc gccgacggcc accgcgccga 31560 tegtgeegge eegeeggegg accageegea ggteeaggtg eagaceggee aeggegaeea 31620 gcagtacgac gccgaactga ccgatggcgt cgagcaggtg gacctggtcg gggtcggcgg 31680 gcagcagcca ccgtccgatg tcgggtgcca gggcccccag caccgagggg ccgagcagca 31740 ccccggtcag cagctcaccg accaccgccg gcaggccgaa gcgttgcgcc acccgtccca 31800 ggacgacggc gagcagcagc agcaggccca cctggagcag gaacagcagt agctggtggg 31860 agcccagcgg gggcaccggc gcggccacga tcacggtcgt tgttcctttc gtctcgacgc 31920 ccggccgggc ccgccggtgg tcaggccgcg atctcgggcg gcaggtccac cgggtcggcc 31980 gagttcatga aggtccgcag ggcccgcagg tcggcggcgg gcttctccca gcccagcccg 32040 gegeaceaat egatgaggga ggteagetee eeggtggeee gaacettgte eteeteggge 32100 aggetgagea cegacatete ggeeggeeae tgeaceaegt tggeeaggte caegtegage 32160 eccteggece gggegaacte cageaggteg egeagecece agaegttgte eegetggggt 32220 gccacetgga gccagaggtt gaceteegag egggeeegge ggaegttege gatgaaggte 32280 teccaetteg egecetgeeg gateegeteg aacaeetege egtageegte geaggaggeg 32340 ccgatgccga tgctcttgaa gtgccggaac cggtcgaaga ccgactccgg caacacggtg 32400

aggttggagt tgtagacgac gtcgacgttg ccggcgttac ccgtctccac cagcaggtcg 32460 agcagggcga agtggcccgg ctgcatgaac ggctccccac cggcgaagta cagccgccgg 32520 atgaggtggg cgttctcgcg cagggtctgc cacagetcgt cgtcgtcccg gtaggcgtcg 32580 atgacegegg acgaceagge eggeegette ttggegeece ageeegaget gacegggtae 32640 gegeacatea egeacegeag gttgeaggtg ttgeegaace ggatgtegag gaagaaeggg 32700 aagtcctcga cggtgccgtc gggcgcggtg cgggcggcca gccggtcggg gtcggcgatg 32760 teceggaace getggttgat etectgeegg taegacageg egeegtggte etegeggtgg 32820 tagcagtagg agcaggcgtc gacccgctcc ccggccagca tcgccagccg ggtccggcgc 32880 atgttggggc tgttgaaggc gtccgccagg cccatcaccc ggccggggtt gtccgccgcg 32940 tagcgggacc gcggcgagca gccgacggcg tcgtcgttga gcaggaactc cggctcctcc 33000 tectgetegt acagettgtt gtggtacate gagtegteca egeageaceg eeegtagaca 33060 ccgtcgatgg acgcgcagag atggatccag ggcagcacgc acatggtccg ggaccgggct 33120 tccgggtcag tcatgaaagt tgatcacctc ggtggtgggg gcggtgtcat cccggtcggc 33180 cgaccgtctc gacccggggc agcggaaaga tcaaccgggt gccgctggcc agcatctccg 33240 cctcccgggc gacgatctcg tcccggaagt gccagggcag gaccaggtag tagtccgggc 33300 gggccgcccg cgactcctgc tcgctgatga tttcgatgtc cgtgccgagg gtgcgcgcgc 33360 ccaccttgtc cggattgcgc tccgcggcgt accggatgag ctcgcggtct atgccgcaga 33420 actgcaggag ggtgttgccc ttcgtcgacg cgccgtagac gtgcaccgtg cggccctggc 33480 cccgcagctc gcgcagcagg gcgctcacct cgtcacggtg ctggcgcacc tgctcggcga 33540 agegetggta eggggegteg cegtecagee ceagegeeag eteceggteg gegagtgeet 33600 tgaccgaacc gtcggcccgg ccgcccacct caccggcccg ggtgaccacg cagcagatcg 33660 agcegeegtt cacceegttg aggetggeac ggacgatete caggeeegee gegeeeagaa 33720 tgcggctcag cgtggccagc gagtagtagg acaggtgctc gtggcagatg ctgtcgtagc 33780 eggegatete cageategee ggeaggtagg egacetegae cacecagaee eegeeegggg 33840 cgagcagcgc ctcgacctga cgggcgaact ccaccgggtc ctcgacgtcg tagaacatcg 33900 cgatcgaggt gaccaggtcg aagctgcccg cgtgcgggac cagctcgggg ctggggaaga 33960 agtegeggat cagattgaag tegtegggeg egtegtegge ggegetggag gggtegatge 34020 cccaccgctg cgcgtcggtc aggttgccca gcagggtgcc gtcgttgcag ccgatgtcga 34080 gcaccttgcc gggccgctcc cccaacacct cgaccgccgc gtccacgacg tcggcgagat 34140 gccggcgcat cgtgtcgttg atccgcgagc ggtaccagta ggtgtcgtag agcagcccac 34200 ccggcagggt gtgccgcaac tgcaccaggc cgcacgggtc accgccgtcg cgttccgcgc 34260 accgggtcag ctccaggggg aagcgcaccc tgggcgggtc cgacacgccg ggcttcacga 34320

agctgccctg	taggtactgg	gcaccgaggt	cgaggaccgt	acgcagggtc	ccgccacaca	34380
cccggcaggt	ggtccgctcg	accacctccg	acgccaactc	ctcgccggcc	gccgccaact	34440
ggctcacgtc	aggtcctcct	cgtctcgtgc	cggtgtgcgg	gaccaggcgc	cccgtcgtgc	34500
ggtttgctgg	cgaccagcag	gatgtccaga	tagaagggct	ggtcggggcc	ctcgctgcgg	34560
ccgagatgcc	ggaacgcccg	gtcgaggtac	tcgtcgagcg	cgcggggccg	cagccggtcc	34620
accagccaca	gggcgcgcag	ggccagaccc	accgggccgc	cggacggcca	gccgtgctcg	34680
cggccgtacc	agcgcagcag	cagcaacagg	ccgcgcggcc	cgcaggtcag	cttgacggtg	34740
cggtcgacgg	tgaagccggc	ccactcggcc	tggcgggcca	gcccgtcggc	ggtccaccgc	34800
cacaggtcct	ggccgccgtg	ctcctcccac	accccgtggg	tggagagcac	cagccggccg	34860
cccgggcgca	gcagccggta	cgcctcccgc	aggtacgcgt	ccgcgtccga	gacgtgttcg	34920
agcacctggg	tggagagcac	cccgtcgaac	gtcccgtccg	gcaccgggca	gcgcccgtcc	34980
cggtcgaggg	cgtggtcggc	cggcagggac	tcaccgcccg	ggatgtcggc	ggtctgcaac	35040
tcggcggagc	ggaacaggcc	ccggtatggc	gaggtgcccg	cgccgtagtc	gagccagact	35100
cccgtggcgt	cccggaccgc	ctccgccagc	gcgtcgcgca	ggtccaggaa	gtgggcgtat	35160
gcccagtccc	cgggccgggg	ctcgatccgc	tcccggaacc	gttcggccat	cacctcgtcc	35220
agcgacgggc	cggtgggggc	ggtgccggca	ccggtcagca	ggggaccaag	cccgggtacg	35280
cgccgcagca	gggtcaccaa	cgccagtact	cctcgtgcgg	gtaccgcatg	gtggtcggct	35340
ccggcaggcc	ctcccagcgc	cgcagcgacg	cggcgggccg	gtactcgaag	ggctgctcgc	35400
cggcgtgctc	cggtgccgcc	cgccgctgcg	ccaggcagga	gagcagcacc	tgctgcttga	35460
gcccgatgta	ctccggcacg	tgcgggccga	ggtccagctc	gacctcggcg	ggccggtact	35520
cgaagtagat	gacccggcgc	cgcttgccgg	tcaccgccgg	cgcggcgtgc	agcatcagga	35580
tgttgtgcag	catcacgtcg	cccgggttca	tcaccgccgg	caccgccccg	gtggtgtccc	35640
actcggtggc	gttcatccgg	gtggtggtct	cgttcgcccg	gtcggtgtcc	cagtagttcg	35700
actgcgggat	gcaccagacg	cagttgtcct	ccggggccgg	gtcaaggtag	atgccgacgt	35760
cgatcacccg	gcccgcgccg	gtgatgccga	ccgcgttctc	cgggtagagg	ccgccgtcgc	35820
ggtgcca gg g	cagccggggc	gccccgcct	cggtcttgaa	gaccatgctg	tcccaggtgg	35880
ggatgaggtt	ggggccgacc	aggtcctcca	tcgcccgcag	cagcaggggg	tggccggcga	35940
gccgggcgac	caccggggac	ttgtcgacca	cgtactcgat	ccgcaccggc	gccgcgtccg	36000
gctcgtgcgg	ttccagcgtc	cagatggtgt	cggtcatcgt	ccgggtgcgc	caggettegt	36060
cgatcagctc	gtcggccgcc	gcctgcacgg	accgcagctc	gtcggggtcc	agcagcccgc	36120
gcaggatcag	cgcgccctgc	cggcggaagg	cggtcaggtg	ctccggaagc	agcccggtct	36180
cgtggatgtg	gcactcgggg	acggcctgct	cggtgcggac	gtccacagtc	gcgctcatgg	36240
ttcggttccc	ttctgccagg	cggacggttc	gtgctgcccg	gagccgccgg	ccgggcccgg	36300

gctcggtcgg tcggcgacga agtaccagtg ctcccgcagc gcgtcggcga accccgcccg 36360 gtccagcgcc ggctgcccgg cgcggcgccc gggcagggta cgcagctcgt aacccagctc 36420 ggtcacgage agegeeeaca ggteggeget ggtggtgeeg tacteeegea tggegtggte 36480 gccgccgtgc tcgaagacga tcaccggccg ccagcggcgg agcagctcca cggcaccgcg 36540 cagggcgagc acctcgccgc cctcggtgtc caccttgacc aggtcgatcc ggcggtcacc 36600 ggggagcacg tcgtccaggc ggacggtgtc gaccgtcagc tcccgcaggg tctcgtccgg 36660 gcggtcgtag ggacgccggc gcagcccgct gtagccgggg ttggagacca cgtggacgaa 36720 gctgtcccgg ccggtgcgct cggcggcggc ggcggccacc accgtcacgc cggggaagtc 36780 ceggegeage cecteggegt acgaeggeag egectegaeg gecaegtgee ggecaegggg 36840 ggcgacccgc agcaggtgac gcaggatgtc gccggcgccg gccccgatgt ccacggtgtt 36900 ggcgtccggt tcgcagatct gctcgatcag cgccacggtg agctggtcgt accagtcgtt 36960 catcgacage gegeeggeet egteggtege ggaaagetea gtggacateg teaegeteet 37020 cggtccggca cgccggtccg gccccggagc cgaccgccgg ggcggtacgg accaggagtt 37080 ccagctcccg cagctcgatc tcggacagct ccaggccggc ggcgcggacg ttctcctcga 37140 cgactccggg cgactgagcg ccgaacaccg gcaccacccc ggccgggtgg tgcagcgccc 37200 aggccagtgc cacctgcgcg acggtgtgcc cacgctcggc ggcgaaggcg gcgaggccgt 37260 cgaccacgtc gagcagttgg gcgtagtcct caccccggaa ggcgtgcgag taggcccgcc 37320 agtcctcggg ggcgaatgcc tggtcgcggt gcagcgcgcc ggtgagcagc ccgtgggcga 37380 gcgcggagcc gcccagcacc ccgacgccgg cctcctggca gcggggcagc acctccttct 37440 cggcaccacg gtcgagcagg ttgaacggca cctggacgac gtccagcagc ccggtcggca 37500 ccagctcggc caggtcgccc gccgtcacgt tggcgaagcc gacatggcgg gccaggccct 37560 egegeaegaa ceeegeeage aceteggegg teteegegag egggaeggte gggtegggee 37620 agtgcacgga gtacacgtcg acgtggtccg tgccgagctg acgcaggctg gccagcagct 37680 cgtcccggag gaacgcgggg tcgctgttac gcaccgtccg tccgggcggg tcgagcttgt 37740 geogtegeac geogggeogg gtetecagee egeoggeogt ggegateacg atetegteee 37800 ggtgcgcggg caacaggtcg gccagcccgc gggcaagggc cgcctcggcg gccccgccgc 37860 egtacgeccg ggaggtgtcg aaaagggtga egeccaggte gaaggeecgg eggaeggeet 37920 geacgeetgg ttegateege eggeeeeact ggeegeegag egeeeaggtg eeeaggeega 37980 gegeegagae cageggeeee egeteacega tgeagegetg cegeaeggeg teetecegee 38040 cggtgcccca cccacgcccg tcggccggcc gtcacgccgc cggctccccg tcgctgcgca 38100 gcgtcaggaa caccacgccg tcgtgattga tcatcttgtc ggtgaccggc gtcagcccgg 38160 ecteggegge gatgeeggte ateaacteea egeegtgeea gtteaggaae eeettgaaet 38220

ccacggggtt cgcgtcgcgg taccgctcgg cgtaggtgtg gaagaagccg cgcgtgttgt 38280 cgccgaggtc caggaagttg aagcagaaca gcccgccggg ccgcaggatc cgccggatct 38340 gacggaagta gaggaagacc tcgaagacgt tgaggtggat gaacacgttc agggagaacc 38400 cggcgtcgaa cgcggcggtc ggcagcttct ccaggaagtc gttctcgatg tggtggtagg 38460 agacgttete ceggeceteg caggtggege gegeettgte gaggaaggat eggetgaegt 38520 cggcgcagag cacggcgcgc acccggtcgg cgagcccggc cgccatgatg ccctcgccgc 38580 tgccgatctc gaagatctcc gattccgggc cgagcccgag ctgctcgacg accagggcga 38640 cettgtegae aeggteetgg aggtaeteet egegeggetg gtageeggeg agetgeatet 38700 geateteete eggegtgtte eacteeeaga egtagttgag gtegeeggtg eteeggageg 38760 gacageeeeg gggggegtee tgeggeggeg gegtegeetg ettegegteg tteateggae 38820 etcactegeg gtettgtegg getetgeggg gacaactggg egggeggetg eggaaaactg 38880 ggcgggcggt gtcacggacg ccgggcgaac tcggcgacgt cctcggggct cagcgcgccg 38940 gtgtcggcca gccgggccag gagttcggcc acctggacgg cggtcggccc ggtggtgacg 39000 gactcccgca tccgctgcgc cgccacccgg aatcggtggt cgtagaggac ggagccgagg 39060 gcctcgtcga cctcctcgcg ggacgccttc aggccgggca gcgtcttcgt cgcgcctgc 39120 gggtcgagcc gccgcccgta gatcagggcg tcgtagttga gcgccagcga caactgcggc 39180 acgeceatgg egagecegtt catgtageag ttggegetge egtggtgeac cageaagteg 39240 cagtegggga ggatgagete cagegggeag ttgetgagea eeegeaegtt eggeggeage 39300 gegeceagee cetecacete ggaggaggeg geggtgatea egacetecae geecegetgg 39360 gcggcggcgt cgacggcgtg ccgcagcgcc ggcacctgcg cgccgaacac gcccgtggcg 39420 gagttgcccc acaccacgca gacccgcttg ccccggcgcg gaccgagcag ccaggggtcc 39480 acgtcctggg agccgttgta gggctggtag cggatcggga tccgcagcgc gtcgcccatc 39540 ggcgggatcg ccacgtcggg cgacgggtcg atggcgtacc ggatctggtg ccggctccac 39600 tegacgeegt aettgeggaa eteggteaee gggtegeegg agaceaggte gageeeggge 39660 teggtetega tggtgeegat gaaceeggge gagaagtaga egetggggat gtggtgeage 39720 teggegacea gegegeeete eaeggeeatg atgtegtgga eeaeeaggte gggeeggtag 39780 tgggcggcgt agtcgaccgc gttgtcgtag ctgcgctgga ccgcggtgac cgtgcgcttc 39840 cagtagtcgg cgagcaggtc ggtgtcgaag tcggcgagcg agtccatcgg ccggcccgtg 39900 aaggggttca acggcagcgg ttgctccacc atgtgctgcg gggtgtagag ggcctggacg 39960 tagaagccca geegggeget etecateatg tegggteegt egageacega gaegggeate 40020 atgcccgccg cggccacgcc ccggacctgg gacggcgaac aggcgacctt gacgtcgtgg 40080 eeggeegeee geagegeeea ggeeagegge accatgeaca tgtagtgeee ggeeeagttg 40140 gacacggtga acagaacctt catcgcagcc tctctgtggc ctgccgaggg gaggttgggg 40200

40260 gtcgcggccg gacggtcagg aggtcaggac cggcaactcc cgcgcgggat cggcgaactc gatcacgatg gtgcgccgcc actggtcgga ggggttcggc ccggagccgt gcaccagccg 40320 tacgtcgtgg acgatgaagt ccccctcctg cgaggggacc ggcacccgcg gcccggcgtc 40380 gcgcacggcc gtgacgtcgg cgtcgtcggg cagcaggtgg gagccgggca cgccctccag 40440 acagoogtto tooggooogg oggtgtocag goagatgotg atgttgcaga cogogtgogg 40500 ggggacgttg acceggteec ggtgecaegg caegeeggee gecegeagtg geteettgag 40560 caccaacgeg aaggeggtgg gcacgacegg ggtgccgagg acgtcggcgg ccaccgcggc 40620 gateteegge eggtgeagea actegeeetg eggeeagtee tgettttega ggttgtggat 40680 ceggtacage aceggeteeg egecetegae etegtagtte eagtagtegg egttggeeeg 40740 cgccggaccg gcgaaccggt cgatcaggct taccgcgccg gccttgagct gggccagcac 40800 ctcggggtcg agcaccggcc cgacgtgcgc gatcccgtcg ctgcgggaacc ggctggccac 40860 ggcctcgcgc tcccgcgaca tggtggtcat cggaggctca ccccttcggt cggtcggcgc 40920 gtgccggtgc ggcggccgac ggcgatgatg tcgcacacct ccggcgaccg gcgctcgtgc 40980 agcaceteca ceteggegaa geeggegttg tgeagggegg egaacaggga eteceggteg 41040 agccagegea egtegaeget gageceeegg geetgegget eggggtgete etegeggaee 41100 tgcttgaccg tgtagccgtc gatcggttgc aggtcgccca cgcctcccca gtagtgggtg 41160 gagaggtaga ttcccgccgc gacgcccgcg atgtccttca gcagggtcca cggctcacgc 41220 acgtggtaga gcaggcccgc gcagaggacg gcgtcgaact cgcccagctc ggtgaagtcg 41280 atcogotoca ogtoggogao gegoagotoc aegttggtga tgeogttgac otocateaco 41340 ageteegege ggegeaggtt eteeggaegg ceeteeaggg caageaeegt egtgeegggg 41400 tgccgggcga gggcaagcgt gtccgcgccc tccagtgcgc cgagttcgag gatccgccgc 41460 gcgtcgggaa acgcaccgaa gaacttcgcg gcccggtcgg ccggggactg gctcagcaga 41520 taaccgtgct gggagccctc ggcgtaacgc actccgtcgt gctcgaatcc attcacccac 41580 ggctcgagcg cggcgacgcg gcgacgaatc tcttcacggt ccatgggatc aaagcctagc 41640 gatgccattg cggttgcgga ctagtgtttt catcatattc agcggctcgc cgtgctgagc 41700 etttegttga ccageeggge ccatteegga ateeggteee egeegatete gatategaag 41760 gacgactgga gttccgccgg cccggcgtcg gccgcccacc tggcggtgcg ggccagtccc 41820 teggecageg gggtgteegt ceagtegeeg aagacegate gggecagete egtegeggtg 41880 tacgcggttc gcacctcgtc ccgcgacggc aggtgggcga tcggatgctc cggcacgccg 41940 geogeogace gracegootg ggocagetee ageaeggtgt tggtgetega egageocaeg 42000 ttgaatgccc gccccacgc ggcctcggtc tcggcggcgc ggctgaccac gttcaccacg 42060 teacegaegt aegtgaaege geggaeetgg eegeegtege egtaeaeggt gateggeteg 42120

cctcgcagga	tctggttgaa	gaagatggcg	accgcgttgc	ggtacgggtc	ccgcatgttc	42180
tgccactcgc	cgtagacgtt	gtgcatgcgg	aaggcggtga	agggcagccc	ctgggtccgc	42240
atcgtcacct	ccagctcgcg	ctcgaccagg	tacttggcca	ggccgtagct	gtccgcgggg	42300
acggggacga	cggactcgcg	catcggcgtc	tegeegtgge	cgtagaccgc	cacggaggag	42360
gcgaaacaga	agaaccgcac	gccggtacgc	agcgacgcgt	tgatcagatt	tatgctgccc	42420
atcacattgg	tgccgtagtt	gagctgcttc	accgaatggc	tgatcgcctc	cgccgcgaag	42480
gcggcaaagt	ggaagacccg	ctcgaatcgg	ttctcggcga	acagtgaatc	gacgaagtcc	42540
acgtcggtca	ccgaaccgac	ggccaggtcc	accccggccg	gaacccgctg	ccggctgccg	42600
ccgctgaggt	cgtccagaac	ggtgacccgg	tgcccattcc	tgaccaatga	ctccaccagg	42660
tgcgagccga	tgaatccggc	accaccagtc	accagacaac	gaaccatccg	gggctccttc	42720
gtcaatagat	ccggaaaggg	ttgaccgagc	gggcgatctg	cggcgcgccc	ttcgtcggcg	42780
aacaccgacc	cccgagagaa	agcttcgcct	cagggcaccg	gcgaccggtc	ggcctgcttc	42840
ttcagcggct	cccaccagtc	ccggtgcgtc	cggtaccagt	cgatcgtctc	ggccaggccg	42900
tcggcgaagg	cgacctcggg	ccggtagccg	agcgcccgca	gtttcgcgtc	cgtcagcgag	42960
tagcggcggt	cgtggccctt	gcggtccggc	acccgctcga	cccggtccca	cccggccccc	43020
aaggcgtcca	gcagccgccc	ggtcagctcc	atgttggaca	gctcagccgt	gccggcgatg	43080
tggtagacct	cgccggggac	accgcggtcg	acgacggtct	ggatgccccg	gcagtggtcc	43140
gtcacgtgga	tccagtcgcg	gacgttcccg	ccgtcgccgt	acagcggcac	ccgtcgcccg	43200
ttcaacagct	cggtgacgaa	cagcgggatc	agcttctccg	gaaactggta	cggcccgtag	43260
ttgttgccgc	accgggtgag	gcagaccggc	agcccgtggg	tgcgggcgta	ggccagggcg	43320
atcaggtccc	cgccggcctt	cgccgccgcg	tacggggagt	tcggcgccag	gggggtgtcc	43380
tcggcccagg	aaccctcgtc	gatgctgccg	tagacctcgt	cggtggagac	ctggaccacc	43440
cgggcgaccc	cggcgtcgag	acacgcctgc	atgagcgtct	ggacgccctg	cacgttggtg	43500
cggacgaact	ccgccgagtc	ggcgatggac	cggtcgacgt	gcgactcggc	ggcgaagttg	43560
accaccacgt	cgtgcccggg	cagcacctcg	gccagcagcg	ccgtgtcgca	gacgtcgccc	43620
tggacgaagg	tgatccggtc	ctggaccggt	tcgaggttgg	cgaggttgcc	cgcgtacgtc	43680
agcttgtcca	gcaccgtcac	ccgggcctgc	gccgtgtcgg	ggtaggcacc	ggtggccagg	43740
tcgcggacgt	actgcgagcc	gatgaaaccg	gcaccgccgg	tgaccaggac	gcgacgcatc	43800
agacccccac	ccggacttcg	ctgtgatcgc	cgaggacgaa	ccggtgcgtc	ttgggcaccc	43860
ggggcccggg	gaccacccgc	gcctcccggc	cgatcatcga	gaactcgatg	cggccgatgc	43920
cctcgatgta	ggcaccgcgc	agcacgatgg	agtgctcgat	ctcggtctcc	agcagggtgc	43980
agtcgcagtc	gatcgaggtg	tacgggccga	ggtaggagtt	gcggatgatc	gagccggctc	44040
cgaccaccac	cgggccgacg	atccgggagc	cgctgacgtc	ggcgccggcg	ctgatcacca	44100

ccgggccgat	cagttcggtg	cggtcgtcga	ccttgccctc	gaccaaaggc	tcgacgctgc	44160
cgaggacgaa	ccggttcatc	tccagcatgt	cggcgaggtt	gccggtgtcc	ttccagtagc	44220
ccgtgatcat	ggtggagtcg	acccggtggc	cgcggtcgat	catccactgc	accgcgtcgg	44280
tgatctccag	ctcgttgcgc	caggacggct	tcagctcggc	cacggcatcg	tggaccaccg	44340
ggctgaagac	gtagaccccg	accagggcca	ggtcgctctt	ggggtgctcg	ggcttctcct	44400
ccaccccgat	cacccggccg	tccgcgccca	tctcggcgac	gccgaaggcg	tgcgggtcgg	44460
cgacccgggt	cagcatgatc	tgcgcgtgcg	gtcgctcctg	ccggaagcgc	tcgacgatgt	44520
ccttgatccc	gccgacgatg	aagttgtcgc	cgaggtacat	gacgaagtcg	tcgtcgccga	44580
ggtagtcgcg	ggagatgagc	acggcgtgcg	ccagcccccg	gggagcctcc	tgcggaaggt	44640
aggtcacctg	gaggccgaac	tgggaaccat	cgccgaccac	gcgctgaatt	tcgggcgcgg	44700
tgctgccgac	gacgatgccc	acctcctcga	taccgccctc	acgaatagcc	tcgagcccgt	44760
agaacagcac	cggcttgttg	gccacgggaa	tgagttgttt	ggcggacgtg	tgggtgatcg	44820
gacgcaatct	cgatcccacc	cctcccgcca	ggaccagcgc	cttcacgaac	gccctcgaaa	44880
ggatgggacc	gagacgggtc	gctggttcac	gagcactcca	ggggtcacgg	tggactgggc	44940
tcttcgtgaa	cgtaccgaag	gatcactcgt	gatttcccta	cttatgggcc	accgaggtgt	45000
gatcggtgga	tctctatgcg	tccgccattt	ccgcaaacgg	gggcctggcc	ggcccgccgc	45060
cgaccagttc	gagcacggcg	gccaggccgt	gcacggtgtc	cggcgggctg	gccggcagca	45120
gcagggtctg	caggccggcg	tacaccgccc	caccgtcggc	cagggtgtcg	cccaccatca	45180
gcgcccgctc	cggggcgacc	ttcagctcgt	cgcaggcggt	gcggaagatc	cggggatcgg	45240
gcttgaccgc	ccccacctcg	tgggagaaga	cgtaggcgtc	caccagctcc	gccatcccgt	45300
acgccgcgaa	ggtgggccgc	aggtcccagg	cgatgttgct	gaccacggcg	gtgcccacgc	45360
cgcgccggcg	caactccgcc	aggaccgggg	cggcgtcgcg	gtagggcagc	cagccgtccg	45420
tgcggaacag	ccggtcgtag	agcgcctcgg	cgaggccggg	atggggcagg	tcgacggtgg	45480
agagcaggcc	cacgtacgcg	ctgcggtgcg	tttcgggcga	gaggtcccgg	cgggcgtaca	45540
cctcggcgag	ccccggcggg	acggcgtgcg	gctccggccc	gccgggacgg	ccggccgcca	45600
gcagcaaccc	ggtcagggcc	tcctgctgcg	ccgggtcgag	ctggacgccg	acggtggccg	45660
ccgccgcccg	cagccaacgc	tgcggcagtt	ccacggcgaa	cagcgtgccg	gagaagtcga	45720
acaggacggc	gtcgatcgga	cggggcaggg	gggtcgtcat	cgctctcctc	ggtgcagccg	45780
cgtcagggcg	gcaccagcct	ggcagcggac	cagccggatg	tccatcatgg	aggaatgcgc	45840
cgggtcgggc	gcgcccgcca	tggccgccgg	tccggacgac	aggcattttc	ggtcactctt	45900
gccttctagg	cggatttctt	caaagatggc	tgtcaattct	tcagcgatcc	tggaggcatc	45960
cgtgacccgt	acccgaaccg	ccctgcgccg	gctgctcgcc	gccggtctgg	ccagcctcgc	46020

caccgctgcc	gcgaccctcg	tcgccaccgc	cggcccggcg	gcggccgcca	ccacccccgg	46080
catcgacgtg	tcccactacc	agggatcgat	caactggacg	agcgtccgca	acgcgggcat	46140
ccagttcgcg	ttcatcaagg	ccaccgaggg	tacgagctac	aaggacccca	acttcaacgc	46200
caactacgtc	aactcctaca	acgccggagt	gatccggggg	gcgtaccact	tcgcccggcc	46260
gaacatctcc	tccggcgcca	cccaggccaa	ctacctggcc	agcaacggcg	gcgcctggtc	46320
ggcggacagt	cgcaccctgc	cggccgcgct	ggacgtcgag	gccaacccgt	acagcggcgg	46380
cacgtgctac	ggcctcagca	cgtccgggat	gcgtagctgg	atccaggact	tcctgaacac	46440
gtacaaggcc	cgcaccggcc	ggtacgcggt	catctacacc	accacgagct	ggtggaacca	46500
gtgcaccggt	agctggaccg	ggccgtgggc	caaccacccg	ctgtggctcg	cccgctggtc	46560
gagcaccccg	ggcaccctgc	cggccggcgc	ttcggtctgg	agcttctggc	agtacacggc	46620
ctccggcagc	gtctccggga	tcagcggcaa	cgtcgaccgc	aacaactgga	acggcgaccg	46680
cacccggctg	atcgcgctgg	cgaacaacac	ctgacccgaa	cgcccgggta	ggcggttggc	46740
ggcagcggaa	ccgattgcga	ccgtacggtc	ggcggccggt	ccggctgccg	ccagcccgtc	46800
acccggcccg	cgtcgcgggc	cgcgccggca	tccggtcctg	ccggcccggg	gtggcccgcc	46860
gtgccatccg	ccaggcggcc	acgcctgcga	cggcgccggc	cacgacaccg	aacagcgcga	46920
acagcaccgg	aagacccgcg	ctgaccagca	gcagcaccac	gtcgccgaag	gcgacgagca	46980
tccacagtgc	cagcccgggt	cgagcgtccc	tgcgtcggtg	tcccatgtcg	cacctcctcg	47040
catcgtccgg	gatcagatac	cccgttcgac	gcaagtacat	gcgaatcgac	atcgcaacgg	47100
cgggaatcgc	ctgctcagcg	ggccgagtcg	gcaatggacg	gccccggccg	ggcgctcagt	47160
cgacccggtc	cggcttgaag	cccttggcga	tccggtcgaa	gtcggccagc	cgcgcctgcc	47220
agtccttgtt	cgccacctćc	caccggaggg	cgtacccccg	gttgctggcc	gtgacgaagc	47280
cccggttgcg	gacgtggatc	cgagtgccgt	cccggttctc	caaccactcc	cagtccgcgc	47340
acgtcttgta	gtagtcgcag	cgcttgatgc	tcagatactg	gtagccgttg	acgtagttct	47400
tccgggccgg	ttccttctct	ttccagtcgg	cgtaggcgtc	gccctccggg	gtgctggtcc	47460
actgcaccag	cagctcgccc	accccgtcgc	gctcgtcgaa	gacgatcgtg	ttctgcccca	47520
cgctgcgccg	cacccagccc	ttcggcaggg	gcagcgagaa	gcccgccggg	tccttgtgca	47580
ggagccaacc	ctcgggcagg	gcgttcgggt	ccacggacgg	gctggcagac	ggcgtcgggc	47640
tgggcggagc	cgcgctgctg	gtcgccggtg	cggccgacgg	cgtcggcgtc	gacacgcccg	47700
cctgcgggtc	gccgccgggc	cccgggtcgt	cgtcaccgct	ccggccgagc	agcggcaccg	47760
ccgccagcag	gccgatcagc	agcaccgcga	cgagcgcgcc	gaccagcagg	ccgcggcggc	47820
gacgctcggg	cttcgtgccc	ccgacgacgg	tggcccggcc	cgtcgacgag	agtgccgggc	47880
cggaggcggc	cggcagcacc	gacgtcgggg	cggcctcctc	gcggggcgcg	acggcgggct	47940
cgcgggccgg	ggcgggcggc	gaaacgggca	cagccgcgcc	cggatcgacc	cgggtgtcgt	48000

cggctcgggt	gtcgtcggcc	cgaccggccg	ccggggcccc	gtcggcccct	tcgtccccag	48060
cctcggcggc	ccggtccgcc	ggcggcccgt	cactccctcc	ggccggcgtg	cccgcagcct	48120
cgtcggcgct	ggtcgcggcg	tcgggggcgg	ggatcttcgc	ggtgggatcg	gccgcctgcg	48180
ggccgaagtc	ggtgaccttc	gcggtcggat	cggcgtcggc	gctcggcagg	tcgaccatcg	48240
cggtcggcgc	ggcgtccacc	cccgccggga	ccttcgcggt	cgcgtcgccg	ccgcccacgc	48300
cggccgccgc	cgcgccaccg	gcggcaagac	caccttccgg	ggtacgcggt	gcgggcgggg	48360
ccgccggccg	gccggtgcgc	tgttcggcgg	ggcgcggtgc	gggcaccacc	ggcggtcgcg	48420
gctcgcgcgg	gccgttcggc	cccggccggc	gtacgccgtc	gagcagcgag	atggtcttgg	48480
cgcgacgccc	ggcggcccgc	cgcaggagcc	gctcggccac	ctcggcgtcg	atccgctcgg	48540
ccgggtcctt	gcggagcagc	ccgttcagca	ccggcttcaa	cgggccggcg	ttcctcggcg	48600
gcggcatcgg	ctcggtggcc	agcgccgcca	gggtggcgat	cgccgacggt	cgggcgaacg	48660
gcgacttgcc	ctccaccgcc	gcgtagagcg	tcgcgcccag	cgaccagagg	tccgcctccg	48720
ggccggcggt	gccgtcccgc	gcccgctccg	gggcgatgta	cgccggggag	cccagcacca	48780
ttccggtccg	cgtcacgttc	gggtcaccgg	ggatggtcgc	caggccgaaa	tcggtcagca	48840
ccacccggcc	gtcggtgccg	agcagcacgt	tgcccggctt	gatgtcccgg	tgcatgacgc	48900
cggccttgtg	cgccgccttc	agcgcgccga	gcacccccag	gccgatctcg	accgccttgg	48960
ccggcgacac	cggcccgtcc	tccgcgagag	tgtcctgaag	ggacttcgac	gccacgtact	49020
ccatgacgat	ccacgggtcg	ccgtcggtgc	gcagaacgtc	gaagatgcgg	accacgttga	49080
cgtggttgag	tcgcgcgatg	gcacgggcct	cccgcagcga	gcgttcccgc	atctcgcggc	49140
gctcctccgg	ggtgaggctg	ggcggcggga	ccagttcctt	gatcgccaca	tcccggtgca	49200
gcacctcgtc	gcgcgccttc	catacccgac	ccatgccacc	ctgaccgagc	ggcgaaatca	49260
gccggtaccg	gtcggcaacg	agttggggaa	gcgcgttcga	catcggtgga	gacggtaccc	49320
ggcggcggcc	cgccgcacac	cgccggcacg	ccactgtgcg	acgaaggtca	agttcgcgac	49380
gcgtacgctg	aacggcatgt	ctgccgaaga	gccgctgttc	cgggtgaccc	ggggcgttcc	49440
gaccgccgag	gaactggccg	cgctggtcgg	cgtcatcgtc	gcccggaccc	gctccgccgc	49500
cgctcacgcg	cccgccgcgc	cgtcggcctg	ggcacgcagc	ggtcggcccg	gcggtacggt	49560
gctcgccgct	cgcccgggag	cctggcgcgc	ctccggtctg	ccccgctgac	gcactcgcca	49620
gcatgtggcc	agtgtggccc	gccgccgagg	cgggtggcgg	cgggggctcc	cggaggtcga	49680
cgacacccgt	taacctcact	cagggagacg	atgccgtgac	ggatagggag	ggtcgatgat	49740
tcccgaggag	gaccgaccag	caccctggtt	gagcggctac	ggcagcatcg	aggccgacat	49800
ccgccagatg	cgcgagttcg	ccgacaaact	ccaggcggag	gtcgagcgga	actacgcacc	49860
gcatctgtcg	tacatagcgg	acgacatgaa	ggcacagatc	cccaaccccg	ccgacgcctt	49920

cgtcgaactg	gtgcagttcc	tcaaggcgca	caacgagacc	cagcaggcca	ccgccacgat	49980
ggtctggtcc	gtcggtgggg	ccaccggcca	cctggccacg	gcagccggcc	ggatcgccga	50040
gcagtacgcc	gactccgacg	ccttctccgc	cgctcgcgtc	tccgacgtgg	agcgggccct	50100
cgccaacccg	ggcgcggcgg	ggcagggccg	ccccacgccg	gctctgcccg	acccgaccag	50160
cccggacggc	gggccggggc	gggtggtgct	gccatgatcg	agcggggcag	cggccggacg	50220
tccggcctca	ccgactggcg	gctgatggac	ctgctgagca	tgtgggcgtg	catccaggac	50280
cacgagaccg	ccgggcactg	gaagcaggtc	gccggctggc	gcaaggtttg	cgacctcgcg	50340
caggcccacc	tgggccgcct	caaggagtac	cggcgcggcc	tggccgaggc	gtggccaccg	50400
gcgaccaacg	ccgccgcccg	ggcgtacctc	ggcgaactgg	acgacctgat	cgacaaggtg	50460
caacgcaccc	acgacgcggc	tgccgcgaac	tacgacgccc	tcgcggccgc	cacccgagcg	50520
atcagcagcg	cccgcaccga	actcaagccg	ctacacgacg	agtacgtgga	gaaactccag	50580
cagaagcggg	cgtacgaggc	gactaccgcc	gatccgaagg	cgctgatggg	cagccggctg	50640
ccggacaagc	cggtgactga	cgccgacctg	gaacgactca	acgcccaggc	ccggaacctg	50700
atgtacgggt	tgagcggcga	actccaacag	gcccaagcaa	tgctccgcca	acccctcct	50760
ccgcaccgcc	caggacgaca	gccgaacaac	ccggatgctt	acgagagcac	aggcacgcct	50820
ccggtcatcc	cgcccgtatt	accagtccca	accattaggc	cttcaattcc	ctcaagcgct	50880
cagcaagcag	agccacgccc	tgttcctgtc	cagagcgcac	cccaaacagg	tcctgtactc	50940
gggggaatcg	ggacgggaaa	caccacttcg	ccatcgggct	ccatttctcc	cggcaccggc	51000
cacccagtga	catccaaccc	ggcaggaggt	gctggcccta	ccctcccgcc	gaacttgcca	51060
cctgccatcg	ccccactgg	acgaggcagc	acaaccggcc	aggtaggaaa	ccagccccgc	51120
tcaaccacgt	cctcacgacc	attcttgcca	ggcggcctga	tcggcggcgg	gcccgcgatg	51180
gggattaatc	aaccccttgg	caatactcct	ccgcgaagga	tcaacccaat	tggaggggtg	51240
atcgggggcg	gtggggctgg	aacctcacca	accggcgctg	caggcactcg	cccgggctcg	51300
ggacgtggtc	cccactttaa	cctgacccct	gcggcgcctc	cgaatggcgc	accgcaaggc	51360
gtcgtaaaca	ccttaggtct	gaatggtgag	ccgtcacgct	catcccaccg	cgagcaaggc	51420
gatactgacg	gccgctactg	ggatcccgac	catccatggg	caaccagcga	gggcgttcct	51480
ccagtagtcc	gcccgcccga	ggcggaggga	ccaatcgacc	cagggccagc	tattggcttc	51540
gaccggtgaa	aaacgctcct	ccagcgggcg	ctaccttcac	cttcctagca	acattgatgg	51600
ttgcatcagc	gtacgccccg	agcgccgtgc	gtgcgagtcc	tgaaaccgat	ggtgccttgc	51660
gaatacgggc	tgaccagtgg	caccttaact	acctgaaggc	ggcggaggct	cagaagctgt	51720
cactgggaga	aggggttgta	gtagcggtcc	cggatactgg	cgttgatcca	caccccgacc	51780
ttcagcgcaa	tctaatcaaa	gggattgaca	tcattcccgg	gggcaatgga	gatggccaga	51840
aagatcgcaa	cagtcacggc	actagcatgg	ctggactaat	cgcagcccac	ggacagggcc	51900

agagcggcgc	cttaggcata	gcacccagag	ccaagatcat	gccaatcctg	tcttccgcgt	51960
cgaacaacct	cggtgatgca	gacggcttgg	ctgcgggtat	agaatttgca	atctcgcatg	52020
gggcggatgt	catcaatgtc	tccagcggag	gcggcgccag	cgttcgactc	atcaaggcaa	52080
tcagagaggc	ggtcgccgca	gacattgtag	ttgtcgcagc	cgccggaaac	agtcccgaag	52140
acatgacaat	tggctatcca	gccagcgagg	aaggagtcgt	cgcagttggc	ggaattgatc	52200
gacagggaga	gcatgcttca	gtttctgtcg	tcggaccgga	agttgactta	gtcgcaccgg	52260
cagtcgacat	ctacagcacc	agttacgacg	ggaagtactc	caaaggcacc	ggtacgtcca	52320
gtgccacagc	gatagtcgca	ggggccgctg	ctctggtccg	atcgaagttt	cccgacctgc	52380
ccgcctcgga	ggtcgtccat	cgcctcactg	ccaccgccat	cgacaaaggg	ccgccagggc	52440
acgacgacca	gtacggctac	ggcgttatcg	acctggttgc	cgcgcttacg	gcagacgtac	52500
ccccggtggg	ctttgagtcg	gcgacggcgg	acgtgcccga	cgtgcctggg	tcgaccacga	52560
cggcggtcgc	cgagccggca	ggcgagggtg	acgatggggc	aacggcccga	ggtctggcca	52620
cgttgggagt	gatcgtggct	gctgcgggcg	cttgggcgct	ggtcgctcga	cggcgtaggt	52680
tgagcgacga	cccgcccccg	cggatcagcc	ggtgaccagc	cagccctgac	gccatgtcgg	52740
cgacattggg	gggtcggggt	gggtgggata	ccgctatttg	gccgacatga	agtcgatcaa	52800
cagcgatcaa	caggcagtgt	gatcggcggg	ggtcggtcga	cggccaggcg	gcgtcgacgg	52860
aggcggggga	agcggtagcg	tcggcgacgt	gccgaactcg	atttcactcc	gactcgtgct	52920
cgcgtcggcg	agccctgccc	gtcgcaagct	cctccacgcc	gccggcatcg	aacccgacgt	52980
gctggtcagt	ggggtcgacg	agtcccaggt	gaccagcgag	cgagccgagg	atctgtgcct	53040
ggagctggcc	cgcctgaagg	cgcaggcggt	cgtcggccgg	ctgcgcccgt	cggccgacga	53100
gcggacgctg	gtgctcggct	gcgactcggt	gctcgccttc	gaccgcgaga	ttctcggcaa	53160
gccggccgac	gaggcggacg	ctacccggcg	ttgggagcgg	atgcgggggc	gcagcggggt	53220
gctacacacc	gggcactgcc	tgatcgacgt	catccacgag	acgcgcgccg	aggcggtcgc	53280
ctcgaccacc	gtgcgtttcg	ctgacatcag	cgacgaggag	attgccgcgt	acgtcgcgac	53340
gggcgaaccg	ctcgcggtcg	ccggcgcgtt	caccatcgac	ggaatgggcg	gggcgttcct	53400
ggagggtgtc	gacggcgacc	cgggcacggt	ggtcggcctc	tccctaccgt	tgctgcgccg	53460
gcttctcggc	gagctggacc	tgcggatcat	cgacctgtgg	acgaaggtcg	cgccgggcgg	53520
ccaggcggtc	gaggcggtgg	gtacggtcca	gccatgacga	cgaagtccct	gccgctgacc	53580
ccggaactgc	atgcgtacgt	ggtggcccac	ggatcggacc	cggacgaggt	gatgcgggat	53640
ctgatcgagg	agaccctcgc	cgcgctgccc	gccgaggcga	ggatgcaggt	ggccccggag	53700
caagccgcgt	tcctgacgtt	cctcacccgg	ttgatcgggg	cgcggcgggc	ggtggaggtg	53760
ggcaccttca	ccggcctgtc	ctccctggcg	atcgcgcgcg	ggctggccga	gggcgggcgg	53820

ttgacctgct	tcgacatctc	ggaggagtac	acgggcgtcg	cgcggcggta	ctgggcgcgg	53880
gccggggtgg	ccgaccagat	cgacctgcgg	atcgggccgg	ccggggacac	gctgcgcggg	53940
ttgccgtacg	aacggcacct	ggacttcgcg	ttcatcgacg	cggacaaggt	cggctacccg	54000
gtctactggg	cggagttggt	gccccgcatg	ctcccgggcg	gggtcatcgc	ggtggacaac	54060
acgttgcgcg	ggggccgggt	gctcgccccg	cgtgacgccg	acgaccgggc	catcgccgcg	54120
ttcaacgacg	aggtgatggc	cgacgtccgg	gtggagccgg	tgctgctgcc	gatcgccgac	54180
gggctgaccc	tggcccgggt	gcgctgacgg	gcgccagccg	gacgatcgtg	ccaggtcgcc	54240
ggcccggcgt	cgtgtgtccg	cctcaccggg	tcgacgaggg	ggtgaggcgg	ggcggggtgt	54300
taggaagggg	cccttcctat	accgaatgcg	ttaacaaggg	gcccctcctt	acacctcaac	54360
ctcagcgcac	gctgcgggcg	aactggcggg	cggcccaggc	gacgccgacg	gcggcaagca	54420
ccgcgatgat	ggtcaggccc	tgccagacct	tgtcgttgcc	gaggtcgccg	gcgaagaggg	54480
cccgggtgcc	gtccacggcc	caggagaacg	ggttccactc	ggcgatgcgc	tggagccagc	54540
cgggggcgaa	ggtgagcggc	agcaggatgc	cggagagcag	cagcaccggc	tgggcgacgg	54600
tgttcatcac	cggggcgagc	gcgtcctcac	tcttgacctt	gagcgcgacg	ccgtacgaga	54660
cggccgaggt	catcagcgcg	atcagggcga	gcatcaggta	cgccagcagc	aggtcgccga	54720
tgaacacgcg	cagctcgaac	aggagcgcga	gcagggtgat	gatgacggcc	tgggcgagca	54780
gcgacacgac	gtcgcgcagg	gcccggccga	gcagcagcgc	gagccggctg	accggggtga	54840
cccgggaccg	ttcgatgacg	ccggcgcgca	gctcggcgat	caggccgaag	ccctggaaga	54900
ggccgccgaa	gatggccagc	agcaccagca	ggccgggcac	gaagatcttg	tacgcctcgg	54960
cctgggtcgg	cgcgttcagc	gcgggcttga	gcagcggggc	gaagaggagc	aggtacatca	55020
ccggctggaa	gacgccgacg	aagacccaga	ccggattgcg	gagcaggagt	tgcatctggc	55080
gctgggcgac	gagccaggtg	tcgcgggcga	acttcatgat	cggactccgg	gtggtcagga	55140
ctcgcgcagc	gagcggccgg	tcttggtgag	gaagacgtcg	tcgaggctgg	ggcggtgcag	55200
ctcgatcgag	ctgagcctga	ggccggactg	gtcgagccgg	cgcaggacct	gcgggatggc	55260
ggtggccccc	tcgtcgacgg	tcaggcgcag	gccgccgccg	tcgacggttt	ccagcttggt	55320
gacgtacggc	tcggtgtcga	gcagttgggc	ggcctgcggg	gtggcggcgg	cgtccagccc	55380
gacgagcagc	acctcgccgg	agatctcccg	cttcagcccg	cccggcgtac	cctcggcgac	55440
cacctcgccg	tggtccatga	tcgcgatccg	gtcgcagagc	gcgtcggcct	cgtccaggta	55500
gtgcgtggtg	atgaagacgg	tcatcccctc	ggcgcgcagc	cgacggatct	cgtcccacat	55560
gtgggcgcga	ctctgcgggt	cgaggccgct	ggtcggctcg	tccaggaaga	caatgcgggg	55620
gtcgtggatg	atgccgagag	cgatctcgac	gcggcggcgc	tggccgccgg	agtaggtctt	55680
gcacttacgg	tcggcgtact	cggtgagctg	gaaggcggcc	agtgcgcgct	cggcgcggcg	55740
gagggcgtcg	gccttgccga	tgccgtacat	ccgggcgtgc	aggaccagtt	cctcgcgggc	55800

ggtggagtcg	tcccaggtgc	tgccgccctg	ggcgacatag	ccgatccggc	gacgcacctc	55860
ggccgggttc	cgcagcaggt	cggccccggc	gatggtggcc	tggccgccgt	cgggggtgat	55920
gagggtggcc	agcatccgca	gggtggtggt	cttcccggcg	ccgttggggc	cgaggaaccc	55980
gaagatctcc	ccctcggcga	cgtccaggtc	gacgccgcgc	acggcgtcga	ccgtcttgtg	56040
ctgtcgaccg	gcgcgggagc	gaaacgactt	ccgcagccct	ctggtctgga	tcatcttcgc	56100
tcctggtcgt	ccttagccgg	accgggccgg	ccctctctcc	gggacgccac	gccacacggg	56160
tggccccgaa	cgtcgcgccg	aggctaacgc	gatataactt	ctctagtcaa	ctttgattaa	56220
tggcgaccgt	cggccccctc	ccccacgttc	cagccgtcct	gactggccaa	cccttcgggc	56280
agatacggca	cgccggcctc	gatccggtcg	gcgacccgct	cacaccaggc	cacctcgacc	56340
tctccccggg	caatccacag	ctcgtacatc	cagctcacgc	cgaccggctt	ggagtcgcgg	56400
atccaggagg	actccatcga	ggcacgcatg	gtttcgacac	tggcccgcag	cacctgcccc	56460
cgactgcgca	gcgcggccac	cgcctccggc	ctgggcagcg	ccggcaggaa	cgcgaacgcc	56520
gccacgaacg	gatcgctcgt	ctgatgattg	ccccaccaca	ggccgcgcag	cagcgtctcg	56580
aactcgtcga	ccccttcgg	ggtgatctcg	tacgtcgtcc	gcgcccgccg	ggcgccgacc	56640
tgctcggtgg	cgacctcgcg	gagcagcccc	tcctcgccga	gcttgcgcag	cgcgtggtag	56700
atcgagccgg	gctgcacgtt	ggcccacttg	tcggcacccc	aactgagcag	ctcgcggcgg	56760
acgtcgtagc	cgtgcaccgg	ctgcatccac	ttgaccaggc	cgagaatcat	catgcgagtg	56820
gcagacaccg	gaaaagcgta	ttagacaagt	ttgactatcc	aagcatctgg	gcagtgcctc	56880
atcccacact	gagcgatcgt	tagggccacg	acgccggccg	ataaactccc	cgtcagtaac	56940
atcccgggag	gagccacgag	gtgcgcaagg	tactcatcgc	caaccgaggc	gagatcgccg	57000
tccgcgtcat	ccgcgcctgc	cgcgacgccg	gcctgggcag	cgtcgccgtc	tacgcggact	57060
ccgaccggga	cgccctgcac	gcgaccctgg	ccgacgaggc	gtacgccctg	ggcggcgaca	57120
ccgccgccga	gacgtacctg	cggatcgaca	agctgatcgc	cgtcgcggca	caggccgggg	57180
ccgacgccgt	ccaccccggg	tacggcttcc	tcgccgagaa	cgccgacttc	gcccaggccg	57240
tcctcgacgc	cgggcttacc	tggatcggcc	cgaccccaca	ggcgatccgc	gacctgggcg	57300
acaaggtcac	cgcccggcac	atcgcccagc	gggccggcgc	gcccctggtt	cccggtacct	57360
cggacccggt	cggcagcccg	gacgaggtga	tcgcattcgc	ggtcgaccac	ggcctgccgg	57420
tcgccatcaa	ggccgccttc	ggcggcggcg	ggcgcggcct	caaggtggcc	cgcacgatgg	57480
aggagatccc	gcacctgttc	gagtcggcca	cccgggaggc	ggtcgcggcg	ttcggccggg	57540
gcgagtgttt	cgtcgagcgg	tacctcgacc	agccccggca	cgtcgaggcc	caggtcctcg	57600
ccgaccagca	cggcaacgtg	atcgtcgtcg	gcacccggga	ctgctcgctg	caacgccggc	57660
accagaaact	cgtcgaggag	gccccgcgc	cgttcctcac	cgacgcccag	cgccggcaga	57720

tccacgacag	cgccaaggca	atctgccggg	aggccggcta	ccacggcgcc	ggcaccgtgg	57780
agtacctggt	gggcacggac	ggcacgatct	ccttccttga	ggtcaacacc	cgcctgcagg	57840
tcgagcaccc	ggtcaccgag	gaaaccgccg	gcatcgacct	cgtccgcgag	cagttccgga	57900
tcgccgacgg	cgagaagctg	cggctggccg	aggatccgac	cccgcgcggg	cactccatcg	57960
agttccggat	caacggcgag	gateegggee	gcaacttcct	gcccgccccc	ggcaccgtca	58020
ccgcgctgcg	gctgcccacc	ggccccggtg	tccgggtgga	caccggcatc	tccgccggcg	58080
acgtgatcgg	cggcaacttc	gactccctgc	tggccaaggt	gatcatcacg	ggcgagaccc	58140
gcaccgaggc	cctggagcgg	gcccggcggg	cgctggacga	gatggtcgtc	gagggaatgg	58200
ccacggcgct	gccgttccac	cgcctggtgg	tacgcgaccc	cgcgttcacc	gccgcgccgt	58260
tcaccgtgca	cacccggtgg	atcgagacgg	agttcgacaa	caccgtcctg	ccgttcaccg	58320
ccgccgccgg	ccccgccgag	ggcccggccg	agcgggagac	cgtcgtggtc	gaggtgggcg	58380
gcaagcggct	ggaggtgacc	ctccccgccg	gcctcggcgc	gggtacggcc	gccgggcccg	58440
ccgcgcggaa	gccggcccgg	cggggcggcg	gggccaaggc	cggcgcggcg	gtcggcggcg	58500
acgccctcac	ctctccgatg	cagggcacga	tcgtgaagat	cgccgtcgcg	gacggggaca	58560
ccgtcgccaa	gggcgacctg	gtcgtcgtgc	tggaggcgat	gaagatggag	cagccgctgc	58620
acgcgcacaa	ggcgggcacg	gtcggcgggc	tgtccgccga	ggtcggcgcg	gtcctcgccg	58680
ccggcgcccc	catctgcacc	atcacctgag	gtgcaaggag	gggccccctg	ttaacgcatt	58740
cggtatagga	agggcccctt	cctaaccacg	cgcccggcgg	ggccgcgccc	cagcccgggt	58800
acgcgtaccg	gccgggggtg	ttttccgcga	ccaccgcgag	cggtgaggac	cggggccggg	58860
aatgatggcc	aggtgcggtt	cctacatggc	gcggttcccg	cgcacgacct	gacctacaac	58920
gacgtcttca	tggcgccgaa	ccgctccgag	gtcggctccc	ggttggacgt	cgacctggcc	58980
acctccgacg	gcacgggcac	caccatcccg	ctggtggtgg	cgaacatgac	ggcggtggcc	59040
ggccggcgga	tggccgagac	tgtcgcccgg	cggggcgcac	tcgcggtgat	cccgcaggac	59100
atcccgatcg	aggtggtggc	caacgtggtc	gcctgggtca	agcaacggca	cctggtgcac	59160
gacacggcga	tcacgctcgg	ccccaccgac	accgtcggcg	atgccatcca	tctgctgccg	59220
aaacggtcgc	atggcgcggt	ggtggtggtc	gacgaggccg	gtcggccgct	gggcgtggtg	59280
acggaggcgg	acaccgtcgg	ggtggaccgc	ttcgcccagc	tccgccacgt	gatgtcgacc	59340
gagttgcaca	cggtgccggc	ggacgcggac	ccgcgtaccg	gattcgaccg	gctctcggcg	59400
ggccggcggc	ggctcgcgcc	ggtggtggac	ggcgacggcc	ggctcgtcgg	ggtgttgacc	59460
cgcaagggcg	cgctgcgcgc	gaccctctac	accccggcgg	tggacgaccg	gggccggctg	59520
cggatcgcgg	cggccgtcgg	catcaacggc	gacgtcaccg	gcaaggccgc	cgcgctgctg	59580
gaggccgggg	tcgacgccct	ggtggtggac	accgcgcacg	gccaccaggc	gcggatggtc	59640
gccgcgctgc	gggcggtgcg	caagcttcac	ccgggcgttc	cggtcgcggc	cggcaacgtg	59700

	acggggcacg	cgacctcgtc	gaggccggcg	ccgacatcgt	gaaggtgggc	59760
gtcggtccgg	gcgcgatgtg	caccacccgg	atgatgaccg	gggtggggcg	teegeagtte	59820
tccgcggtgc	tggactgcgc	ggcggcggcg	cgggacctcg	gccggcacgt	ctgggccgac	59880
ggcggggtac	ggcacccgcg	cgacgtggcg	ctggccctcg	ccgccggcgc	gtcgaacgtg	59940
atgatcggtt	cctggttcgc	cggcacgtac	gagtccccgg	gtgacctgta	cacggacgcg	60000
gacggccgga	ggtacaagga	gagcttcggg	atggcctcgt	cgcgggcggt	cagcgcgcgt	60060
acggccgagg	acagcgcgtt	cgaccgggcc	cgcaagggga	tcttcgagga	gggcatctcc	60120
tcggcccgga	tgtacctcga	cccggatcgc	ccgggcgtcg	aggacctgat	cgacgagatc	60180
atctccgggg	tacgcagcgc	gtgcacgtac	gcgggcgcgc	gcagcctggc	ggagttcgcg	60240
gagcgggcgc	tggtcggggt	gcagagcacg	gccggctaca	ccgaggggat	gcccctaccg	60300
acgagttggt	gaccccgcgc	ccggcggtga	gaagggttcc	cctctctacc	ggaggcgtca	60360
acaaggggcc	cttccttcgt	gcgcggctgg	gtatcggcgt	gaccgactgc	cgcacgcgcc	60420
gccgcacact	gagccgccgc	ccgtcgaggg	cccaccgaac	gggcgccggg	gtcagtcgaa	60480
gaggcgacgg	atgacggtcc	gggcggcggc	ctccgggtcc	gggccggtgc	cgggcgggag	60540
cgccccggcc	agccagagtg	tcacgaagcc	gtgcacgatc	gaccaggcgg	ccagggcgtc	60600
cgcctcctgg	tccgggtcgg	tttcccggcg	cgggagggcg	gccaccccgg	cccgcagcgc	60660
cgcgccggcc	cgatcacggg	cggctgtcac	ctcggggtcg	tcgcgacggt	agagctccgg	60720
gcggaacatc	acctcgaagt	gggcccggtg	gtcgaccgcg	aaccggacgt	acgccacgcc	60780
ggcgtcgagc	aggtcgccgg	cctcgcacag	cgccccggcc	agcaggtcga	atccctcgac	60840
ggcgagcgcg	gtgagcagcc	ccgccttgtc	gccgaagtgg	tgcgcggggg	cggcgtgcga	60900
gaccccggcc	cggcgggcca	ggtcgcgcag	gctcagggcg	gccggcccgg	cgtcggtgat	60960
cgcgtcgacg	gcggcggcga	gcagggcgcg	acgcaggtca	ccgtgatggt	agccacgcgg	61020
tccggtcatg	ccggcagcct	aacttgtcat	tgacaagata	gccaggccga	agcaatctag	61080
gcaatgacaa	gttgccttcg	accgaggaga	accccgatgg	cgcccctgat	cgctctcatc	61140
gccggctcgg	ccctggcccg	actcgccggg	ctactcaacg	tcgacgccct	ggccggctgg	61200
caccccgccc	tgcgggtcgg	getegeggee	atgttcgcgc	tcaccgggat	cgcccacttc	61260
acctcccgac	ggcccgacct	ggtcgccatg	gtgccgcccc	gactgcccca	cccggggctg	61320
ctggtgaccg	tcaccggcct	gctggagttg	gccggcgcgg	tegegetget	cgtccccggc	61380
acggcgcggt	gggcagcggc	cgggctgggg	ctgctgctgc	tcgcgatgtt	cccggccaac	61440
gcctcggccg	cccggcgcgg	gctgaccctg	gccggccggc	cggtgacccc	gctcgtcccc	61500
cgcgcgctgc	tccaggtgat	cttcctcacc	gccgccgccg	cgatttcgtt	tgggccctga	61560
ctatcaggga	gctaacatga	cccgcatgga	gctgataggg	ctgcgagacg	tgccactcgg	61620

ccggctgctg	gtgaccgccg	gccacgtcgt	cggccaacgg	tggaaccgct	acctcgccga	61680
ggagcacggc	ctcacccagg	cgggcatggt	caccctgatg	accctggccc	ggcacggcga	61740
gctgccgcac	cgggcggtcg	ccgaggcgtg	cttcatccgc	ccggccaccc	taaccggcat	61800
cgtcgacaca	ctggagcgcg	acggcctcgt	cgagcggcaa	cgcgacgacg	tcgaccggcg	61860
cagcgtgcgg	ctcgtcctga	cccccgccgg	tcgggaacgg	gtcgccgcgc	tcaccaacgt	61920
catgcagtcc	ggacgaccga	tgacctcggt	cgacgccgac	ccggcgaagg	ccgccgtgat	61980
ccggcagttc	ctgctcgagg	tcatcggcag	tggagaggaa	cctcgggtga	cggccctcga	62040
cgcgaggccg	gaggctccgg	catgctgatc	cggctgctcc	gcgcccacct	gcgcccgtac	62100
cgtcgaccgc	tggcggcggt	gatggcgttg	cagttcgtcg	gcacgatggc	ctcgctctac	62160
ctgccgagcc	tcaacgccga	catcatcgac	cagggtgtgg	cccggggcga	caccggctac	62220
atcatgcgta	cgggcggctg	gatgctgctg	gtcagcctgg	tgcagatcgc	ctgctccacc	62280
gccgcggtct	tcctcggcgc	gcgctccgcg	atgggcttcg	gccgggacgt	acgcgccgag	62340
gtcttcgccc	acgtcaaccg	gttctccgcc	cgcgaggtga	cccgcttcgg	cgcaccctcg	62400
ctgatcaccc	gcaacaccaa	cgacgtgcaa	caggtgcaga	tgctcgtcct	gatgagctgc	62460
accatgctgg	tcgccgcgcc	gatcatgagc	gtcggcgggg	tgttcatggc	actgcgggag	62520
gacgtcgggc	tgtcctggct	gatgctggtc	agcgtgccgg	cgctggcgat	cgccctgatg	62580
ctgatcatcc	ggcggatggt	gcccgggttc	cggctgatgc	agacccgcat	cgacgcggtc	62640
aaccgcgtgc	tgcgcgagca	gatcaccggc	atccgggtgg	tccgggcgtt	cgtccgcgag	62700
ccgtacgaga	cggcgcgctt	cggccgcgcg	aacgccgacc	tcaccgcgac	cgccctgcgc	62760
accggtcggt	tgatggccct	gatcttcccc	gtggtgacgc	tggtgctcaa	cgtctccagc	62820
gtcgccgtgc	tgtggttcgg	cgcggaccgc	gtcgacgccg	gccagatcca	ggtcggcgcg	62880
ctcaccgcct	tcctgcagta	cctcatgcag	atcctgatgg	ccgtcatgtt	ggccaccttc	62940
atcctgatga	tggtcccgcg	cgccgcggtc	tgcgccgagc	ggatcgtcga	ggtgctcgac	63000
accgactcga	cggtgatccc	gccggccgcg	ccgacggccg	aggtgaccgg	ccggggcgaa	63060
ctggaactgc	gcggcgtccg	gttccagtac	ccgggggcga	gcgcgccggt	gctgcacgac	63120
atctcgttcc	gggccacgcc	cgggcgcacc	acggccatca	teggeageae	gggggccggc	63180
aagacgaccc	tgctgacgct	gatcccccgg	ctgatcgacg	ccaccgccgg	ggcggtgctg	63240
gtcgacgggg	tggacgtgcg	tgacctggcc	ccggacgatt	tgtggcggcg	gatcgggctg	63300
gtgccgcagc	ggccgtacct	gttcagcggc	acgatcgcca	gcaacctgcg	gtacggcaac	63360
ccggacgcca	ccgacgcgga	gctgtgggcc	gccctggaga	tcgcccaggc	gcgcgacttc	63420
gtcgccgagt	tgcccgaagg	gctgaacgcc	ccgatcacgc	agggcggcac	caatatctcc	63480
ggcgggcagc	gccagcgcct	cgcgatcgcc	cgggccctgg	tccgcaagcc	ggagatctac	63540
ctgttcgacg	actcgttctc	ggcgctcgac	ctgggcaccg	acgcccggct	gcgcgcggcg	63600

ctacgaccgg	tcaccgcgga	cgcgacggtg	ctgatcgtgg	cccagcgggt	ctccacgatc	63660
gtcgacgccg	accagatcat	cgtgcttgag	gacgggggca	tcgtcgggat	gggccgacac	63720
gccgaactac	tggaagactg	cccgacgtac	gcggagatcg	tcgcctccca	gcagacggcg	63780
ggggtgccgg	catgacggcc	gtaccggatc	agcggcccac	cgcgcggccg	gcggaggggc	63840
cgacgccgaa	gcggctgccc	tccggcaacc	agggcagcgg	cccgaggtgg	atgagcgccg	63900
gcatgccggc	cgagaagtcg	atgaacttcg	ggccgtccac	ccgccggctg	ctgcgccggc	63960
tgcgaccgca	ccgcctccag	ctggccgcca	tcgtcctgct	ctcgctggtc	agcgtcggtt	64020
gcaacgtgta	cgggccgaag	gtgctcggcc	acgccaccga	cctgatcttc	agcggggtga	64080
tcggccggca	gttgccggcc	ggcaccaccg	ccgagcaggc	ggtcgcggcg	gcccgcgcgg	64140
ccggtaacga	cagcttcgcc	gacatgctgg	cccggatgga	cgtggtgccc	ggʻggtgggca	64200
tcgacttcac	cgccctgggc	cgggtgctgc	tgttcgtgct	cgccctctac	ctggcggcca	64260
gcgtgctgtt	gtggtggcag	ggctggctgc	tcaacggggt	ggtgcagcgc	acggtgctgc	64320
ggctgcgcgc	cgacgtggag	gacaagctga	accggctgcc	gctgccgtac	ttcgaccggc	64380
agccccgggg	cgagttgctc	agccgggtca	ccaacgacat	cgacaacatc	tcgcagagcc	64440
tccagcagac	gctgagccag	ctgctcacct	cgctgctcac	cgtggtcggc	gtactggcca	64500
tgatgttctg	gatctcgccg	ctgttggcgc	tggtgtccct	ggtcgcggtg	ccgatgtcgg	64560
tggtggtcac	cagcctggtc	gcgaagcggt	cacagcagcg	gttcatcgcc	cagtggacgc	64620
ataccggaga	gctgaacggc	cagatcgagg	aggcgttcac	cggacacgag	ctggtcaagg	64680
tcttcggccg	gcagcgcgag	gtggaggccg	ccttcaccgc	caagaacgag	gagctgttcc	64740
gggccagctt	cggcgcccag	ttcatctccg	ggatcatcat	gccggcgatg	atgttcatcg	64800
ggaacctcag	ctacgtcgcg	atcgccgtgg	teggeggget	gcgggtggcg	tcggggtcga	64860
tgagcatcgg	cgacgtgcag	gcattcatcc	agtactccct	ccagttcacc	cagccgctga	64920
cccgggtcgc	ctcgatggcc	aacctgctcc	agtccggggt	ggcctccgcc	gagcgggtgt	64980
tcgcggtgct	cgacgccgag	gagcagagcc	cggacccggc	ggtgccggcc	cgggtcgccg	65040
accagcgcgg	tcgcgtcgaa	ttcgaccacg	tctcattccg	gtacgagccg	gacaagccgc	65100
tgatcaccga	cctgtcgctg	gtcgccgagc	cggggcacac	ggttgccatc	gtcgggccga	65160
ccggcgccgg	caagaccacc	ctggtcaacc	tggtgatgcg	cttctacgag	ctggacgccg	65220
gccggatcac	cctcgacggg	gtcgacatca	ccacgctgag	ccgcgacgac	ctgcgcggcc	65280
ggatcggcat	ggtgctccag	gacacctggc	tcttcggtgg	cacgatccgc	gacaacatcg	65340
cgtacggccg	gccggacgcg	agcgaggagg	agatcgtcgc	cgccgcccgg	gcgacgttcg	65400
tggaccggtt	cgtgcgtagc	ctccccgacg	gctacgacac	cgtcatcgac	tccgagggca	65460
gcaacgtcag	cgccggcgag	aagcagctca	tcaccatcgc	ccgggcgttc	ctggccgagc	65520

cgtcgctgct gatcctcgac gaggcgacca gttcggtgga cacccgcacg gaggtgctgc 65580 tccaacgggc catggcggcg ctgcgctcgg accggaccag cttcgtcatc gcccaccgtt 65640 tgtccaccat ccgcgacgcg gacctgatcc tgatgatgga gcacggtcgc atcgtcgagc 65700 agggcaccca cgagcagete etggcegece ggggegegta ceaeeggett taccaggeee 65760 agttcaccca gccggacccg gccgccgtcg gggaccccga gccccagccc gcctcggtcc 65820 ggggctgacc gtcgtggccc ggtacatccc gcccagctcc ccgacccgca ggggcagctc 65880 ccggggcccc gggcgcggaa gaccagagcg tggtgcgggc agagcgccgg gcggagcacg 65940 aactcgtcgt cggggcccag ccgcatcggc gggaacatgt cgtcggcgaa gtggccgagg 66000 teggggeete gatgaeggtg aegteagtge ggegeegg ggtteeeega egtegtggte 66060 cgtaccgcgc tgcgcatggg gagacggtag gccggccggg ggcgggcgcg catccgaatt 66120 eggggeegge eegaegeage egagaegeat eeggttaceg egaagggega caggeegeea 66180 gtcgctacag tcggcaaccc ggccgatgca cagcgcgcct cggggcgggc cgccggcacg 66240 66300 ggacctgccg gcggcccatg gcggcccggt cgtcggctac ggggggtccg acactcgagg eegegeegae taeggtaege eggeegtegg egateegeeg acegeeteea eeegtaegee 66360 gaggttgccg gccccagcgg gtccccggcc cgccgcgctg cccgaccgcc gcgtcgccgg 66420 cccgacgacc cggttcgtgg cgggtgccgg cgaggtggag ccgcccagtt actccagctc 66480 gtggagcatg agctggcggg cggcctcggt gatcgagccc gacaggctcg ggtagatggt 66540 gatggtctgg gccaactcgt tgaccgtgag gttgttctcc accgccatgg tgatcggcag 66600 gatcageteg etggeetteg gtgeeaceae cacacegeeg atcacetgge egetggeegg 66660 geggeagaac agetteaega ageegtegge gaggtegtee atettegeee gggegttgee 66720 egacagegge ageateacet ggegggeegg ggtettgeeg gegteeacet egteetggga 66780 gacgccgacg gtggccaact ccgggtcggt gaagacgttc gcggccaccg tacgcagccg 66840 cagoggoogg accgcotogo ogagogogtg coacatogog atcoggocot goatggoogo 66900 66960 gacgctggcc agcggcaaca ccccggtgca gtcgccggca gcgtagatcc cggggacgtt ggtgcgggac acccggtcga cggtgacgta gccgcccgg gccagctcga cgccgtactc 67020 67080 ggcgaggccg aggttggcgg tgttggggat cgagccgacc gcgatgagcg cgtgcgagcc gtgcaccage eggeegtegg ecagttegae etceaceeeg teggegatge getggaceet 67140 cteggegegg gagttgttga ggategteat geeeegggag eggaacaege getegatege 67200 catggcggcg tcggcgtcct cgtgcggcat cacccggtcc cggctggaga cgagggtgac 67260 cgggaccccc atggccaggt acgcgctggc gaactcggca ccggtgacgc cggaaccgac 67320 gacgatcagg tgctcgggca ggtgcggcag gtcgtacacc tgccgccagg tcaggatgcg 67380 ctegecgtec ggcacggccg tggggagctg geggggggtg gegecggtgg egaccagcac 67440 ggtcgacgcg tcgatcgagt gcttctcgga gccgtcggcc ggcgtgacga cgacgcggtg 67500

ggtgtggccc	agcatgtcct	cgccgagccg	ggccgtgccg	gccacgaagg	tgacgccggc	67560
tttcaccagc	ttcgcgtgga	tgtcggcgga	ctgggccagg	gcgagccgct	tgacccgctc	67620
gtgcacggcc	cgggcgtcga	cggtgaccgc	ctccagcccg	tcggagtgca	ccccgaactc	67680
ctcggtgtcc	cggtacccgg	tgaccacctc	cgagctggcg	atgaacgttt	tcgacggtac	67740
gcagtcggac	agcacgcagg	caccgccggc	cccctcggcc	tccaccacgg	tgacatcagc	67800
gtccaactgg	gcggcgacca	gggccgcctc	gtacccggcc	ggccccccgc	cgatgatcac	67860
gatctggctc	acagctatcg	cccctcgtcc	gtgctcacag	tgactttctt	ctccccgacg	67920
cgtccgacac	gcaccgtcgt	attctcccc	agccgtccgc	cgggctatcg	tcatcgccgt	67980
gcgtcactac	gccgcctacg	gctcaaacct	ggaccccgcc	cggatgcgcg	cctactgccc	68040
gcactccccg	atggtcggcg	teggetgget	ggagggctgg	cggctcacct	tcgcgggtga	68100
gggcgcgatc	ggctgggagg	gcgcggtcag	caccatcgtc	gagtcccccg	gtgatcgggt	68160
gttcgtggcg	ctctacgaca	tccacccgta	cgacgccgtc	cagctcgacg	agatcgaggg	68220
ggtggcctcc	gggacgtacc	gcaagctgca	cgtccgcgtc	tccaccctcg	acggcgacgt	68280
gaccgcgtgg	gtctacgtct	tcgacgggta	cgagggcggc	ctgccgacgg	cgtggtatct	68340
gtcggagatc	gccaacgccg	ccgagaaggc	gggcgcgccc	gacgactacg	tcagcgagct	68400
gcggtcccgc	cccaccggca	cggcgtcggc	gtagcgcgtc	tcccacactc	ccagtctgct	68460
ccgcccgaga	cggggccgca	cggcggcccc	cgccgggggt	cgtctgtcac	acatcatggt	68520
cgcgcccgtc	acaccgccgt	ggcggcgggg	acggtgcgct	cgtacatgtc	ggtccagcgc	68580
atctcgcgca	gccccaccga	gcggtagagc	gtcgccgggg	aggtcgggtt	ggtcaggtcg	68640
acgccgaggc	cggcgtgccg	ccgtcccttc	gccgcgtaga	ccgtgaaggc	ccgccacagc	68700
agcgcggcgc	cgaccccgtg	ccgccggtac	ttcggcagca	ccgacagggt	ccgcacccag	68760
cccgagtcct	gttccagcgc	ctggtcggac	gactgcaacg	cgccggccgg	ctccccgtcg	68820
acctcggcga	cgaaccactc	gtcccaggtc	ctgtcgtacg	cgggcagacg	ctcccgccag	68880
tggtcgtacc	cggccggctc	gtagtccggg	gtgtcccgga	acgccgtgtc	gtagatccgg	68940
tggaacaggc	gcaggtcgtc	ctcgtcgccg	gcgcgcagcg	gccggaccgt	caccccgggt	69000
gggggcggcg	gctcggcggg	cagcccggcc	aggtcacgac	tcatccgtac	gtaccgcttc	69060
acccggctga	aaccggcctc	ggtcagctcc	gtcacccagc	gggtctccgg	cgggtaggcc	69120
gaggcgcgga	cggtcagcgc	gggcaggctc	cgctccgcgg	cccgctcggc	gacccggtcc	69180
agcatcagag	cgagcagcgg	ggcgcgtacc	gcctcggcgc	gctccgggtc	gacgaggacg	69240
tcgacgaact	cccggcccac	cccggtcggg	ttgtccacca	ccgaccaggc	gacgagccgg	69300
ccctgcgggt	cgctgaccag	ccaggagtcg	cgcgccgggt	cgaagaaggg	ggccgtcagg	69360
gcggccttga	cgtcttcggc	gtcgaagtcc	gggtggccga	tcgcgaaggt	gtctgcggcg	69420

tgcacgacgg	cgaggatccc	agggacgtcg	tcgagggtgg	ggcggcgcgc	cgcccagtca	69480
gcgggaagag	tcacggggcg	atcctggcag	ccaccccggt	cccgcgcccc	tcattttcaa	69540
ccgccccgcg	ccctgccccc	gccgccgcac	gcgctcgccg	gcgagagggg	accctttcta	69600
ccccaggcgt	tagtaagggg	cccttccttg	caccacggcg	cgtgcggtgg	tcagcaggtc	69660
gagcagcgcg	gtgccctcgg	ccggcgtgag	cgcccggaat	ccggtcgaca	ccagccggtc	69720
ggtcaccgcc	tccgaccaca	gccggcggcg	caccagcggc	ccgacccggg	ggtacggcgg	69780
cggccagccg	caggccagcg	ccccggcctc	cccctccggc	ccggccagca	ccgcctccag	69840
cggcgtcatc	ccgccggccc	gcaccgccag	caggtacgcc	ccggcgaagt	gctcccgaag	69900
cagcagcagc	ccggcggcgg	cacgggcccc	cggggtgtcg	tccggcggcg	gcacggcccg	69960
ccaggcggca	aagagtggca	tcccgctggc	gtccgcggcg	tcgaccaccc	ggtgcagcag	70020
cgtcgccaga	cggatcacgc	cgggcacggc	ggtcaggtgc	tcgctgcccc	accggcagca	70080
ctcggccagg	ttcgccgtgg	ccacctccag	cggagcgtgc	acgcgggcgg	cggcgtccca	70140
cccgtcggcg	accgcgtcgg	gggcgacgaa	gccgagggcc	gcgctcaccg	tggcggcccc	70200
gacgtcgccg	agcaccccgg	cccggccggc	gatgtggaag	gcccagccgg	agatgcccag	70260
cagacgggcc	cggtgcaggg	tggccgggca	gcgggcgaac	atctccccga	gctccagcac	70320
caacggcttg	ctcgcggcgg	cgacctgctc	cggcgtcatc	gggttcagtc	tgccccgccg	70380
gggccttccg	tgacagcccc	gtcttcggcg	tcgaccgcct	cgatcgcccc	ctcgatttcg	70440
ccggtgcggc	gctgggcggc	ggtgacggcc	cgttccgccg	cccgccgggc	cagcttccgc	70500
cggctgagtt	cctgctcggc	ctctgcgcgc	gatcgctcca	gctcggccag	cgaccgctcg	70560
atgccggtca	gttcctcggc	accgtcgtgc	tcggcctcca	ccgcgccggc	cagctccgcc	70620
teggeeeget	cctggtcggt	acgcgcccgc	gccagttccc	gttccagcat	ccggcgttgc	70680
cgggcccgct	cggcacgggc	ggcgcgctcg	gcctcccggg	cggcccgctt	cgcgcgcggt	70740
ggtgggtggg	tgggcggtgg	ctgctcctcg	ccgccggtga	ccaaacggag	ctgggggcgg	70800
ggcacctcgc	cgaagccggc	gtagctggcg	gcccgcagca	gccggccgga	gcgcacctgc	70860
ccggccacct	ccgtgtcgga	gagcgcggcg	tcgagcgtcg	cctccacctc	gcccagcggc	70920
agcttcccgg	ccggcgggcc	gccctcggcg	teggeggeea	gccggcgcgc	ctcggcgacc	70980
agcgcggcga	ccgccgcccg	ccgctgggcg	gagagttccc	gcagccgggg	gccgcgcagg	71040
tcgcgctggg	cgcggcgcag	cgcctcggcg	agttgggtca	ggtcggcgac	cagctcgggg	71100
cggcgcaggg	cgagcaggtt	gaccagccac	gcggccacgg	tegggeggeg	cagccgggcg	71160
atctcgcggg	ccgtggccgg	gtcgccggag	cgccgggcct	cggcgacggc	ggcgtcgcgg	71220
gtggcgacga	acttctccgg	cggctcggtg	tagagccgcc	ggaggaggct	ctgcgggggc	71280
ggcacggctc	agacgtcgag	ccggctgccc	ggctcgaggc	gctggtagtc	ggtccccgac	71340
agcgcggcgt	actgacggtt	gaggacggcg	aggccgttgt	cgttgagcag	cccgtcgtgc	71400

agggcgaagg	ctcggcgcgg	ggcgaccgcg	cggatgaagt	cgagcacctc	ggagaacttc	71460
gaccaggggg	cgtggatcgg	cgcgaagagg	gtgtccacgg	gggcgtcctc	gggtgccacc	71520
agggcgtcgc	cggggtggta	gacgacgtcg	ttcagcagat	acccgaggtt	gtccacgacc	71580
gggatgtcgg	gatggatgac	ggcgtgccga	ccgccgtacg	cgcgcaccgc	cacgcccgcc	71640
gcggtgaacg	cctgcccggg	tgagatgggc	tccagggctt	cggccacgtc	gccgagggca	71700
ccggccagcg	aggccgggcc	gtagatgcgg	aacggccagc	ggtcgagctg	ccgggtgaga	71760
gccgcgacgt	ccacgtggtc	ggggtgctca	tgggtgatca	gcaccgcgtc	cgcaccgtcc	71820
agcgcggtcg	ggtcgctgaa	gacgcccggg	tcgacgacca	gcacaccgcc	gtcgtgctcg	71880
acgcggaggc	aggagtgggc	gaatttggtg	agctgcatcg	tgactcctcg	attgacccaa	71940
tcgtgatgtc	cctcagcgca	gtctgccgga	accggcgcgg	tgccgcgtcg	cgtctgaggt	72000
atcgcccgat	ggggcgtaga	cgatcggagc	gggaatggac	ggacacgcaa	gacgcaggtt	72060
gctgaccgcg	gtggggctgg	tggcgctgct	ggcggccggt	ggttgcagcg	ccgacagcga	72120
tggggcggga	gagccttcgg	cggcggtggc	gcccgagcag	gcggcacctg	ccgacggggg	72180
caaggcggag	cagggtgccg	atgccggggg	aacgcggtcc	ggcgcgggtg	gcggctcacc	72240
ggacctgcgg	gtcgaccagc	ggtcaatcat	ctacaccgga	accatgcggg	tgcgggtgga	72300
cgatgtggac	gccgccgccc	ggtccgccat	cacggcggtc	accggcgtcg	gcggcttcgt	72360
cggcggcgac	gagcgcagca	gcggcggaac	cgccgacgcc	cgggcggagt	tgcaactgcg	72420
ggtgccggcg	gagcggttca	cggccgtcct	ggaggagttg	gcgaggctcg	gccggcagga	72480
gcagcgggcg	atccgcacgg	aggacgtgac	cgaggagacc	gtggatctcg	acgcgcggat	72540
cgccacccaa	cgggcccggg	tcgagagcgg	tcgcaagctg	ctggcgcggg	ccacctcgat	72600
cggcgacctg	gtgacgctgg	agagcgaggt	ggctaggcgg	gaggccgacc	tegeeteget	72660
ggaggcgaag	aagcgccggc	tggccgacct	gacctcgctc	tccaccatca	ccctcaccct	72720
ggtcggtccg	gaggcggagg	cccgggacac	cgagcccgac	accggcttcg	tggtcggcct	72780
gcgcggcggc	tggacggcgt	tcgtcgcctc	gctgggcgtg	ctgctcaccg	tgctcggggc	72840
gctgctgccg	ttcgcggtgg	ccctcggcgt	gccggtggcg	gtgctgcttg	cggtgctgcg	72900
gcggcgccgg	cgtcgaccgc	cggcgccggc	cgtcaacgcg	ccgccgccag	tgcccgcagc	72960
gcggtctgca	ccatgacccg	gatgccgacc	gcgatggccc	cctcgtcgac	gtcgaacgag	73020
gcccggtgca	ggtcgacgtt	cgggccggac	cggccgacgc	cgaggcgggc	cagcgcgccg	73080
gggacgtact	ccaggtacca	ggagaagtcc	tegeegeeca	tgctctgcgg	ggtctccgcg	73140
accccctccg	ggccgagcgc	ggcgtgggtc	gccgccgtga	gcacctggat	cgcccgggcg	73200
tcgttggtca	ccggcggccg	gccgcgtagg	tactccaggt	cgacggtggc	gccggtgggg	73260
gcgatgacgt	cccgcaccac	ctgagcgacg	atcttggggg	cctggtccca	ggtgtcgcgg	73320

tccatcaccc gcagggtgcc ggacgcggac gcctcggacg ggatcacgtt gtaccgggtg 73380 ccggccgagg cgtggccgaa cacgagcagc agcccgctgt tggccggcac ccggcggctg 73440 accagggctg gcacctcggt gaccagccgg ccgagcgcgt cgaccaggtc gacggtcagg 73500 tgcgggcgag cggtgtgccc gccggggccg gtgagccgga cggtgacgtt gtcggcggcg 73560 geggtgateg ggccgacceg caggccgacc ttgccgacgg gctggttggg gtcgcagtgc 73620 agtgegaaga tetgeaegae gtegtegaga eegeeggeet egatgaeete cagegageeg 73680 cagggcagga tetectegge eggetggaag ateageegga eeeggeegte caattegeeg 73740 aggttggcga gttgggccag cagcacgccg acgccgagca gcacggtggt gtgcacgtcg 73800 tggccgcagg cgtggcagac accgtccttg gtggaccggt agggcacgtc cttgacgtcg 73860 gteageggea gegegtegat gteggegegg agegegaeea eegggeegte ggggeggeeg 73920 tegatgtege agatgaeece gttgeeettt ggeageagge gegggegeaa eeeggegage 73980 74040 gacagetege gggegateag ggeegeegte tegaacteet egeeggagag eteegggtgg gagtggatgt gccggcggt ggcgataagg ccgggcatcc ggagggcgag cagatggtcg 74100 agetegaagg geaaaggetg egaceeggae ggegaeteeg geeaggeega egacgeeagg 74160 tggctgccgt tcggcagcgt caacgcactc gtcacgtcga aatctcgatc actagaaacg 74220 gatggatcat cagggatgac agccgccagc ctagaccttc gacggtgact ctgtgcaaca 74280 tcattcccgt agcgatcgga ccgcgcagcg tcacgaatac cctggtggaa gggctccata 74340 atctgcggga cagcaggtag atcgcggttg aacgccgtca tctgcccccc acctcctaca 74400 accegtaace gatteggegg teaegaaate acegtegate eggggeegte getaeegaat 74460 tgtcgcatta gtcgtctcgg ttaactgccg ctcggacaag taaccgaccg cactcggcag 74520 74580 teggacgact ceegacggtg acacgacggg cegacetget eeegcacatg etgteegtee caatcacccg gacgggttac ccactgcccc gggtggcaca caccgggctg ccccgggtgg 74640 cacacacacc aggogaccgt agccccgaac ggttacgccc cgcgacccct catccgagac 74700 aaggggtcag aaccggtcgc tggggcggta cgtccccac acctggcgca gggtgccaca 74760 gacctegece acegtggece gggecegeag egecteette ategggtgea geaegttege 74820 cgtaccetcg geggeggece geageteace eagegegee tegaeggegt egetgtegeg 74880 ctccactege agettggeca geogetegge etgggeagee tegategteg ggtecaceeg 74940 cagoggeteg tacggetegt eggegtegae egtgaacegg ttgaggeega ecaecaeeeg 75000 ctcgcccgag tcgatctcct gggcgatccg gtacgcggac tgctcgatct cccgcttctg 75060 gaagecegee tegatggegt egaceacega geegtggteg geeaceeget eeateagete 75120 caccaccgcc gcctcgatct cggcggtcat cgcctccacc acgtacgacc cggcgaacgg 75180 gtcgacggtg gcggtcaggt ccgtctcgta cgcgagcacc tgctgggtgc gcagcgccag 75240 ccgggcggcc ttctcggtgg gcagcgcgat ggcctcgtcg aagctgttcg tgtgtagcga 75300

ctgggtgccg	ccgagcaccg	cgcccagccc	ctggatcgcc	acccggacca	ggttcacctc	75360
gggctgctgg	gcggtgagct	gcacgcccgc	cgtctgggtg	tggaagcgca	gcatcatcga	75420
cttcgggttc	ttcgcgccga	actcgtcgcg	catcagccgg	gcccagatcc	gccgggcggc	75480
acggaacttc	gcgacctcct	ccagcagggt	ggtccgggcg	acgaagaaga	acgacagccg	75540
gggcgcgaag	tcgtccaccg	ccagcccggc	ggcgagcgcg	gcccggacgt	actcgacgcc	75600
gttggccagc	gtgaacgcga	tctcctgcgc	gggcgacgcg	ccggcctcgg	ccatgtggta	75660
gccggagatg	gagatggtgt	tccacttcgg	cacctccgcc	cggcagtagg	cgaacgtgtc	75720
ggcgaccagc	cgcagcgagg	gcttcggcgg	gaagatgtac	gtgccccggg	cgatgtactc	75780
cttgaggatg	tcgttctgga	tggtgccgtt	gagcgccgcg	cccggcaccc	ccgcctcctc	75840
ggcgacgagc	tggtagagca	gcagcagcac	cgaccccggg	gcgttgatcg	tcatcgaggt	75900
ggaaaccttg	tccaacggga	tgccgtggaa	cagcagccgc	atgtcctcga	tcgagtcgat	75960
ggcgacgccg	accttgccga	cctcgccgtg	ggcgatcggg	tcgtccgagt	cgtaccccat	76020
ctgggtgggc	agatcaaaag	cgacggagag	gcccatggtg	ccggcgcgca	ggagctggtg	76080
gtagcgcgcg	ttgctctccg	tcgcggtgcc	gaagccggcg	tactggcgca	tcgtccacgg	76140
ccgcgaggtg	tacatggtgg	agtagacccc	acgggtgtac	gggaactccc	ccggctcgcc	76200
cagccgctcg	ggcagaccct	ccggcaggtc	cctctgggtg	tagacaccct	tgatcgggaa	76260
gccggactcg	ctcgaccgcg	gttcactcat	ccccggatgg	taggacgtgc	caccgcgccg	76320
gagggtgagg	gattgcgcac	atcgcacccc	tgtctttccc	cgccgactcc	gagggtgaac	76380
acctggccac	gttcgctccg	attaggtaaa	cgttccgccg	cgtcgggttt	cgcatcgggc	76440
gtcggaacca	gcaagataga	ggagttgtgt	cccagccccc	tcgatttccc	ccggtggctc	76500
ttctgtgact	cagatcccga	cgtggagcgg	cggaccagtc	agcccacccc	acggacgtgc	76560
ggcagccggc	accaccatcg	gtgaccggta	ctcgctccgg	tccgcggtgg	gcaatggcgg	76620
catgggcacg	gtctggcgtg	ccacagacac	cctgctgcgg	cgcgacgtgg	cggtgaagga	76680
ggtcgtcctc	ccgcccggcc	tcgccccgag	cgaccgcgac	gccatgtacg	aacgcacgct	76740
gcgcgaggcc	cgcgcggcgg	cggccatcca	gcacccggcc	gtggtccagg	tgtacgacgt	76800
ggtcaccgag	ggtggtcgcc	cctggatcgt	gatggagctg	ctggacgccc	gcagcctggc	76860
cgacatggtg	atcgaggacg	ggccggtggc	ccccgcgcg	gtcgccaaga	tcggcatcgc	76920
cctgctcggc	gcgctggagg	tggcccacgc	gatcggggtg	ctgcaccgcg	acgtgaagcc	76980
ggccaacgtg	ctgatctgca	ccgacggccg	gtgcgtgctg	accgacttcg	gggtggccaa	77040
gctccccacc	gacgtgcagc	tcaccacgcc	ggggatggtg	ctcggctcgc	cgcacttcat	77100
ctcccccgag	cgggccatgg	gccaggagtt	cggcccgccg	agcgacctgt	tctccctcgg	77160
cgtcacgctc	tacacggcgg	tggagggccg	gcccccgttc	gacaggggcg	acccgatcga	77220

gaccatgcac gccgt	ggtcg aggacccgc	c ggccacgccg	cagcgcagcg	gcccgctgac	77280
ccgggtgctg atggg	gctgc tggagaagg	a cccggcccgc	cgcctcgacg	tgcacaccgc	77340
ccgcgcgatg ctccg	cgagc tgctcgccg	g cccgctgacc	agcaccgcca	ccgccgtcaa	77400
ctcggtcacc gaccc	gtacg cggtggtgc	c ggtcaagcag	cgcccggccg	tcgccccacc	77460
gccctccgct gcgga	gccga agccgagcg	g gcagatcggc	ggccgggcga	tgctcgcccc	77520
cggcgagtcg ctgac	cgacc ggctggcgg	c cctgcgccgg	ggcgagaaga	cgaggaagag	77580
gaagacgacg accgc	cgccg cgctggacg	a caccagcgcc	gacgcgcttg	ccggcccgct	77640
gcacaccccc accgg	ggcga tgcccgcgc	c cccgcccgcc	ggccggacgt	acggcggttc	77700
gtcggaggcc accca	gcggg tcgacgcgg	g gaccgcgccg	gaggccaccc	agcggatgac	77760
gtacggcagc ccgccc	cgacg ccacccago	g ggtgtcccac	gggagcggcc	cgtcggaggc	77820
cacccagcgg gtgccc	ctacg gcggcggct	c ggcggacgcc	acccagcagg	tgcccttcgg	77880
tegeeggeee gaege	gacgc agcgggtco	c ctacggcagc	cagcccggcg	cgacgcagcc	77940
ggtccccggc ttcgg	cgcgt cgccggacg	c cacccagcgg	gtcggcgggg	cgtacggcgg	78000
cggccagtgg tcggtg	gcccg gcaccggcc	a gccgtgggcc	accccggcca	ccgcgcccgc	78060
cccggccacc gccgg	cggcg gcggggtcg	g ccgcctcgtc	gccacggtca	agggctggcc	78120
gcgcaaggtg cagcto	cgccg cggccggcg	g cgtcgccgtg	ctgctgctga	tcggcgtgtt	78180
cgccctcttc ggcgg	cgacg acccggago	a gccgaccacc	ccgcaggggc	agccgagcgc	78240
cggggcgccc gccgg	ccccg gggtggaga	t gcaggagcag	tcggccaagg	gcgtcacggt	78300
gcaggtgccc aaggg	ctggg agcggcgca	g tgccgacggg	ggcgtgtggg	tcgactacat	78360
cgatccggag gacaac	cagee geaaggtge	g catcctcgcc	gagcggtgga	gcggcacgtc	78420
gacgcgctgg gccgag	gaccg ccgcgaacg	g gctgcggacc	cggtcggcct	cctgccagaa	78480
gccgtacaac caggto	gtcga tgaccgago	a ggagctcgac	ggcaaggcgg	cggccgagtt	78540
cgagtacacc tgcgg	cgacg gcgagggca	a gcggcacggc	gtgtggcgcg	gggtggtgca	78600
cgagggcaag gtcta	ctcgt tctacctct	c ctcgaccgac	gcccgcttcg	ccgagagcaa	78660
gccgatcttc gatcag	gatgg tggcgtcgt	t caagctccgc	gggagcgact	gagccgggcc	78720
gggggccgac gcgac	gccgg ccgggcggg	c cgacgcgacg	tggtgagccg	ccgccgtgct	78780
atcaagagcc atggc	ggcgg acaccactg	a cctcgacgac	acgcgcgatc	tggacgacct	78840
tegegacegg geeeg	geggt gget e gaeg	a cgaccccgac	ccggccaccc	gcgacgagct	78900
ggaggccgtg ctcgad	cgggc tgccggcga	g cgcggccgag	ctggccgacc	ggttcgccgg	78960
gccactgacc ttcgg	caccg ccgggctgc	g cggcccgctg	cgcgccggcc	ccaacgggat	79020
gaacctcgcc gtggto	caccc aggccgccg	c cgggctcgtc	gcctggctcg	ccgcccagga	79080
cgccaccggg ccgct	ggtca tcgggtacg	a cgcccggcac	ggctcgcggg	agttcgccga	79140
gcgcaccgcc caggto	ggcca ccggcgcgg	g ccgcccggcg	ctgctgctgc	cccgcccgct	79200

gcccaccccc	gtgctggcgt	acgcggtgcg	gcagctcgac	gcggcggccg	gcgtgatggt	79260
gaccgccagc	cacaacccgc	cccaggacaa	cggctacaag	gtctacctcg	gcgcgcagct	79320
cggcggcgag	ctgggcgcgg	gggcgcagat	cgtgccgccg	gccgacaccg	gcatcgaggc	79380
cgccatccgg	gcggtcggcc	cgctggccga	cgtaccgctg	ggcccggccg	ggcaggtcgt	79440
cggcgacgac	gtggtcgtgt	cgtacgtcga	ccgggccgcc	gccgtggtcg	acccggcggg	79500
gccccggagc	ctgaaggtgg	cctacacgcc	gctgcacggc	gtgggcgcgg	ccgtgctgac	79560
cgccgccttc	gcccgcgccg	gcttcggcat	ccccggcgtg	gtgcccgagc	aggcggtgcc	79620
ggacccggac	ttccggaccg	tcagcttccc	caacccggag	gagccggggg	cggtggacct	79680
cctcgtcgcg	ctcgccgagc	gcaccggggc	ggacctggcg	atcgccaacg	accccgacgc	79740
ggaccgctgc	gcggtggccg	teegegaegg	ccgggcggcg	ggcccggcac	cggtgagtgg	79800
gggcgcctgg	cggatgctgc	gcggggacga	ggtgggggcg	ctgctcgccg	accatctcat	79860
gcgccgtggc	gtccacggcc	tgtacgccac	caccatcgtg	tcgtcgtccc	tgctacgggc	79920
catgtgcgcc	gcccgtggcc	tgccgtacga	cgagacgctg	accggcttca	agtggatcgt	79980
ccgggccggc	ggcggaccgc	tgggtgaggc	cggctccgac	ccgctggtct	tcggctacga	80040
ggaggcgctg	ggctactgcg	tcgccccgga	gcacgtccgc	gacaaggacg	gcatcaccgc	80100
cgcgctgacc	gtcgccgagc	tggccgccgg	gctgaaggcg	caggggcgca	ccctcaccga	80160
ccggctcgac	gagctggccg	ccgagttcgg	cgtgcaccac	accgaccaac	tctcggtgcg	80220
ggtggacgac	ctgcgcatca	tcgccgacgc	gatggcccgg	gtccgggcgg	ccaccccgac	80280
gaccctgctc	ggccgcccgg	tgaccgaggc	gcgggacctg	ctccccgagg	cggacgtggt	80340
gatcctgcgt	accgacgggg	cacgggtggt	gatccgcccg	tcgggcaccg	agccgaagct	80400
caaggcgtac	ctggaggtgg	tggagccggt	ggcggacggc	gacgtgccgg	cggcccggac	80460
gcgcgcggcg	gccacgctgg	cggcactccg	cacggaaatc	gccgccctgg	tgcagggatg	80520
aggtgtgctc	ccgcttccga	cgctctctca	gcgggttggc	gtgtcgcccc	caggttcgtg	80580
gtgatatgcg	gccaggtaag	ccaccgtcct	gccactatcc	atgtcgtaga	acatgatgcg	80640
tgccacttgg	atgtagtagt	aggtgaccaa	tgaggtgaac	ccggggccct	gtttgagcgt	80700
gtacgtagcg	ccgaagccac	tggcagtcac	atcgtcacgg	cgggctttcc	cgttagcgct	80760
cgcgtagctc	agcgcagcag	gaacatcctc	cccgccatag	ggatacagca	gctggctggt	80820
gtatcccttc	tcgaagggct	ttgcaggttc	tgccggcaag	ggcgagaggt	cctgggcgtc	80880
cgtcttgatc	acgatetegt	agagccggac	atcggccgtc	tcggtgttgt	acgccaggat	80940
gaccggcacc	ggcaaggtgt	ttgggagcgt	gaccgaaatg	gacgtgaacc	cgggtccggg	81000
gcgctgcgtc	ggccgctgcc	cggcttgggt	ggcgggcccg	tccgaggaat	aactacggaa	81060
catgcaactg	ccgtctgtct	tgttgtacag	gaacagccac	tgccgctttc	caccctcgcc	81120

gttcacctcg aagggcgcta cggacgacca tccagcgccc cagttgtcct tctggccatc 81180 aggeggeeae acctgetege aaccgtette gttgteeaea acctgeeaea eggegetgtt 81240 gccggtaagg gcatcgtaga gctggacata ccgcctgtcg ttctgcacga cgggaacgac 81300 ggaggtccac cccttcccga aattgcgctg ccagcgggga ggccactcgg gtggcatctc 81360 gtcgtgggca ttgactggac cgaaggcggc cgtgccgtca ttgctgttgt agaacagcac 81420 cgctgggcca ctgtagtgcc cgtcgaaatg cagagatatg acgtgcgtga accctggtcc 81480 gagttggaca tcatagagag cattccggag tgacatgggt ttaccccgtc ctagggatca 81540 ctgcttctca acaagatcat caacggtgtg cggcaggctg cacaatcggg tggaagaaga 81600 gccagcaccg ggcctcactg gccatcacag tatcgtctga cctcttcgac cgggcccgaa 81660 acgggcgaac cgagagcgtt ccgcgcatct gtcggtcggg cgtgtcgaag gtgcggctgt 81720 tegecaegtg egeggegage agggtgeeet eegegeegte aegggttetg eeaegaggeg 81780 gccaggaccc agacggtgac cagccggccc agggtgccgg tcacgatgaa ccgcttgcga 81840 ccgctggctg cgccgctccg gcggccctcc gcgccggacc gggaacgcgg cacgctcacc 81900 ccgcgtgatc ccttgcccac gaagggctcg tctgaatagc atcagcacat caggccccac 81960 cattaccegg caccattggc attegettte ttegacgttg eggetgeggt gecegggegt 82020 tgcatttccg gcggaaaggt gttgcacggt gcgtgaaaca aatggctcga ccgtgccgcg 82080 acggcagete ggcaggetge teacceaget eegegagage geceatatea geategaege 82140 ggcggccggc gagctggact gctcgcggca gaagctctgg cggatcgagc gggggctgac 82200 eteggeeaag acaceggaeg teegggtget etgegagetg tacegggeea egeeegaeea 82260 ggcgagcgtg ctgctcgggc tcgccgaggt gagccgggcc gaggggtggt ggcacgccca 82320 eggcagetee gtgeeggeet ggtteteget etaegtegge etggagaaeg tegegageag 82380 catteggeae tacaaegegg agetggtgee ggggetgttg cagaececeg getaegecae 82440 cgcgctcttc gagcacaacc ggcccgagct gggcgaggag gagcgaaaga aggcggtggg 82500 ettecggact cageggcagg ggetgetgge ceggeggetg ceceeggeee cegagetgae 82560 cgtgatcctc agcgaggcgg tgctgcgccg cccggtgccg ggccgatcgg tgatggccga 82620 ccagctccgg cacctgctgg ccgtcggcga acggcacaac atcaccgtac gggtgctgcc 82680 getggeegee gggeegeege tggeegeega ggeeggeaeg ttegtgetge tegaetteee 82740 gctctcggcg ctcggcagcc cgaccgagcc gccgaccgtc tacgtcgagg ggctcaccgg 82800 cgcgctctac ctcgaccagc cgacggagat cgccgcgtac gaacgggtct ggaggggtct 82860 ggattegete geeeteggeg egegacaate ageggagetg ategatgeea teeggggaga 82920 gtgctatgag tgatctgacc ggcgcccgct ggcgcaccag cacccgcagc ggcaccaacg 82980 geggggaetg egtegaggtg geegacaace teaceggeat egteggegte egggaeagea 83040 aggacccggg cgggccggcc ctgaccgtcc cgcccgccgc ctggtccgcc ttcgtcaccg 83100

aggtcaaggc	caaccgcctc	accegetgae	agctccgcaa	cgaaccaacc	cccggctacg	83160
cctcagacgc	ggccagcgcc	ccagggctgc	ccacgcctca	gacagcccgc	gcctcagacg	83220
tgcctgcgcc	tcagacagcc	cgggccgcag	gggcgcgtgc	gcctcagacg	gcccgggcct	83280
caggcgcgct	tgccgagggc	ggcgtcgacc	gccttgccca	gggcggtgac	gaccagggcc	83340
accgagggc	ggaccaccga	gtcgtccagg	ctgacggtgc	cggagaagcc	ggccccgccc	83400
gcgatctcct	ccagccgacg	ccgggcgtcg	acggcggcgt	cgccggtcag	gccgagcgcc	83460
ggctccatcc	ggagcaccgc	gaccagggtg	gccagcgccg	ccgtcgcctc	gtcggggatc	83520
tgcccgccgg	ccagcgcctc	ggccagccgc	cgccgggagt	cctcctccac	ggtggcgtcc	83580
gccgtcgggt	agcggtgcac	gtggatgaag	cccagctcgg	tctcctcgac	gtcgcgcacc	83640
acgccccggg	cgaccaggtc	gccgaggatc	cggtcgcgca	ggccgtggcg	cagccgctgc	83700
acccaggagg	acggggtgtg	cggcgtgtcg	gcggccatcc	ggcccaggac	ctcgtccagg	83760
atcggttcgc	cggtgggcgc	ggggtccgtg	accaccaggt	tcccatcgac	gtacgcgacc	83820
cggccggcga	gggccagctc	gatcaggacg	gcggcggcca	tcccgaggtc	gaggctgatc	83880
cgcggcatgg	tegeettgee	ggattcgtcg	tcgtacgcga	ggagcagcaa	ttcctcggcc	83940
agcgcaacac	cagtcatggc	cggagacggt	agcgcctgag	cgcaccccgt	gcgcccccaa	84000
ctcgcccacg	agcgcactcg	cccggtgaga	ggggaacccc	gctataccgc	aggcgttaac	84060
agggggccct	tccttgcgat	cagaagcggg	gcataccgcc	gaactggcgg	tcgccggcgt	84120
cgccgaggcc	cggcacgatg	aacatccggt	cgttgaggct	ctcgtcgatc	gcggcggtga	84180
cgaggcgcag	cggcaggccg	gactgctcca	gccgggcgat	gccgacgggc	gcggcgagca	84240
cgcagagcac	ggtgatgtcg	gtgcagcccc	gctcggccag	cagccggcag	cagtgctcca	84300
gggagccgcc	ggtggccagc	atcgggtcga	ggaccagcac	gggcaggccg	gcgaggtcgc	84360
gcggcagcga	ctccatgtac	gcgcgcggct	cgtacgtctc	ctcgtcgcgg	gcgaggccga	84420
cgaagcccat	ggacgactcg	gggagcaggg	cgagcgcggc	gtcggccatg	ccgagaccgg	84480
cccgcagcac	gggtaccagc	agcggcgggt	tggccagccg	ggtgccctcg	gcgtcggtga	84540
cgggggtctg	caccgggtac	ttctcgacgg	ggaaggagcg	ggcggcctcg	tacacgagca	84600
tggtggtgag	ctcgtgcagc	gcggcccgga	agttggagga	gtcggtgcgc	gcgtcccgca	84660
tggcggtcag	ccgcgactgg	gcgagcggat	ggtcaatgac	gtgtacgtcc	acgatcgccc	84720
aacctaccga	acgcccgggc	cccgagacac	gaggagcgac	gccgctcacc	cggcccgtgc	84780
ggcaaccctg	gacggttggc	gttcgaaggt	agggcaggtg	cccaaggtcg	ggcccgacct	84840
cgccgcgtga	tcaagatcac	gaggcgtgcg	ggtgcgtaga	cttccgggca	tgacggcgac	84900
agcgacgtcg	gcccggtcgg	acctctccga	gctgggacga	tccgagaccg	ctttgcggaa	84960
cttcctgcac	ggcctgccgg	gcgtggacca	ggtcggcgcg	gagcagcggg	cggcccagct	85020

cggcacccgc tcgatcaaga ccacggccaa ggcccgggcg atcgacctgg cgatccggat 85080 ggtcgacctg accaccctgg agggggccga caccccggc aaggtgcggg cgctcgcggc 85140 caaagcactg cgccccgacc cggccgaccc gtcctgcccg cacgtcggcg cagtctgcgt 85200 ctacceggeg atggtecegt acgtggeega ggtgetgege ggateegeeg ggteegggeg 85260 gccgtccggc ggaccggacg gcaacgcgcc ggccggaccc ggcgtggtgc acctggccag 85320 cgtggccacc gcgtttccgt ccgggcaggc acccctggag gtcaagctcg ccgacacccg 85380 ggccgcagtg gcggctggcg cggacgagat cgacatggtg atcaaccggg gcgcgttcct 85440 ggccggccgc taccgcgagg tctacgacga gatcgtggcc accaaacagg cgtgcgggga 85500 cgcccacctc aaggtgatcc tggaaaccgg cgagctggcc acgtacgaca acgtgcgccg 85560 ggcgtcctgg ctggccatgc tggccggcgg cgacttcatc aagacctcga cgggcaaggt 85620 tecegtegeg gegaceetee eggtgaeget ggtgatgetg gaggeggtee gegaetteeg 85680 cgccgccacc gggcggcagg tcggcgtgaa gccggccggc ggcatcaaga acaccaagga 85740 cgcgatcaag tacctggtta tggtcaacga gaccgtcggc ccggactggc tggacccgga 85800 ctggttccgg ttcggcgcgt ccagcctgct caacgacctg ctcatgcagc gcaccaagct 85860 gacgaccggc gtctactccg gtcccgacta cttcaccctg gactgagcgt gatcttcgaa 85920 tacgcgcccg cccccgagtc ccgctcggtg gtggacctca agccctcgta cgggctgttc 85980 gtcgacgggg agttcgtcga cccggccgac ggcggcggct tcaagtcggt caaccccgcc 86040 teegaggagg tgetegeega gategeegag gegggeageg eegaegtgga eegggeggte 86100 86160 egegeegeec ggaeggegta egagaaggtg tggggeeega tgeegggeeg ggaeegggee aagtacetgt teeggatege eeggateate eaggageget eeegegaget ggeegtgetg 86220 86280 gagteeetgg acaacggcaa accgateegg gagteeeggg acgtegaeet geegetggte gccgcgcact tcttctacta cgcgggctgg gcagacaagc tgccgtacgc gggcttcggc 86340 cegaacecee ggeogetegg egtggeegeg caggteatee egtggaactt ceegetgete 86400 atgetegeet ggaagatege eeeggegetg geegeeggea acaeggtggt geteaageeg 86460 geggagacea eccegetgae egegetgetg ttegeegaga tetgeeagea ggeegagetg 86520 ccggccggcg tggtcaacat cgtcaccggc gcgggcgaca ccggccgggc gctggtcgag 86580 caccegggeg tggacaaggt egegtteace ggetegaceg aggteggeaa ggecategee 86640 86700 cggtccgtcg cgggcaccgg caagaaggtc accctggagc tgggcggcaa ggccgcgaac atcgtcttcg acgacgcccc ggtcgaccag gcggtcgagg ggatcgtcaa cggcatcttc 86760 ttcaaccagg ggcacgtctg ctgcgccggg tcgcggctgc tggtccagga gtcggtcgcc 86820 gagcaggtgc tggagtcgct gaagcgccga atggcgctgc tgcgggtcgg cgacccgttg 86880 gacaagaaca ccgacatcgg ggcgatcaac tcggccgccc agctcgcccg catccgcgag 86940 87000 etgteegeeg egggegagge egagggggeg gagegetggt egeegeegtg egagetgeee

gagcgcgggt	tetggttege	gccgacgatc	ttcacggggg	tcacccaggc	gcaccggatc	87060
gcccgggagg	agatcttcgg	tccggtgctg	tccgtgctga	ccttccgcac	cccggccgag	87120
gccgtcgaga	aggccaacaa	cacgccgtac	gggctgtcgg	ccgggatctg	gaccgacaag	87180
ggctcccgga	tcctgtggat	ggccgaccgg	ctgcgcgccg	gggtggtgtg	ggccaacacg	87240
ttcaacaagt	tcgacccgac	ctcgccgttc	ggcgggtaca	aggagtcggg	ctacggtcgc	87300
gagggcggcc	ggcacgggct	ggaggggtac	ctcggtgtct	gagcgggtcg	cggtacgcaa	87360
gacgtacaag	ctcttcatcg	gcgggaagtt	cccgcgcagc	gagtcgggac	ggtcgtatct	87420
cgtgcaatcc	gcgaacgtgt	cgctggcctc	ccgcaaggac	gcgcgggacg	ccgtggtcgc	87480
cgcccgcgcc	gccgtgaagg	gctgggccgg	ggcgaccgcg	tacaaccggg	gtcagatcct	87540
ctaccgggtc	gccgagatgc	tggagggccg	ccgcgagcag	ttcgtcgcgc	tcggcgtgcc	87600
ggccgacgag	gtcgacgcgg	cgatcgaccg	ctgggtctgg	tacgcgggct	ggtccgacaa	87660
gctcccccag	gtgtacggcg	gtgcgaaccc	tgtcgccggg	ccgtacttca	acctgtccgc	87720
gcccgagccg	acgggggtgg	tggccgtggt	ggcccccgag	gcccccgcgc	tgctcggcct	87780
ggtcagcgtg	atcgccccgg	cgatcgtcac	cggcaacacg	gtggtggtgg	cggcctcgcc	87840
gacccagccc	ctggcctcgg	tgaccctggc	cgaggtgctg	gccacctccg	acctgcccgg	87900
cggggtggtc	aacgtcctga	ccggtgcgat	caccgagacg	gtgccgacgc	tcgcggcgca	87960
cctggacgtc	aacgcgatcg	acctgaccgg	ggtgggcgac	gcgtcgctcg	ccaccgagct	88020
ggaggtcagg	gcggcggaga	acctcaagcg	ggtgattcgg	ccggccccgg	ccgaccacga	88080
ctggtacgcc	gacccgggcc	tcacccggat	gacgacgctg	ctggagacga	agacggtctg	88140
gcaccccaag	ggcgtctgag	cccaccgacc	cgtccaccga	cccgcccgcc	acccggccgc	88200
cggaggcagg	ggtgggcggc	gggtggggtg	gatctactac	gaggggtagg	attgccgcgt	88260
gactcggttg	ggtgatcttg	agcgggcggt	gatggacgtg	ctgtgggaca	ccgtcccggg	88320
cacgtcggac	ggggtgacgg	tgcgcgaggt	cgccgaggcc	ctcgacggcc	gcgagctggc	88380
gtacacgacg	gtgatgaccg	tgctggaccg	gctcgccggc	aagggcatgg	tgcggcgcca	88440
gcgggagggg	cgggcctggc	gctaccaggc	cgcggccagc	cgcgaggcgc	acatcgccca	88500
gctcatgctc	gacgcgctgg	acctcggcgg	cagccgggac	gccgcgctgg	tgcgcttcgc	88560
ccggtcggtg	accggcaccg	aggccgaggt	gctgcgcgcc	gccctcggcg	ccgaggcggg	88620
cggcccgctg	accgaccgcg	tcgacgcgcc	gcgcgccgac	cgggccgggc	agccggccct	88680
ggccgacgag	gcgacggacc	ggtagggccg	ccgtcatggc	gtacgccgtg	cacttcgccg	88740
cgacggtcct	ggcctgctac	ctgaccgctc	aggtcctggc	ggcgtccacc	tggacgtggc	88800
gggcccccg	gatcgcgatc	gtctgctggc	aggcggtcgg	gctcgcgctc	gggctctccg	88860
cgatgggcct	gccgatggcg	ctcggcgtgg	ccgcgtacga	ccggccgacc	ggcagcgcgt	88920

tgctcgccct ggccaccgac ctgacccacg gcaccctgcc ggccgggctc ggcgcggtcc 88980 accteggtet ggteggggte gggtteggea teggggegge getgetegee acgaeggtae 89040 gcagcgtgca ggcgaccgtc cgggcccagc ggcagcaccg ggacctgctc gccctggtgg 89100 cccggcggga cccggaggtg ccgggggcgc tggtgctgga ccatccgagc gcggcggcgt 89160 actgcctgcc gggcgtgcgg ccccgggtgg tggtcagcgc cggggcgctc agcatgctcg 89220 accgggccga gctggcggcg gtgctgaccc acgagcgggc gcacgcccag gagcgccacg 89280 accttgtgct gctgccgttc accgcgctgt gccgtgcgct gccctggttc cgttgggtac 89340 gcgacgcgca cgagcgggtc gccctgctgg tcgagatgcg cgccgacgac aaggcccggg 89400 agetgeaege egaggeteee etegeggggg egttgegeeg gttegeegeg geeggeeaee 89460 ggategegee ggeeggeace eteggeetgg gegaeeggga eetggaegte egggteeage 89520 89580 ggctgctggt cgccgaccgg ccgcccggc tgatcggggc cgccgcgctg gcggtggcgg teaccetggt egegetgeeg gtetecetet teetgagetg aegeeegaee eggaeaegte 89640 egacceggae aegegegaee ggaeaegtee gaeeeggaeg eetegeeega gttgggeeeg 89700 tgtcccacgg ggccggctcg cctgcccgtt gccgggccac cgacatgcgg ggcgataggt 89760 agagagccta cgtgtagtct tcctacgaca agggagccta ctaccggagg gcggccatgg 89820 atcaactgct cctcgcccgt ctccagttcg ccacgaccac ctcgctgcac ttcctcttcg 89880 tegtegteae geteggtetg gteaecetge tegteggget ceagaeggee tggaegatea 89940 ccggcaatcc cgtccacgag cggctgaccc ggttctgggg tcagctctac gtgatcaact 90000 acgtgctcgg catcgccacc ggcctgctca tggagttcca gttcgggctg aactggagcg 90060 gcctgtcgcg ctacgtcggc aacgtcttcg gcgccccgct ggcgatcgag accctggtcg 90120 egttetteet ggagteeaeg tteeteggga tgtggatett eggetggeae eggetgegee 90180 ggggcgtgca cctcgcgctg ctgtggggcg tggcgctgac cgcgtacgcc tcggcgttct 90240 gggtcatggt ggcgaacgcc tggctgcaga acccggtcgg ctacgaggtg cgcgacgggg 90300 tggcccacct gaccgacttc ggcgcgttgc tgaccaatcc caccttcggc ctggccttcg 90360 ggcacgtggt cgccgccgcc ctgctcaccg gcgggatgct gatggcggcg gtgagcgcct 90420 ggcacctgat ccggcgcacc ccggaccacg cgctgttccg cacgtcgctg cggatcggcc 90480 tggtcaccgc ggcggtctcg atcagcctgg tgcagggctt cggcttcgcc cagttcgggc 90540 eggtegggea gaegeageee aceaagtteg geggeggege geagegegae geeetggteg 90600 ccgaatggac ctcccggttc gggcccggcg actacacccc gcccgtgctg gccgacgtcg 90660 ggctcggttt catgatcctg atcggcctcc tcctgggctg tctgtggctg ctgctcccc 90720 tgctctggcg ggactggttc atccggctgc gcttcccgct ctggctgatc ctgctggcgc 90780 tgccgctgcc cttcgtcgcg gtgatcctcg gctggatcgc ccgtgaggtg ggccgccagc 90840 cctgggtcgc gtacgggctg ctttccaccg agcgggcggt ctcgccggtc gcgcccgggg 90900

tgatgctcgc	ctcgctgatc	ggcttcaccc	tgctgctcgg	cgggctcgcc	gtcgccaact	90960
gggtgctgtt	cgcccggtac	gccgcccggg	gagccgccga	tcccgcccta	ggccgccggc	91020
ccggcccagc	cgccgacgag	tcccgtcccg	tccccgtcct	cggctgagga	ggcccctgtg	91080
gaactcgcct	ggtacgccct	gctcgggctc	ttcctcgccg	gctacctggt	cctcggcggc	91140
tacgactacg	gcgtcggcct	gctgctcgcc	cggggcggcc	cgccggcccg	ccgccgggcg	91200
gccctcaccg	ccgtgggccc	gttcttcctc	ggcaacgagg	tctggctggt	ggcgaccgtc	91260
ggcattctgt	teggegegtt	ccccaccctg	gagggggaac	tgctgtccgg	cttctacccc	91320
gtcgtcgccg	ccgcgctggc	cggggtgatc	atggtgaccg	tcggcgtgca	actgcgcagc	91380
cgcccgaccg	acgagccgac	ccgcgccgcc	tgggaccgga	tggtggccgc	cgggagcctg	91440
ctcgccgcgt	tcggctgggg	ggcgctgctc	gccgggctgc	tccagggcgt	accgctggcc	91500
gccgacgggc	acgtcacggg	cgtcggccac	gtggccaccc	cgttcgcggc	cctcgccggg	91560
ctggcgatga	cggccctggt	ggcggtgcac	ggtgcgacgt	tcctcacgct	ccggctgtcg	91620
gccgccgacg	ccgcaccgct	ggcccgtacc	gcccgccggc	tggtcgcggt	ggcgctcgcc	91680
gccgtcgccc	tggccgccgt	cgcgggcgcg	ctctccgatc	gggtacgcgc	cgcgacgcag	91740
cgcccgctgc	cggccgtact	gctgccgttg	gtactggtgg	cggcgctgct	ggtggcccgg	91800
gcggcgcacg	cgcggcacct	gcccggggtg	gccttcgccg	ccacttcggc	ggcgctggcg	91860
ctgccggtgg	cgggagtcgg	cgcggcgttg	tggccctacg	cgctggtctc	caccgtcgca	91920
ccgacggcat	cactgagcgt	gaccgacgcg	gcggccagcg	ggccgacgct	gacggtgctg	91980
ggctggctgg	cgctaccgct	cctgccggcc	ctactaggct	tccaggcgat	gtgctggtgg	92040
gtgttccggg	gacgaaccga	cggcagggca	ccggtgtact	ggtgagccgc	cgtcccttcg	92100
acccacgtct	gctccgccgg	gtccccgcgg	cccggcgcga	cctcgccgtg	ctcgcggtgc	92160
tcggcgggct	gacggcgctg	ctggtcgtgg	ggcaggccac	cgcgctggcc	acggtgctgg	92220
ccgccgcgct	cgacgggcgg	ttggcccggc	cggcgctcgc	cggtttcctg	gccgccgtgg	92280
tggggcgggc	gctggtcgcc	tgggcccagg	gcacggtggc	ggcgcgggcc	gccgcgacgg	92340
tcaaggcggc	gctgcgggcc	gacctgctcg	ccgccgtcgg	ccggcacggt	cccggctggg	92400
tcgccgggca	gcgggccggg	cagctcgcca	ccctggccgg	gcgggggctg	gacgccctgg	92460
acgcctactt	caccgggtac	cttccgcagc	tcgtgctcag	cgtcaccgtc	ccggtggccg	92520
tgctggcccg	gatcaccttc	gccgactggg	gctcggccgt	catcgtcgcg	ctgaccctgc	92580
cgctgatccc	ggtcttcggg	gcgctgctcg	gctggcaggc	gcaggccgcc	accgagcggc	92640
agtggcggcg	gctgtcgacg	ctcggcgggc	acttcctcga	catggtcgcc	ggcctgccca	92700
cgctgcgcgc	gttcggccgg	gcccggggcc	aggtcgaggt	ggtccgccgg	atggccgacg	92760
ggcaccgcgc	cgcgacgatg	cgcacgctgc	ggatcgcgtt	cctgtccgcg	ctggtgctgg	92820

agetggtege caccetgteg gtggegetgg tegeggtgee ggtgggeate eggetgeteg 92880 geggegget ggegetgtee accgegetge tggtgetget geteacceeg gaggegtace 92940 tgccgctgcg ggcggccggc agccggttcc acgccagcat ggaggggctg gccgcgctgg 93000 acgaggeact gaccetetee geegeegace egacegeeae ggeeacegee gggtegegge 93060 cegteceega egggegegee gagateeggt tegagggegt gaeegtegeg taegagegga 93120 ccgtggcgct acgggacgtc acgctgacaa tccggcccgg cgagcggatc gcgatcgtcg 93180 ggccgagcgg cgcgggcaag agcaccctgc tcaacctgct gctcggcttc gtcgccccga 93240 cgcagggccg ggtcaccgtg ggtggcgtcg acctggccgg cgcggacccg gacggctggc 93300 ggcgtcaggt cgcctgggtg ccgcacggg cccacctctt cgccgcctcg ctgaccgaca 93360 acateegget eggtgeeece ggeaegeeeg aegeegeget egeeggegeg gtegeegeeg 93420 ccgcgctgga cgaggtggtc gccgccctgc ccgacgggct cgacaccgtg ctcggtgagc 93480 gegggeaegg cetgteeage ggeeagegge agegggtege cetggeeegg gegtteetge 93540 gggacgcgcc ggtggtgctg ctggacgagc cgaccgcgcg gctggacacc gccagcgagg 93600 eeggggtget ggeegeeace egeeggeteg tegeegggeg aacegeeetg ttggtggeee 93660 accggccggc gctgctctcc gacgccgacc ggatcctgcg ggtcgaggaa ggccgggtca 93720 ccgagctgac caccacccg gccacagggg tgacccccgg ccccggcgag gcggctgccg 93780 gaccggccgg gcaggtcgcc cccgcccgg ccggagaggg ggcggcccga tgagcaccgg 93840 tecegeegae gaegeetteg ceateeeget geeggeegae ggggeeeegg tggeeggegg 93900 cagegteegg geegeegage gggeegtget eeggetggee eggeegtace tgggeegget 93960 ggtcggcgcg ggtctgctcg ccgccgccac cgagttcgcc gggctggccc tgatggccac 94020 egecacetgg etgetgatga gegeegeegg teggeeacca etggaeegge teaeegtgge 94080 gategtegeg gteegggege tggegateag eegaggegtg tteegetaea eegagegeet 94140 cgccggccac gatgccgtgc tgcggatgat caccgacgtc cgggccgggg tcttcgccgc 94200 ectggccgcc cggcgcgacg ccgcccggca gcgcaccggg gacgcgcttga gccggctcgt 94260 gtccgacgtg gaggccgtgc aggacctgct gctgcgggtg ctcgtcccgg gggccgccgc 94320 cacggtggtc agcgtgctgg ccgtggccgg ggccaccacc atctcgctcc ccgccgccgg 94380 ggtgctggcg ctgggcctgc tcgtcgccgg ggtggccctg ccgctcgcgg ccaccgcgct 94440 gacceggeac geogeogace gggtggeece getgegegge gegetegeea eggacgeegt 94500 ggaccttgtc cacggcgccg ccgacctggc cgcgttcggt gccaccgggt acgcgctgga 94560 egeegeegee gategggeee geeggetgge ceggetggaa egaeggeteg eegeeaeegg 94620 ettegeegtg gaegeegeg gggegetegt egeeggggtg acegeeggea eggtggtggt 94680 caccgcgctg cgcgacggcg tcggcggggt gctggtcggg gtgctggcgg tcggttccct 94740 ggccgccgtc gaggtggcgc tggcgctggt cggggccgcc cggcagcgca cccagctccg 94800

ggccgggctg gtccgggtgg ccgccctgct gaccgccccg caggccgacg cgcccgccgc 94860 94920 caccccgccc ggtgccgccc gtgccgccgc cgtcggtgcc ggcccgcacg acgtgcgctt cgacgcggtc accgtgcggt accggcccgg caccgccccg gccctggacc gggtcaccct 94980 ggacctgccg gccggccgcc gggtcgccgt ggtcgggccg agcggcgccg gcaagagcac 95040 cctcgccgcc gtcctcaccg gcacggtgcg acccgagcag ggccgggtca ccctcgacgg 95100 ggccgacctg teggcgtacc eggtcgagga actgcccegg gccgtcggcg gcctgctcgc 95160 cgaggcgtac gtcttccacg ccacggtccg ggagaacctg ctgctcggcc ggcccgccgc 95220 95280 cgacgaggcg gagctgaccg ccgcgacccg ggcggccggc ctgctggact gggtgcacgc ccagccggcc gggtgggaca ccgtggtcgg cgaggagggc ggacagctct ccggcggcca 95340 geggeagege etegegetgg ecegggeget getegeegeg eceggggtge tggtgetega 95400 cgagccgacc gaggggctcg acccgtccgc cgccgacgcg gtgctcgcct cggcgctggc 95460 ggcgaccccc gccgggcact cggtgctgct gatcagccac cggctcagcg ggctcgccga 95520 cctcgacgag atcgtggtgc tcgacgccgg ccgggtggtc cagcgtggcc ggcacgacga 95580 gttggtcgcc gcgccgggct ggtaccggga ccagtggctg ctccaggagg cggccgagcg 95640 95700 egggtacetg geeetgacge eeegeeeetg ageeggetee gggatteeee eggaegegte ggcagtcacc gcatggcagg ctcgtcgcat ggtgcgctgc gacgacgtac tcgtgaagga 95760 geggetgege gagttgageg aceggetgea eggeceggea eggeteaagg eegacetget 95820 ggccgaggcc cgccacgcgt tgcaggacgc cgtcgaggcg taccgggacg gcgggctgcc 95880 ggcggcggag gccgagcggc gggcagtggc cgagttcggc gagccggccc ggctcgcccc 95940 96000 ggcgtaccag gcggagctgg cggccgggtc gctgcgcggc ctgtccctgc gggtgctcgc ggtcgccggc gtcctggtcg tcgcgggcga tctgacctgg caggggtcga gctggagcgg 96060 eggeeeegge eegeeggegg cetacegeet getgteegee teggtggaeg geatetgget 96120 gggcgcggtc gtgctgtcgg tggcggggtt gctgctggtc gccgcctcgg cccggtgggc 96180 gcacceggee etgeceegge tegecegget gaceggtete gggeteaceg ceaegetegt 96240 cetgggegtg gegaceggeg eggeeetgta egeetggteg ategggetet gggaggegge 96300 ccgcacctgg ccgccgatgc tcgtgggcgc gctggtctgc ggcgcggggt tcttctggat 96360 eggtegggeg geeeggteet ggetgetete ggeaegeega eeggeeggae eggegtagte 96420 gggtgggcgg cgggcgggt caggccggcg tggcgggggt gtcgccgagg aactggccga 96480 eggtegeget gaacteeege eageeggeee gtteeeegge gagggeeegg eggeeggagt 96540 eggteagete gtaggtgegg egetegegge egttgaeggt geteeaactg etgaecaegt 96600 gccccgcccg ctccagccgg cgcagcgccg ggtagatcgt cccggtaggc agatcgaggc 96660 tgccctcgct gcgcgcgcgc agcgcctcga tgatggcgta gccgtgcagc gcgccccgtt 96720

ccagcaccgc gagcagcagc gcgtcgaggt gtccgtgcag cgcctgggcc ttcataggta 96780 gcaagactac ttgtgggcca ctcgcgccgc caccggggtg cgggcaccgg gcctcctaag 96840 ccgcccacta gggtatgtgc ccagagtcac tcggcggccg gagacgccgc cgggtgggca 96900 gcccgaagca cacggaggtc agcgtggccc gccagtcgcc ccaacggccc gacgccgacg 96960 agectgaget egacgagace gaeggeaceg cegeagaggt egaagaggae ggegegeee 97020 cgtcggcgca ggacgccgac cgcgcgctct gggacgagct gcgcatcgac ccggtcgaga 97080 tegecetgee egeeggeace ggetacaege tgegggegta eeggeeggea egggagttga 97140 ccccgaccga cgtcgccgag cgcgaccagg acgacccgtt cctggcccgc cggcaggcgg 97200 97260 tegagacega egaggaegag gaegaggtea teateetega egaggaggtg geegeegagt 97320 tegeegagge ggaegeggag gaggeeggeg ggaagteeeg etecegeaag eeeegegeeg acgeggaete egaegaegee ggageegeea cagaegegga egeggaggag gageeggaet 97380 ccgacgagga cgaggcggc gacgaggagg ttccggtctt cctcagccac cggggcaggc 97440 tgctgctgtt caagacgccc gaatccctcg tcagcttcgt ccggtccggc gcacccaacg 97500 acatgtetea actggacage tggaatgaac tgteegaacg ggtggageeg geegacateg 97560 tecegetega egaggaeace tacgagetegg acctggtegt ggagaacetg eggggtggge 97620 acgacacctg ggactcggcg ctgctgatcg agccggcgag gtggcccggg acgtcgcgta 97680 tgccctgcgt ctgcccgccg tgttggacat gctctccgcc ggctccagcc tcgacgacct 97740 ggacgaggcg ctgcgcgcca cggccaacgg cgggctcggg ggcttcctcg gccgccggcg 97800 97860 gctgaggaaa atcggcgcgc agacggcgag tctcggttgg cgcaccattg tcggcaagat 97920 etetgeggte gtggaetgge gegaetgaea egtteeaggg ageateagte tetggeagag 97980 aaagaccagt cccgggagga ggacgacgct gtggcgctcg tgcgcgtgta ctgcggtctg gecteggegg atceggeega eegaceggee teggeeggtt eggegetgae gteegetgtg 98040 gtcgacgacg caggtcggct gctccatgtc tgcgagatcg gcgacgaccc agccggctac 98100 98160 geteagetgg tegtgetaet egtggagegg tegggeggge egagegggge tgegategee gccgacageg acgaccacac ggtcaccteg ctgctgagtg ccgccgggcg tccactggcg 98220 98280 atcgcggacg acgactcggt ggacgacttc gccgagcggt tcgccgacga cgactcgctg gaggagatge agteegegee ggeegagegg egggggteg ggetggeeeg ggegeteeag 98340 gccggcgcgc tctcggcggt caccctcccg gcgccccggg atctcgccgg ctacaagcag 98400 gtcctctcgg cgcacgccgc gctcgccagc ggccggcact ccgccgccgt ggcgctgcgc 98460 gaggtgetge gggageteta eeeggeegee etgegegegt acceggaeee ggeegageeg 98520 gtcgccctgg ccgtgttgga cgccctgccc gagcccggca tgctgggcgg gacgatcgcc 98580 cggggccggg aggtgtcggt ggcggcggac gccatcgccg cccacctcgc ggccgacggg 98640 gtggccgacg aaggcaagat caacgatgcg gtgaccgcgc tgcgggtcgc catcgccgag 98700

98760 accccccgcc gcgcggcggt cagccgggcg ctcacctccg ccgtggcgga gacggtccgt 98820 caggeggtgg ceteggtgeg ageatgegae gegggetgeg aggeeetggt eggegegete gacgcccggg tcaccacccc caccccggtg ccgggccggc gggccgccgc ccgccggggc 98880 gageeggteg eegagttgee eggegeegge etgegegeae tgeggeeeae agageeegag 98940 99000 ccggtccccg gccggcgcag ccgtcccgag ccggtccccg gcggcagcct gcccgcccag ccccgcccgc tcggcccgcc gccggtcgcg ccggagcccg tcgccccgcc gccggtcgcc 99060 ccgcgcccga tcaccccggc cgcctcggcc accccgccgg tctccggccc gccgtcgccc 99120 99180 gagecgegee geetgatega caacceggee aaccggeegg teteegegee geegeeeeeg ccaccgggga tcaccccgat cgcgccgagc cagcgcgagc gcgggtccgt gccgccggcc 99240 99300 gaggccggtg agccgttccg gcccacgctg accaccgccg cgatccagaa cgcgcgggcg gageggeage geaceateat ecegeetege eceaagaega egggegagte egegeegeeg 99360 99420 cccaccggcg gettcagcgc caccgacctg agcgtcccgg tgccgacccc gcgtcccggc caggagtccg ctcccccgg ctcgcgggcg aactggccgc tggtcaacaa ccccgaggac 99480 cccgccgaca gctccccgaa caatcccgtc gcgcggcggc ccttggagga tcgggcgaag 99540 cggcagatcg acgcgccgac ccaggtggtc ccgccggccg agggccgggt caccccgccc 99600 99660 tggctcgccg acgacctgcc ccaggagcca ccgatgctgc ggctggtcga gccgccaccg 99720 ctggccgacc gggcactgcg ggatgggccg ggccaggctg ccgacccgcg cctggagccc 99780 ccgccgctgc ggctggtcga ccgcggcgag gcagcccgcg ccggccgtcc cgcgccggag ccccgccccg agcgggcccc cgcggaacac cggtccccgc tgggtcagcg ggtcccgttg 99840 gaggagegge cegacatgga acateggace geceegeege ageegtegeg gteegegeeg 99900 99960 atggagegge gtacceegee gateteegae gagggggaeg gegacetget gatettegee 100020 gccgccaagt cggcctggtt cgtcgggcac ggcgacgagt ccgagatgga ctggtcgagc 100080 accgccgaca ccgggtggca ggccgccgag caggccgccc gcccggcggt gggcgccgat 100140 accaaggccg ggttgcccaa gcgggtgccg caggccaacc tggttccggg ctcccccctg 100200 cgcgaggagc gtcccctacg gatagtccgc gacgcggcca gcctcgccga gaacacgacc 100260 ggctacttcc ggggctggcg tcgcgggcag gagatcggcg ggttcgccgt cggcggccgg ccgggccgcg aggcggccgg cggctgggac ttcacccggg acaccggcga ccgagacgac 100320 100380 gaccgggagt acgagtaccg gtccgccggc taccgctcct gaccatcgcg ccggggtggc gggcaccgcc gccccggccg cgcccgccgt gctggcgtac ggccgtagca acccgacgcc 100440 100500 caccegaceg aceggtggga ccacacegaa gageaaceet ggeeggeege etgaegteee gcagggacgg tgacggctac tggccgtccc cccgggaagg ttgcgaggcg gtcggggcgc 100560 acaggegetg teagggeege teetgageeg eectaeggaa tgggetagee etaeggaate 100620 gagcgccggc cgcccgccgg tggcgtcgag ttcgcctcca gccggtcccc aaacagccgg 100680 acgcgcccga cggcccggcg ggtgccggtc gtcgggcgcg tcccgtcgtc gatcaggccg 100740 100800 gcqcgaccgc gcgcgagcgg cgcatcgtga gcacgtactc gaccagcgag atcagcacgt gettegtega eteceggtte egggegtege aggeeaceae eggeaegteg tgegagateg 100860 cgagcgcgtc ccggacgtcc tgcgggtcgt ggtactgcat cccgtcgaag cagttgatgg 100920 100980 ccaccaggta cggcagccgc cgatgctcga agaagtcgat ggccgcgaag cagtcggcca gccgccgggt gtcgaccagg accaccgcgc cgatggcgcc ccggaccagc tcgtcccaca 101040 tgaaccagaa ccgggtctgg ccgggggtgc cgaacaggta caggatcagg tcccggtcga 101100 101160 togagatacg googaagtoo atogocacog tggtogtogt ctogocoggc acotgooggg tgtcgtcgac gcccacgccg gcggaggtca tgatcgcctc ggtggtcagc ggcgtgatct 101220 101280 ccgagaccga gccgaccagc gtcgtcttgc cgacgccgaa cccaccggcg ataacgatct tcgccgacgt cacgcgcccg ctcgggacag gcgggcggtg cgacatgtca gagcctgcga 101340 101400 agtocactca gcaccototo cagoagttoa gtgoccacog ogtogtogga gtogtocagg atggtcggct cgtggactgc gaccaggccg tccgtcgcca tgtcggcgat gagcacccta 101460 gccacgccga gcgggagctg catccgcgcc gcgatctcgg caagcgactg cacgcgtccg 101520 101580 togoacagog oggogatgta otggtgotot oggocotggo cacogttgot actggcagog gcccgaccgc gcaccgtcgt ctcgacgagc gcctccaacg cgatgtccag ccgagggcgg 101640 101700 gtacgaccgc gggtgacggc gtacggacgg accaacgcgc cagtcggctc gtcacgatcc 101760 atgtcgccgc tcacctcctt cgtccccgac accggctgaa cccggtggaa cccgtcgttc 101820 ttgtccttgc caccccgccc gacccatcgg ccagcgcgtg ggtcagccca tcatccccac 101880 agtcgtacgc ggctgcgggg tcaacgcgtc gcccacccgg tcgaccagga gggccatctc gtatccgacc tgcccgacgt cgcagctacg ggcggcgagc acggcgaagg acgagccgtc 101940 102000 cgagatggac atcaggaaca ggaagccgtt gtccatctcg accacggtct gcagcaccgc accgccctcg aagcagcgtg ccgctccctg cgtgaggctg accagcccgg acgcgatcgc 102060 102120 qqcgagctgg tcggcccggt cacgcggaag gtctcgtgac gacgccagga gcagaccgtc 102180 cgcggagacg gcgaccgcgt gcgcgacacc gggcacccgg tcggcgaagt tggccagcag ccaaccgaga tectgegtag ttgtcatect tgttgeteet tetgeeeget eeeggeeace 102240 gggcctgagc cagactgcga ggattgctgc ccacccggag ctgcctccgg gttggtcggg 102300 ttgccgtcgg gctcggtacg cccacgctgc acgcctcgat ggtatgccga gagcagaccg 102360 102420 cggacgccct ccggcgtacg gcgctggacc gacgtggtgg gcttctccac cccgccaggc 102480 acgagttggg ccatcggcac ccgcttcggc aggcccttgc gggtggtctc cgccaccggg acctcggtgg ccgccgaggc ggcccgccag ccgtcgtccg cggcagtctg ccaggcgtgg 102540

gcctgcggcg	tgggccgccg	gccggcgaag	ccctcggcgg	gaccggggcg	ggtgccaccg	102600
ttggtcggcg	acccgttgtc	gcgcggcatt	cctccggcca	tcggggtgtc	tgccatcggt	102660
gcgttacctg	tcgtcccggg	tgctggtgtc	tggacgggcc	ggccggtgac	gtcgaccgcg	102720
gagaactgtt	gggtcacggc	ggcgttcgcc	gggctcccgg	cgccattggt	cgcgcgctgg	102780
gcgacgccgg	ccgtctcctc	cgaacccgag	cggcgggtac	ggaaccaggc	cgactcgagc	102840
tcccggaaga	tcggcagctc	catcgtctcg	tccgcgtacc	gctgctgccg	gttctgggcc	102900
tgcacgggcg	tcgaccgcgc	cggcgtgggc	ggggtcgtcg	gctgggtggc	cggcgtgctc	102960
ggcacctcgg	tgctcggcac	ccggggcagc	tccgtggtca	tgtccagggc	tgcggcgagg	103020
cgctccggca	ccggcggggt	gaccggctcc	ggcgcggcca	ccggcggcca	ggccggcggc	103080
gccacgggcg	cctgggccga	cgggaccggc	cgactgggca	gcggctgcgc	cgagtacggc	103140
tgaccggaca	cgggcgtgcc	gaacggctga	ccggagacgg	gcgtgccgaa	cggctgaccg	103200
gacaccgggg	cggccgagac	gggctgaccc	gagaccggga	agacggaaac	cggcggtgcg	103260
gacaccggcg	gcaccgagac	cggtggcggg	gtccagcccc	gggcctccgg	gctgctcggc	103320
agctgtcggg	ggatggccgg	ctgctggccg	ctgctggccg	gatcgccgtc	gccggacgcc	103380
cgccgctgcg	gcagcgggtc	gctcgactgg	ccattcgagg	tgcggccggc	ggcggcaccg	103440
ccagcggtgc	cactggcccc	ggtcaggtcc	gaccaggccg	gcatcgaccg	catggaaccg	103500
gtcgacgcgg	gcgtgccgtg	gccgttgcgc	gaggccgggt	cgaacgaccg	gccgcccagg	103560
gttacctggt	tgcccgagtg	ccccggccgc	tgggtgggcg	ccggtgtcgc	cgggttgttg	103620
ccgaaggccg	cgaaggcacc	cagggccggg	ggggccccgc	cgggctgcga	gctggtgagc	103680
gaggcgggag	gggccggcag	cgcgccgggc	tgctggaacc	ggccggagag	cgcccggggc	103740
accagcacgg	tggtgggcag	ggtgacgtcg	gcgacggtcc	cccggtcggt	gccgggccgc	103800
agctcgacct	tgaccccgtg	ccgggacgcc	aaccgggcga	ccacaaccag	gcccatcatc	103860
cgggagacgg	ccacgtccac	ctgcggcggc	gaggcgaggc	ggtcgttgag	gtcgtgtagc	103920
tgctcggcgc	tgatgccgat	gccccggtcc	tcgacgtaga	ggttggcccg	gtcgccgacc	103980
cggcgggcct	ccaccatcac	ctgcgagtcg	ggcggcgaga	aggcggtcgc	gttgtcgaac	104040
agctcggcga	ccaggtggac	caggtcgttg	accgcgtgcg	cggcgacctc	gatgtcacgg	104100
tcgatcaccc	cgaactcgat	ccgggtgtag	tgctcgacct	cggactgggc	ggcccgcagc	104160
acgtcgatca	gtgccgccgg	ctcgcgctgc	acgcgggtgg	agtcggcccc	ggcgagcacc	104220
agcaggttct	cgtcgttgcg	gcgcatccgg	gtggccaggt	ggtcgagctg	gaacagctcg	104280
gccagccggt	ccgggtcctc	ctcgccgcgc	tccagccggt	cgaggtggcc	gatcagccgg	104340
tcgaccagga	tctgcgaacg	gcgggccagg	ttgacgaaca	tggtcgcgac	ggaggcgcgc	104400
agcgcggcct	gctccgccgc	cgtccgtacg	gcctccaggt	ggaccgcgtt	gaacgcctcg	104460
gtcacctggc	cgaactcgtc	cttgctgcgc	accggcagcg	gctcggcgat	ctggttggcc	104520

gcctgcaccg gggagagctg gctggaaaac tgcggatcgc gcagccgggc aacggcctgg 104580 ggcaaaccgt actgggcgat gctgagcgca ccctggcgca ggtcgcgcag cgagcgggcc 104640 atcgaccggg cgaccaggta cgcgaacagg atggccagca gcagcatgcc gagcagcagg 104700 ceggtetgga ggaacacegt gegetgtacg teggagegga gegegtegge etgettgace 104760 acgttgccgt cgagcttcgc ctcgaccgta cggatcagtt tggcgctggc gaccatggcc 104820 gegteecact gateeggeec gaaeggegeg ttggeeatge tgeegttggt gttgeegteg 104880 agccagcegg tgtagttetg egectegege eggtegeege eggegaeggt etggtegtge 104940 aggtccgact cgtccaggct ggccaccgcc ttgaagcttt gcagtgcctg ctgctggccg 105000 gtgccgctgg cgatgtagtc ggtgcgcagg atgggggtca actcgcgctg gatcagcgcc 105060 cggtgcacca cgacccggcg gaccgagagg tattccttct cccgggcgac ggctgccgcg 105120 gcccgcatcc ggtcgctcag gtcgttgtca ccggcgaggt gggtggcgga gtcgcggatg 105180 gacagcaggt cgttgatcag gcctcgtac gcctgcatgg cgtcgatgat cttcaacttg 105240 ccgttgaaga cctggctgcg ggtgccgggg aggtccttca ggttctggtc gatcccgtcg 105300 aggaggeeet ecaggetget eggeaggeeg tegaceteee ecegetgttg eaggtaegge 105360 accttgtcct ggtcgacccg gatgttgacc cggttgtacg cctcctggta ctgcgccttg 105420 gcctggtcgc cgctcgcccc gagcagcaac accgcggagg tgcgttcgtc ctggaggctg 105480 ttgaccaggt cgcccgagta gcccaccaga ttggccaggt cgccggagcg gttggcgttg 105540 ttcagcgttt ccaggttgtc gacgaggcca ctggtgccga cgacgaccgt ggcgatggtc 105600 ggcacgatca tgatgagacc gagcttggac cagatcggca tgtcgcggag ccggccgacc 105660 ggccgacgca gtcgcgacag gaaggaaccc gccgtcttcg gtcgtttgct cacgtcaccg 105720 ccctcgcgat cacagcgttc gcgcgttgcc ccgggcaacg ctcagcgacc gacccggcgg 105780 gteggaeete egagatteea teaegeegtg tteeaaagag aaageeeagg etggeegteg 105840 ccggaggtgt gatgagatgt tgatgcaatt tgctcgcaat ccgtccagcc ggagtgactg 105900 acagtaatgg atcacccca ccgcctcgtc ctgctcgccg gcccttcggg ctccggaaag 105960 tegtacatag cecaacaaac egggetteet gttetttgte tggaegaett etacaaggat 106020 ggtgatgacc ctacgttacc gcgccaaaac ggtcttgtgg actgggactc accccagtcg 106080 tgggacgccg gggcggccgt ggaaacgatt gcccggctgg cgcgggacgg caaggccgaa 106140 gtgccggttt atgcgatcgg cgcggaccgg cgggtggcca cccggacatt cgaggtcgcc 106200 ggatcgccac ttttcgtcgc cgaagggatt ttcgccgccg agatcgtcga ggaatgccga 106260 eggegaggge tgetegeegg ggegtaegeg etgegeegge egegeggeae eacettttte 106320 eggeggeteg eeegegaeet ggeegageag egeaaggete eegggatget getgeggege 106380 ggcctggccc tgctgcgcgc ggagccggcg gtgctgcgcc gccaggcggg gctcggcgct 106440

cacccggccc	cggcccgcga	ggtgctgcgc	cgggtggccg	acctgctcgc	cggccacccg	106500
caccacccct	gatcagccca	gcagcttccc	gtacgccggc	ttgatcacct	cgtcgatgat	106560
ggccagccgc	tcgtcgaacg	ggatgaacgc	gctcttcatc	gcgttgatgg	tgaaccattg	106620
gagctccttc	cagccgtagc	cgaaggcctc	cgccagcagc	gccatctccc	gggacatcga	106680
ggtgccgctc	atcagccggt	tgtcggtgtt	caccgtcacc	cggaaccgca	gatcgcgcag	106740
aagcccgatc	gggtgctcgg	cgatcgacgc	cgccgcgccg	gtctgcacgt	tcgacgacgg	106800
gcacagctcc	agcgggatcc	gcttgtcccg	cacgtacgcg	gccagccggc	ccagcacggg	106860
cgggtcgccg	ggggtgatgt	cgtccacgat	gcgcaccccg	tggccgaggc	ggtccgcgcc	106920
gcaccactgg	atggcctgcc	agatcgacgg	cagcccgaac	gcctcgccgg	cgtgaatggt	106980
gaagtggaag	ttctcccgct	gcaggtactc	gaaggcgtcc	aggtgccggg	tgggcgggaa	107040
tcccgcctcc	gccccggcga	tgtcgaagcc	caccacgccg	gcgtcgcggt	gccgcaccgc	107100
cagttcggcg	atctcctgcg	accgggcggc	gtgccgcatg	gcggtgagca	gggtgccgac	107160
ccggatcgga	tggccggcgt	cggcggcgag	cgccgcgccc	tcggcgaacc	cggcgacgac	107220
cgcctcgacc	acctcgtcca	gggtcaggtc	ccgctccagg	tgctgctcgg	gggcgaaccg	107280
cacctcggcg	tagacgaccc	cgtcggcggc	caggtccagc	gcgcactcct	gggccacccg	107340
ccgcagtgcg	ggcgcggtct	gcatgaccgc	cacggtgtgg	gcgaacgtct	ccaggtagcg	107400
ctccagcgag	ccggagttcg	ccgccgcgac	gaaccagcgg	ccgagcgctt	ccgggtcggt	107460
ggtgggcagc	tcgtggccga	cctcggcggc	cagctcgacg	atcgtcgccg	gccgcaggcc	107520
gccgtcgagg	tggtcgtgca	gcagcgcctt	ggggaccttg	acgatgtcct	cgtatgagat	107580
tgcgaccatg	cccagaccct	agtagcgacc	ggccgggtcg	ccgacgcgac	cggctgggag	107640
gatgtccagg	tgatggaccc	ccgcatcgtc	gaccggctgc	gttgcccggt	ctgcgcggaa	107700
ccgctcaccg	aggccgccgc	cgggaccacc	cgggcgctgc	gctgcccgcg	ccggcacagc	107760
ttcgacgtgg	cccgccaggg	gtacgtcgac	ctgctcgccg	gccgggcccc	gcacgtgggc	107820
gacaccgccg	agatggtggc	cgcccgcgcc	gacttcctcg	ccgccgggca	ctacgacacg	107880
ctctcggccg	cgctcgccgc	cgccgcgctc	gccgcgctga	gccacccgcc	ggaggccccc	107940
ggagcggacg	cgtcggccgg	caaagacggg	caggatgccc	aagccgggcg	ggatgcgtcc	108000
gctggacatg	acgcgtccgc	cggacagccg	gccgtcggga	cgtacccgct	ggtggtggac	108060
gccggggcgg	gcacgggccg	gcacctcgcc	gcggtgctgg	cggcgctgcc	cgacgccgtg	108120
ggcctggccc	tggacgtctc	caagccggcg	ctgcgccggg	cagcgcgggc	ccacccgcgc	108180
gcggcggcgg	cgctcgccga	cacctggcgg	cggcttccgc	tggccgacgc	cagcgtcgcc	108240
gtgctgctcg	acgtcttcgc	cccgcgcaac	ggcgcggagt	tccgccgggt	gctccacccg	108300
gccggcgcgc	tgctcgtggt	cacccccgcc	gaggaccacc	tcgccgaact	ggtcgactcg	108360
ctcgacctgc	tgaaggtcga	ccccgacaag	gcggaccggg	tcgccgggag	cctggccggc	108420

```
cacttegage agacegeega gagegtgetg egggeeegge tggaacteae eggeeggeag
                                                                    108480
gtggccaccc tggtcgggat gggacccagc gcctggcaca ccgacccggc caccctcgcc
                                                                    108540
gcccggatcg ccgcgctacc cgagccggtc cgggtgaccc tcgcggtacg gctcggcgtg
                                                                    108600
taccgcccc gctgaccggg gcgcggcccg ccgctcaggt ggaaaggtcg acctcttccc
                                                                    108660
agcccggcgg ctcctcgtgg tagggccctc gcaggaccac cgcccactcc agcgcccacc
                                                                    108720
ggcgctgccc gatcgcgttg gcgtcgacca ggccgggcgg cgaccgcccg tcgcgctcca
                                                                    108780
getecaggta egeceagteg aggeagtagt geaggtegag eagggeegee gegteggeeg
                                                                    108840
ggtgctgggg cgcggccagg atgcgggagc gccactgctg gaagctctcc ccgcccgcga
                                                                    108900
tgtgcggcag ccgctccacc agccgctcgt cgaccggcag cgtcgggtcg agctgcttgg
                                                                    108960
ccaggccgag cacccaggcc agcgagaaca gcgcgtcgtg gtgcagcacg aacgaccggt
                                                                    109020
ggtcgccccg gccgcccatc acgaactgcc actccggcgg ggtgaccagg tcgaccaggt
                                                                    109080
gggagttgag cagccagctc atcgccgcct gcgccggcat gccgaaacac cgggccagga
                                                                    109140
teaegtgeag caeggegatg egegeetega tetegaeggt eggeegeage tegatetegt
                                                                    109200
cgcccggctc ccacaccagg ggaaactggc tcggtggcag cggcagcccc agccgggaca
                                                                    109260
gctcgtccag gctggcgtca cggacctctc gcgggtcggg agcggaaacg cgcacggctc
                                                                   109320
agatecetgt cagtegeate ggeteagtge eggtegteee eettggeetg ggaggatage
                                                                   109380
ggttcacgac gagcggcacc acggcgggcg ggggcggggg cggttcagcc gatccgctcg
                                                                   109440
atgaccageg getgegggt eggggeggte ggegagatee gtacegeeeg gacegeeteg
                                                                   109500
gccagcgccg ccgggatcc
                                                                    109519
<210> 2
```

```
<211> 1248
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1248)
<220>
<223> evdA
<400> 2
atg acc gat tea gee gae gge acg eee egg ege gge ace tge egg geg
                                                                   48
Met Thr Asp Ser Ala Asp Gly Thr Pro Arg Arg Gly Thr Cys Arg Ala
  1
tgt ggc ggc acc acc gcc cag ttc ctc gac ctg ggt cgg cag ccg ctc
                                                                   96
Cys Gly Gly Thr Thr Ala Gln Phe Leu Asp Leu Gly Arg Gln Pro Leu
             20
tcc gac cgg ttc ctc acc gag gac cag ctc gcg gac gag ttc ttc ttc
                                                                   144
Ser Asp Arg Phe Leu Thr Glu Asp Gln Leu Ala Asp Glu Phe Phe
         35
                             40
                                                  45
```

						tgc Cys 55										192
						gag Glu										240
						atg Met										288
						gcc Ala										336
						gtg Val										384
						gag Glu 135										432
						gtg Val										480
						acc Thr										528
_				_		atc Ile				_						576
						ccg Pro										624
			_		_	gac Asp 215	_	_			_	_			-	672
						tcg Ser										720
						gtc Val										768
						atc Ile										816
gag Glu	cgg Arg	gtg Val 275	gcc Ala	gcg Ala	ctg Leu	atc Ile	ggc Gly 280	gag Glu	gag Glu	gac Asp	gcc Ala	cga Arg 285	gly aaa	gtc Val	gcc Ala	864
						agg Arg 295										912
acc	gac	ctg	ctc	gcc	ctg	ctg	aac	tcg	ctc	aag	gcc	gag	ggc	aag	cgg	960

Thr 305	Asp	Leu	Leu	Ala	Leu 310	Leu	Asn	Ser	Leu	Lys 315	Ala	Glu	Gly	Lys	Arg 320	
										gcc Ala						1008
										gtg Val						1056
										cac His						1104
										tac Tyr						1152
tgg Trp 385	aac Asn	cac His	gcc Ala	gac Asp	gag Glu 390	atc Ile	atg Met	gcg Ala	aag Lys	gag Glu 395	cag Gln	gag Glu	ttc Phe	cgc Arg	cgg Arg 400	1200
										cgc Arg						1248
<210)> 3															

<211> 416

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evdA

<400> 3

Met Thr Asp Ser Ala Asp Gly Thr Pro Arg Arg Gly Thr Cys Arg Ala

Cys Gly Gly Thr Thr Ala Gln Phe Leu Asp Leu Gly Arg Gln Pro Leu

Ser Asp Arg Phe Leu Thr Glu Asp Gln Leu Ala Asp Glu Phe Phe

His Leu Ala Val Gly Val Cys Ala Gly Cys Thr Met Val Gln Leu Met 55

Glu Glu Val Pro Arg Glu Glu Met Phe His Gln Asp Tyr Pro Tyr His

Ser Ser Gly Ser Ser Val Met Gln Lys His Phe Ala Asp Thr Ala Arg

His Leu Leu Glu His Glu Ala Thr Gly Pro Asp Pro Phe Val Val Glu 105

Ile Gly Cys Asn Asp Gly Val Met Leu Arg Thr Val His Glu Ala Gly 115

Val Arg His Leu Gly Phe Glu Pro Ser Gly Gly Val Ala Asp Val Ala

Arg Gly His Gly Val Arg Val Val Thr Glu Phe Phe Glu Glu Ser Thr

145 150 155 160 Ala Arg Arg Val Arg Glu Thr Asp Gly Pro Ala Asp Val Ile Phe Ala 165 170 Ala Asn Thr Ile Cys His Ile Pro Tyr Leu Asp Ser Ile Leu Arg Gly 180 185 Val Asp Ala Leu Leu Ala Pro Asp Gly Val Phe Val Phe Glu Asp Pro Tyr Leu Gly Asp Ile Leu Asp Lys Thr Ser Phe Asp Gln Ile Tyr Asp 215 Glu His Phe Phe Phe Ser Ala Arg Ser Val Gln Ala Leu Ala Ala 230 235 Arg Phe Gly Phe Ala Leu Val Asp Val Glu Arg Leu Pro Val His Gly Gly Glu Val Arg Tyr Thr Ile Ala Arg Ala Gly Ala Arg Gln Pro Ala Glu Arg Val Ala Ala Leu Ile Gly Glu Glu Asp Ala Arg Gly Val Ala Asp Arg Ser Arg Leu Asp Arg Phe Ala Ala Asp Val Glu Gly Ile Arg Thr Asp Leu Leu Ala Leu Leu Asn Ser Leu Lys Ala Glu Gly Lys Arg Val Val Ala Tyr Gly Ala Thr Ala Lys Ser Ala Thr Val Thr Asn Phe 325 330 Cys Gly Ile Gly Pro Asp Leu Val Ser Trp Val Cys Asp Thr Thr Pro 345 Ala Lys Gln Gly Arg Leu Thr Pro Gly Thr His Ile Pro Val Arg Thr Pro Asp Ala Phe Thr Pro Asp Ala Val Asp Tyr Ala Leu Leu Phe Ala 375 Trp Asn His Ala Asp Glu Ile Met Ala Lys Glu Gln Glu Phe Arg Arg 390 395 Ala Gly Gly Gln Trp Ile Leu Tyr Val Pro Arg Val His Val Thr Ser 405 410

<210> 4

<211> 1119

<212> DNA

<213> Micromonospora carbonacea

<220>

<221> CDS

<222> (1)..(1119)

<220>

<223> evdB

<400> 4

	acc Thr															48
	gac Asp															96
	ctc Leu															144
	gac Asp 50															192
aag Lys 65	ctc Leu	gca Ala	ctc Leu	cag Gln	gcg Ala 70	ctc Leu	gac Asp	gtc Val	gly ggg	ccg Pro 75	ggc Gly	gac Asp	gag Glu	gtc Val	atc Ile 80	240
	gtc Val															288
	gcg Ala															336
	acc Thr															384
	ccg Pro 130															432
	gtg Val															480
	cac His															528
	gct Ala															576
	ggc Gly															624
cgg Arg	cgg Arg 210	ctg Leu	cgc Arg	tac Tyr	tac Tyr	ggc Gly 215	atg Met	gaa Glu	cag Gln	gtc Val	tac Tyr 220	tac Tyr	gtc Val	gtc Val	gag Glu	672
-	ccg Pro				_	-		_			_	_			_	720
	cgc Arg															768
gtg	gcc	cgg	cgc	tac	gag	gag	ggc	ctg	gcc	gac	atc	gcc	gac	cag	gtc	816

vai	Ala	Arg	Arg 260	Tyr	Glu	Glu	Gly	Leu 265	Ala	Asp	Ile	Ala	Asp 270	Gln	Val	
					gtg Val											864
					cac His											912
					gcg Ala 310											960
					gcc Ala											1008
					gcc Ala											1056
					acg Thr											1104
			gcg Ala													1119
<210> 5 <211> 373 <212> PRT <213> Micromonospora carbonacea																
<21:	l> 37 2> PI	RT	monos	spora	a cai	cbona	acea									
<213 <213 <213	l> 37 2> PI 3> Mi	RT LCTO	monos	spora	a cai	cbona	acea									
<213 <213 <213 <223 <223	1 > 37 2 > PI 3 > M3 0 > 3 > ex	RT icror vdB			ı caı Trp			Leu	Pro 10	Glu	Tyr	Glu	Lys	Glu 15	Arg	
<21: <21: <21: <22: <40: Met	1> 37 2> PF 3> M3 0> 3> ev 0> 5 Thr	RT icrom vdB	Arg	Val 5		Gly	Tyr		10		_		_	15		
<21: <21: <21: <22: <40: Met 1	1 > 37 2 > PI 3 > M3 0 > 3 3 > ev 0 > 5 Thr	RT icror vdB Ile Leu	Arg Leu 20	Val 5	Trp	Gly Val	Tyr Gln	Thr 25	10 Val	Phe	Glu	Ser	Gly 30	15 Asn	Leu	
<21: <21: <21: <22: <40: Met 1 Asp	1 > 3° 2 > PI 3 > M: 0 > 3 3 > ev 0 > 5 Thr Asp	rT icror vdB Ile Leu Gly 35	Arg Leu 20 Ala	Val 5 Asp	Trp Ala	Gly Val Arg	Tyr Gln Gly 40	Thr 25 Phe	10 Val Glu	Phe Gln	Glu Glu	Ser Phe 45	Gly 30 Ala	15 Asn Ala	Leu Tyr	
<21: <21: <22: <22: <400 Met 1 Asp	1 > 3° 2 > PI 3 > M: 0 > 3 3 > ev 0 > 5 Thr Asp Leu Asp	rT icror vdB Ile Leu Gly 35 Met	Arg Leu 20 Ala Pro	Val 5 Asp Ser	Trp Ala Val	Gly Val Arg Val	Tyr Gln Gly 40 Thr	Thr 25 Phe Val	10 Val Glu Asp	Phe Gln Asn	Glu Glu Gly 60	Ser Phe 45	Gly 30 Ala Asn	15 Asn Ala Ala	Leu Tyr Ile	
<21: <21: <22: <22: <400 Met 1 Asp Ile His	1 > 3° 2 > PI 3 > M: 0 > 5 Thr Asp Leu Asp 50 Leu	Ile Leu Gly 35 Met	Arg Leu 20 Ala Pro Leu	Val 5 Asp Ser His	Trp Ala Val Cys Ala	Gly Val Arg Val 55 Leu	Tyr Gln Gly 40 Thr	Thr 25 Phe Val	10 Val Glu Asp Gly	Phe Gln Asn Pro 75	Glu Gly 60	Ser Phe 45 Thr	Gly 30 Ala Asn Glu	15 Asn Ala Ala Val	Leu Tyr Ile Ile 80	
<21: <21: <22: <22: <400 Met 1 Asp Ile His 65 Thr	1 > 3° 2 > PI 3 > M: 0 > ev 0 > 5 Thr Asp Leu Asp 50 Leu Val	ration of the second of the se	Arg Leu 20 Ala Pro Leu Asn	Val 5 Asp Ser His Gln	Trp Ala Val Cys Ala 70	Gly Val Arg Val 55 Leu	Tyr Gln Gly 40 Thr Asp	Thr 25 Phe Val Val	10 Val Glu Asp Gly Val 90	Phe Gln Asn Pro 75 Leu	Glu Gly 60 Gly	Ser Phe 45 Thr Asp	Gly 30 Ala Asn Glu Asp	Asn Ala Ala Val Ala 95	Leu Tyr Ile Ile 80 Val	

Leu Pro Val His Leu Tyr Gly Gln Cys Val Asp Met Asp Pro Val Leu 130 135 140

Arg Val Ala Arg Glu His Gly Leu Lys Val Leu Glu Asp Cys Ala Gln 145 150 155

Ser His Gly Ala Arg Arg Gly Gly Arg Leu Ala Gly Thr Met Gly Asp 165 170 175

Ala Ala Phe Ser Phe Tyr Pro Thr Lys Val Leu Gly Ala Tyr Gly
180 185 190

Asp Gly Gly Val Val Thr Ala Asp Ala Val Ile Asp Glu Arg Leu 195 200 205

Arg Arg Leu Arg Tyr Tyr Gly Met Glu Gln Val Tyr Tyr Val Val Glu 210 215 220

Thr Pro Gly His Asn Cys Arg Leu Asp Glu Val Gln Ala Glu Ile Leu 225 230 235 240

Arg Arg Lys Leu Cys Arg Leu Asp Asp Tyr Ile Ala Gly Arg Arg Ala 245 250 255

Val Ala Arg Arg Tyr Glu Glu Gly Leu Ala Asp Ile Ala Asp Gln Val 260 265 270

Gly Leu Thr Leu Pro Val Thr Ala Thr Asp Asn Glu His Val Trp Tyr 275 280 285

Val Tyr Val Val Arg His Pro Ala Arg Asp Arg Ile Leu Glu Gln Leu 290 295 300

Ala Ala Arg Asp Ile Ala Leu Asn Ile Ser Tyr Pro Trp Pro Val His 305 310 315 320

Thr Met Thr Gly Phe Ala Lys Leu Gly Tyr Gln Thr Gly Ser Leu Pro 325 330 335

Thr Thr Glu Arg Leu Ala Gly Glu Ile Phe Ser Leu Pro Met Tyr Pro 340 345 350

Ser Leu Pro Pro Glu Thr Gln Asp Arg Val Ile Asp Ala Leu Arg Asp 355 360 365

Val Leu Ala Ala Leu 370

<210> 6

<211> 1236

<212> DNA

<213> Micromonospora carbonacea

<220>

<221> CDS

<222> (1)..(1236)

<220>

<223> evdC

<400> 6

gtg gcg gcg gat ctt cgc gcg ccg ctc acg ccg gcg ggg cgc acg gtg Val Ala Ala Asp Leu Arg Ala Pro Leu Thr Pro Ala Gly Arg Thr Val 18

1				5					10					15		
						gtg Val										96
						acc Thr										144
						ggc Gly 55										192
						tac Tyr										240
						acc Thr										288
						tac Tyr										336
cgc Arg	gcg Ala	atg Met 115	gcg Ala	gag Glu	cgg Arg	ctg Leu	ctg Leu 120	cgg Arg	gcg Ala	atg Met	gcg Ala	gag Glu 125	ggc Gly	gag Glu	gcc Ala	384
						aag Lys 135										432
cat His 145	tcc Ser	gac Asp	ggc Gly	gcc Ala	ggc Gly 150	ggc Gly	tgg Trp	ctg Leu	ctg Leu	tcg Ser 155	ggc Gly	cgc Arg	aag Lys	gtg Val	ctg Leu 160	480
						gcg Ala										528
				Gly	Ser	gtg Val	Phe	Leu	Āla							576
						gtg Val										624
						gag Glu 215										672
gcc Ala 225	gac Asp	gag Glu	ctg Leu	ctg Leu	gag Glu 230	cgc Arg	ggc Gly	ccg Pro	gtc Val	999 Gly 235	gcc Ala	cgg Arg	cgg Arg	gac Asp	gcc Ala 240	720
						gtc Val										768
						gcc Ala										816

ggg cgc ggc g Gly Arg Gly G 275														
ctg gac acc c Leu Asp Thr A 290														
acc aac gcc g Thr Asn Ala A 305					_									
cgc ggc cga c Arg Gly Arg A														
aac gag ctg g Asn Glu Leu A 3														
ggc ctc gcc t Gly Leu Ala T 355														
gtg cgg gcc g Val Arg Ala G 370														
gac tac ctg a Asp Tyr Leu S 385														
atg agc gtg c Met Ser Val A					1236									
<210> 7 <211> 412 <212> PRT <213> Micromonospora carbonacea														
<220> <223> evdC														
<400> 7 Val Ala Ala A 1	sp Leu Arg 5	Ala Pro Leu	Thr Pro Ala	Gly Arg Thr 15	Val									
Val Asp Leu L	eu Ala Gly 20	Val Ile Pro 25	Arg Ile Ser	Ala Glu Ala 30	Ala									
Asp Arg Asp A	rg Thr Gly	Thr Phe Pro	Val Glu Ala	Phe Glu Gln 45	Phe									
Ala Lys Leu G 50	ly Leu Met	Gly Ala Thr 55	Val Pro Ala 60	Glu Leu Gly	Gly									

Ala Glu Ala Asp Ala Ser Thr Ala Leu Ala Trp His Val Gln Leu Ser 90

Leu Gly Leu Thr Arg Leu Tyr Asp Val Ala Thr Ala Leu Met Arg Leu

70

Arg Gly Leu Thr Leu Thr Tyr Glu Trp Gln His Gly Thr Pro Pro Val 105 Arg Ala Met Ala Glu Arg Leu Leu Arg Ala Met Ala Glu Gly Glu Ala Ala Val Cys Gly Ala Leu Lys Asp Ala Pro Gly Val Val Thr Glu Leu 135 His Ser Asp Gly Ala Gly Gly Trp Leu Leu Ser Gly Arg Lys Val Leu Val Ser Met Ala Pro Ile Ala Thr His Phe Phe Val His Ala Gln Arg Arg Asp Asp Gly Ser Val Phe Leu Ala Val Pro Val Val His Arg 185 Asp Ala Pro Gly Leu Thr Val Leu Asp Asn Trp Asp Gly Leu Gly Met Arg Ala Ser Gly Thr Leu Glu Val Val Phe Asp Arg Cys Pro Val Arg 215 Ala Asp Glu Leu Leu Glu Arg Gly Pro Val Gly Ala Arg Arg Asp Ala Val Leu Ala Gly Gln Thr Val Ser Ser Ile Thr Met Leu Gly Ile Tyr 250 Ala Gly Ile Ala Gln Ala Ala Arg Asp Ile Ala Val Gly Phe Cys Ala Gly Arg Gly Glu Pro Arg Ala Gly Ala Arg Ala Leu Val Ala Gly Leu Asp Thr Arg Leu Tyr Ala Leu Arg Thr Thr Val Gly Ala Ala Leu Thr Asn Ala Asp Ala Ala Ser Val Asp Leu Ser Gly Asp Pro Asp Glu 305 310 315 Arg Gly Arg Arg Met Met Thr Pro Phe Gln Tyr Ala Lys Met Thr Val 330 Asn Glu Leu Ala Pro Ala Val Val Asp Asp Cys Leu Ser Leu Val Gly Gly Leu Ala Tyr Thr Ala Gly His Pro Leu Ser Arg Leu Tyr Arg Asp 360 Val Arg Ala Gly Gly Phe Met Gln Pro Tyr Ser Tyr Val Asp Ala Val 375 Asp Tyr Leu Ser Gly Gln Ala Leu Gly Leu Asp Arg Asp Asn Asp Tyr 385 395 Met Ser Val Arg Ala Leu Arg Ser Arg Thr Ser Ala

<210> 8 <211> 1167 <212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1167)
<220>
<223> evdD
<400> 8
gtg aag ata ctg ttc atc gca gga ccg acg aag tcc agc cta ttc ggc
Val Lys Ile Leu Phe Ile Ala Gly Pro Thr Lys Ser Ser Leu Phe Gly
ctg gcc cca ctg gca atc gcc gcc cgg atg agc ggg cac gag gtc gtg
                                                                   96
Leu Ala Pro Leu Ala Ile Ala Ala Arg Met Ser Gly His Glu Val Val
atg get tee acg cag gag gte gta eeg geg acg atg tee gte ggg etg
Met Ala Ser Thr Glu Val Val Pro Ala Thr Met Ser Val Gly Leu
cog god tto cog ctg gog gog ctg acc ctc god gag ctc atg acc acc
                                                                   192
Pro Ala Phe Pro Leu Ala Ala Leu Thr Leu Ala Glu Leu Met Thr Thr
                         55
                                             60
gac egg gee gge gat eeg etg ege ate eeg gee gag gae gee gee tte
                                                                   240
Asp Arg Ala Gly Asp Pro Leu Arg Ile Pro Ala Glu Asp Ala Ala Phe
gtc ccc ttc gtc ggc cgg atg ttc ggc cgg ctg gcg gcg atc agc ctg
                                                                   288
Val Pro Phe Val Gly Arg Met Phe Gly Arg Leu Ala Ala Ile Ser Leu
                 85
                                     90
gat ccg ctg cgc gac ctg gtc ggc ggg tgg cgg ccc gac ctg atc gtc
                                                                   336
Asp Pro Leu Arg Asp Leu Val Gly Gly Trp Arg Pro Asp Leu Ile Val
            100
                                105
ggc ggc ccg cac gcc tac gcc gcg ccg atc ctg gcc acc gaa ctt ggg
                                                                   384
Gly Gly Pro His Ala Tyr Ala Ala Pro Ile Leu Ala Thr Glu Leu Gly
        115
                            120
gtg eec tge gtg egg eac etg etc ace gge aac eeg gtg gae ege gag
                                                                   432
Val Pro Cys Val Arg His Leu Leu Thr Gly Asn Pro Val Asp Arg Glu
    130
                        135
ggc acc cat ccg ggg gtc gac gag gag ctg cgg ccg gag ctg gcc gcg
                                                                   480
Gly Thr His Pro Gly Val Asp Glu Glu Leu Arg Pro Glu Leu Ala Ala
145
                    150
                                        155
                                                             160
ctc ggc ctg gcc cag gtg ccg ccg ttc cac ctg gcc ctg gac atc ttc
                                                                   528
Leu Gly Leu Ala Gln Val Pro Pro Phe His Leu Ala Leu Asp Ile Phe
ccg gcc agc acc cgg atc gac gtc ccg ccg gcg cag ccg gtg cga
                                                                   576
Pro Ala Ser Thr Arg Ile Asp Asp Val Pro Pro Ala Gln Pro Val Arg
            180
                                185
ccg ctg cgc tgg att ccg acc aac cag cag ccg gtg gcg ccg tgg
                                                                   624
Pro Leu Arg Trp Ile Pro Thr Asn Gln Gln Pro Val Ala Pro Trp
                            200
                                                205
atg etc teg ege ggg eeg egt ege egt gte etg gte ace gee gge agt
                                                                   672
Met Leu Ser Arg Gly Pro Arg Arg Val Leu Val Thr Ala Gly Ser
    210
                        215
                                            220
```

	gtc Val															720
	ctg Leu															768
	ggt Gly															816
	ccg Pro															864
	ggc Gly 290	_	_			_		_	_						_	912
	atc Ile															960
	acc Thr															1008
	gcc Ala															1056
	acc Thr															1104
	acg Thr 370															1152
	tgc Cys			_												1167
<21 <21	0> 9 1> 38 2> PI 3> M:	RT	monos	spora	a ca	rbona	acea									
<22 <22	0> 3> e	/d D														
_	0> 9 Lys	Ile	Leu	Phe 5	Ile	Ala	Gly	Pro	Thr 10	Lys	Ser	Ser	Leu	Phe 15	Gly	
Leu	Ala	Pro	Leu 20	Ala	Ile	Ala	Ala	Arg 25	Met	Ser	Gly	His	Glu 30	Val	Val	
Met	Ala	Ser 35	Thr	Gln	Glu	Val	Val 40	Pro	Ala	Thr	Met	Ser 45	Val	Gly	Leu	

Pro Ala Phe Pro Leu Ala Ala Leu Thr Leu Ala Glu Leu Met Thr Thr

50 55 60

Asp Arg Ala Gly Asp Pro Leu Arg Ile Pro Ala Glu Asp Ala Ala Phe Val Pro Phe Val Gly Arg Met Phe Gly Arg Leu Ala Ala Ile Ser Leu Asp Pro Leu Arg Asp Leu Val Gly Gly Trp Arg Pro Asp Leu Ile Val Gly Gly Pro His Ala Tyr Ala Ala Pro Ile Leu Ala Thr Glu Leu Gly Val Pro Cys Val Arg His Leu Leu Thr Gly Asn Pro Val Asp Arg Glu 135 Gly Thr His Pro Gly Val Asp Glu Glu Leu Arg Pro Glu Leu Ala Ala Leu Gly Leu Ala Gln Val Pro Pro Phe His Leu Ala Leu Asp Ile Phe 170 Pro Ala Ser Thr Arg Ile Asp Asp Val Pro Pro Ala Gln Pro Val Arg 185 Pro Leu Arg Trp Ile Pro Thr Asn Gln Gln Pro Val Ala Pro Trp Met Leu Ser Arg Gly Pro Arg Arg Val Leu Val Thr Ala Gly Ser 215 Leu Val Thr Thr His Asn Phe Asp Phe Leu His Gly Leu Ala Gly 230 235 Thr Leu Ala Glu Gln Asp Val Glu Val Val Ala Ala Pro Pro Glu Val Gly Arg Ala Leu His Asp Val Pro Gly Val Arg His Ala Gly Trp Leu Pro Leu Asp Val Val Leu Pro His Cys Asp Leu Ile Val His His Ser Gly Thr Met Thr Ala Leu Thr Ala Leu Asn Ala Gly Val Pro Gln 295 Leu Ile Val Pro Gln Glu Ser Arg Phe Ile Glu Trp Ala Arg Asn Leu 310 Ser Thr Leu Gly Val Ala Gln Thr Leu Ala Pro Gly Glu Asp Thr Pro 330 Glu Ala Val Gly Lys Val Ala Arg Leu Leu Glu Asp Pro Val His 345 Ala Thr Ser Ala Ala Ala Ile Ala Arg Glu Ile Ala Glu Met Pro Gly 355 Pro Thr Glu Val Val Gly Gln Leu Thr Glu Phe Ala Thr Arg Gly Leu 380

Thr Cys Ala Ser Ser 385

```
<210> 10
<211> 924
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(924)
<220>
<223> evdE
<400> 10
gtg acc ggc gga gcc ggg ttc atc ggc tcc cac ctc acc gac gcg ctg
                                                                   48
Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Thr Asp Ala Leu
                                     10
ctc gaa cgc ggc gac agc gtc acc gtg ctc gac gac ctg tcc acc ggg
                                                                   96
Leu Glu Arg Gly Asp Ser Val Thr Val Leu Asp Asp Leu Ser Thr Gly
cgg ccc gag cgg ctg ccc gcc ggg gtg ccg ctg cac cac ggg tcg atc
                                                                   144
Arg Pro Glu Arg Leu Pro Ala Gly Val Pro Leu His His Gly Ser Ile
ace gae egg gee ggg ttg ace egg etg gee gag eag tgt ege eeg gag
                                                                   192
Thr Asp Arg Ala Gly Leu Thr Arg Leu Ala Glu Gln Cys Arg Pro Glu
gte ate tge cae etg gee gee cag geg gae gtg ege aac teg gtg gee
                                                                   240
Val Ile Cys His Leu Ala Ala Gln Ala Asp Val Arg Asn Ser Val Ala
                     70
gac gcc acc tcg gac acc ggg gtc aac gtg gtc ggc acc gtc aac gtc
                                                                    288
Asp Ala Thr Ser Asp Thr Gly Val Asn Val Val Gly Thr Val Asn Val
ctg gag gcc gcc cgg gcc atc gac gcc cgg gtg gtc ttc gcc tcc agc
                                                                    336
Leu Glu Ala Ala Arg Ala Ile Asp Ala Arg Val Val Phe Ala Ser Ser
            100
                                105
ggc ggc gcc ctc tac ggg gag gtc gac gag ctg ccc tcc ccc gag gac
                                                                    384
Gly Gly Ala Leu Tyr Gly Glu Val Asp Glu Leu Pro Ser Pro Glu Asp
                            120
gtc cgg ccg gcg ccg tgg gcg ccg tac ggg gcc gcc aag tac tgc gcg
                                                                   432
Val Arg Pro Ala Pro Trp Ala Pro Tyr Gly Ala Ala Lys Tyr Cys Ala
                        135
gag cag tac ctg gcg ctc tac aac cgg ctc tac ggc tcg acc cac gcg
                                                                   480
Glu Gln Tyr Leu Ala Leu Tyr Asn Arg Leu Tyr Gly Ser Thr His Ala
geg etg egg ete gge aac gtg tac ggg eea ege eag gae eeg ace gge
                                                                    528
Ala Leu Arg Leu Gly Asn Val Tyr Gly Pro Arg Gln Asp Pro Thr Gly
                165
                                     170
                                                         175
gag gcc ggg gtc gtc tcg atc ttc tgc ggc tgc ctg gtg gcc ggg cgc
                                                                   576
Glu Ala Gly Val Val Ser Ile Phe Cys Gly Cys Leu Val Ala Gly Arg
            180
                                                     190
egg eeg aeg gtg tte gge gae gge gag eag aee egg gae tae ate tae
                                                                   624
Arg Pro Thr Val Phe Gly Asp Gly Glu Gln Thr Arg Asp Tyr Ile Tyr
```

195 200 205 gtg gcc gac gtg gtg gag gcg ttc ctg ctc gcg gtc ggg cac ggt ggc 672 Val Ala Asp Val Val Glu Ala Phe Leu Leu Ala Val Gly His Gly Gly 210 ccc ggc ctg tgg aac atc ggc acc ggg acc tcc acc agc atc cgc aaa 720 Pro Gly Leu Trp Asn Ile Gly Thr Gly Thr Ser Thr Ser Ile Arg Lys 225 235 cta ctg gac ctg gtc ggc cgc acc gcc ggg cgc gtc ccg gac ccc cgc 768 Leu Leu Asp Leu Val Gly Arg Thr Ala Gly Arg Val Pro Asp Pro Arg 245 250 tte gag eea eee ege etg gge gag etg aag eae tee geg etg gag gtg 816 Phe Glu Pro Pro Arg Leu Gly Glu Leu Lys His Ser Ala Leu Glu Val 260 265 ace ege geg gee egg gag etg ege tgg geg gee ega acg agg ete gee 864 Thr Arg Ala Ala Arg Glu Leu Arg Trp Ala Ala Arg Thr Arg Leu Ala 280 gac ggc atc gcg aag gtc tac aag tgg gtc gag gcg gac gaa ccg gtc Asp Gly Ile Ala Lys Val Tyr Lys Trp Val Glu Ala Asp Glu Pro Val 912 290 295 300 cgg ggg gag cga 924 Arg Gly Glu Arg 305 <210> 11 <211> 308 <212> PRT <213> Micromonospora carbonacea <220> <223> evdE <400> 11 Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Thr Asp Ala Leu Leu Glu Arg Gly Asp Ser Val Thr Val Leu Asp Asp Leu Ser Thr Gly 20 Arg Pro Glu Arg Leu Pro Ala Gly Val Pro Leu His His Gly Ser Ile Thr Asp Arg Ala Gly Leu Thr Arg Leu Ala Glu Gln Cys Arg Pro Glu 55 Val Ile Cys His Leu Ala Ala Gln Ala Asp Val Arg Asn Ser Val Ala Asp Ala Thr Ser Asp Thr Gly Val Asn Val Val Gly Thr Val Asn Val Leu Glu Ala Ala Arg Ala Ile Asp Ala Arg Val Val Phe Ala Ser Ser Gly Gly Ala Leu Tyr Gly Glu Val Asp Glu Leu Pro Ser Pro Glu Asp 120 Val Arg Pro Ala Pro Trp Ala Pro Tyr Gly Ala Ala Lys Tyr Cys Ala

130 135 140 Glu Gln Tyr Leu Ala Leu Tyr Asn Arg Leu Tyr Gly Ser Thr His Ala 150 155 Ala Leu Arg Leu Gly Asn Val Tyr Gly Pro Arg Gln Asp Pro Thr Gly 165 170 Glu Ala Gly Val Val Ser Ile Phe Cys Gly Cys Leu Val Ala Gly Arg Arg Pro Thr Val Phe Gly Asp Gly Glu Gln Thr Arg Asp Tyr Ile Tyr 195 Val Ala Asp Val Val Glu Ala Phe Leu Leu Ala Val Gly His Gly Gly 215 Pro Gly Leu Trp Asn Ile Gly Thr Gly Thr Ser Thr Ser Ile Arg Lys Leu Leu Asp Leu Val Gly Arg Thr Ala Gly Arg Val Pro Asp Pro Arg Phe Glu Pro Pro Arg Leu Gly Glu Leu Lys His Ser Ala Leu Glu Val 265 Thr Arg Ala Ala Arg Glu Leu Arg Trp Ala Ala Arg Thr Arg Leu Ala Asp Gly Ile Ala Lys Val Tyr Lys Trp Val Glu Ala Asp Glu Pro Val Arg Gly Glu Arg 305 <210> 12 <211> 1041 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1041) <220> <223> evdF <400> 12 atg acc cgc gag ggg tca acg ccg gtt agg gtc gcc acc atc acg 48 Met Thr Arg Glu Gly Ser Thr Pro Pro Val Arg Val Ala Thr Ile Thr gtc ggc acc aac gag atc cgt tgg ctg gac cgc gcg ctc ggc tcg ctg 96 Val Gly Thr Asn Glu Ile Arg Trp Leu Asp Arg Ala Leu Gly Ser Leu 20 ctc gcc agc gac acg gcc ttc gag ctg acg gtc ttc tac gtg gac 144 Leu Ala Ser Asp Thr Thr Gly Phe Glu Leu Thr Val Phe Tyr Val Asp aac gcc tcg gcc gac ggc agc gtg gcg cac gtc atg tcg gcg ttt ccc 192 Asn Ala Ser Ala Asp Gly Ser Val Ala His Val Met Ser Ala Phe Pro

55

60

50

	_		_		cga Arg 70			_							240
					cgg Arg										288
					gac Asp										336
_	_				cag Gln			_	_		_			_	384
					gac Asp										432
_		_	_	_	gcc Ala 150			_		 _				_	480
					cat His										528
					ctg Leu										576
					gtg Val										624
					gag Glu										672
					gcg Ala 230										720
					gcc Ala										768
					tat Tyr										816
_	_	_			gcc Ala	_	_		_		_	_	_		864
					cgg Arg										912
					tgg Trp 310										960

cgt cgt cgg cgg cac cgg ctg ctg cgg gca cga ggg acg ggc gtg gac Arg Arg Arg His Arg Leu Leu Arg Ala Arg Gly Thr Gly Val Asp 325 330 cgc gcc cga gag cgg aag gaa acc gtg cgg gga Arg Ala Arg Glu Arg Lys Glu Thr Val Arg Gly <210> 13 <211> 347 <212> PRT <213> Micromonospora carbonacea <220> <223> evdF Met Thr Arg Glu Gly Ser Thr Pro Pro Val Arg Val Ala Thr Ile Thr Val Gly Thr Asn Glu Ile Arg Trp Leu Asp Arg Ala Leu Gly Ser Leu 25 Leu Ala Ser Asp Thr Thr Gly Phe Glu Leu Thr Val Phe Tyr Val Asp Asn Ala Ser Ala Asp Gly Ser Val Ala His Val Met Ser Ala Phe Pro Gly Val Arg Val Ile Arg Asn Pro Arg Asn Leu Gly Phe Thr Gly Ala Asn Asn Val Gly Met Arg Ala Ala Leu Ala Glu Gly Phe Asp His Ile Phe Leu Val Asn Pro Asp Thr Trp Thr Pro Pro Gly Leu Val Arg Gly 105 Leu Val Glu Phe Ala Gln Arg Trp Pro Gln Tyr Gly Val Ile Gly Pro 115 120 Leu Gln Tyr Arg Tyr Asp Pro Ala Ser Thr Glu Leu Thr Asp Phe Asn Asp Trp Thr Gln Val Ala Leu Tyr Leu Gly Glu Gln His Thr Phe Ala Gly Asp Leu Leu Asp His Pro Ser His Val Thr Ala Thr Val Arg Asp 170 Arg Ala Pro Arg Thr Leu Glu His Ala Tyr Val Gln Gly Ser Ala Leu Phe Val Arg Ala Ala Val Leu Arg Glu Val Gly Leu Leu Asp Glu Val Phe His Thr Tyr Tyr Glu Glu Val Asp Leu Cys Arg Arg Ala Arg Trp 215 Ala Gly Trp Arg Val Ala Leu Leu Leu Asp Leu Gly Ile Gln His Lys 225 Gly Gly Gly Thr Ala Ala Ser Ala Tyr Ser Arg Ile His Met Arg

250

Arg Asn Arg Tyr Tyr Leu Leu Thr Asp Val Asp Trp Pro Pro Ala Lys Ala Ala Arg Leu Ala Ala Arg Trp Leu Phe Ser Asp Val Arg Gly 280 Arg Gly Val Thr Gly Arg Thr Ser Ala Gly Val Gly Ala Arg Glu Thr 295 Phe Val Ala Leu Gly Trp Leu Ala Arg Gln Ala Pro Val Ile Arg Glu Arg Arg Arg His Arg Leu Leu Arg Ala Arg Gly Thr Gly Val Asp Arg Ala Arg Glu Arg Lys Glu Thr Val Arg Gly <210> 14 <211> 1053 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1053) <220> <223> evdG atg agc agg cca cgg att ctc gtc gcg ggc aac ttc cac tgg cag gcc 48 Met Ser Arg Pro Arg Ile Leu Val Ala Gly Asn Phe His Trp Gln Ala ggg ttc agc cag acc gtc gcc gcg tac gtg cgg gcg gcc cgg gag gcc 96 Gly Phe Ser Gln Thr Val Ala Ala Tyr Val Arg Ala Ala Arg Glu Ala 20 25 gac tgc gag gtg cgg ctc tgc ggc ccg ctg tcc cgg gtc gac gcc gag 144 Asp Cys Glu Val Arg Leu Cys Gly Pro Leu Ser Arg Val Asp Ala Glu 35 40 acg gcc cgg cac ctg ccg gtc gag ccg gac ctc cgc tgg ggc acc cac 192 Thr Ala Arg His Leu Pro Val Glu Pro Asp Leu Arg Trp Gly Thr His 50 55 ctg gtg atc atg ttc gag gcc aag cag ttc ctc acc gag gcg caa ctg 240 Leu Val Ile Met Phe Glu Ala Lys Gln Phe Leu Thr Glu Ala Gln Leu gac etc gtc gag gcg ttc ecc ega eag ege egg gcc atc gtc gac ttc 288 Asp Leu Val Glu Ala Phe Pro Arg Gln Arg Arg Ala Ile Val Asp Phe gac ggg cac tgg ggt gcc gag gag ggc ggg gac ggc gac agc gcg tcg 336 Asp Gly His Trp Gly Ala Glu Glu Gly Gly Asp Gly Asp Ser Ala Ser 105 ggc cgg tac tcc gcg gag agt tgg cgg cgg ttg tac tcg acc ctg agc 384 Gly Arg Tyr Ser Ala Glu Ser Trp Arg Arg Leu Tyr Ser Thr Leu Ser

120

125

gac Asp	ctg Leu 130	atc Ile	ctg Leu	caa Gln	ccc Pro	cgg Arg 135	ctg Leu	ggt Gly	ccg Pro	ctc Leu	ccg Pro 140	gcc Ala	ggc Gly	gcc Ala	cgg Arg	432
					ggc Gly 150											480
					cag Gln											528
					tgg Trp											576
					ccg Pro											624
					tgc Cys											672
					gcg Ala 230											720
					gag Glu											768
					gtc Val											816
					tcg Ser											864
					gtc Val											912
ggc Gly 305	gac Asp	gac Asp	ccg Pro	gcc Ala	gga Gly 310	acg Thr	ctg Leu	agc Ser	cgg Arg	ctc Leu 315	tcg Ser	gcc Ala	gag Glu	cac His	gaa Glu 320	960
cgg Arg	tac Tyr	gga Gly	cga Arg	ctg Leu 325	gtc Val	ggt Gly	gag Glu	att Ile	cag Gln 330	gac Asp	cgg Arg	ctc Leu	cgc Arg	gtc Val 335	gag Glu	1008
					gtc Val											1053

<210> 15

<211> 351

<212> PRT <213> Micromonospora carbonacea

<220>

<223> evdG

<400> 15 Met Ser Arg Pro Arg Ile Leu Val Ala Gly Asn Phe His Trp Gln Ala Gly Phe Ser Gln Thr Val Ala Ala Tyr Val Arg Ala Ala Arg Glu Ala Asp Cys Glu Val Arg Leu Cys Gly Pro Leu Ser Arg Val Asp Ala Glu Thr Ala Arg His Leu Pro Val Glu Pro Asp Leu Arg Trp Gly Thr His Leu Val Ile Met Phe Glu Ala Lys Gln Phe Leu Thr Glu Ala Gln Leu Asp Leu Val Glu Ala Phe Pro Arg Gln Arg Arg Ala Ile Val Asp Phe Asp Gly His Trp Gly Ala Glu Glu Gly Gly Asp Gly Asp Ser Ala Ser Gly Arg Tyr Ser Ala Glu Ser Trp Arg Arg Leu Tyr Ser Thr Leu Ser 120 Asp Leu Ile Leu Gln Pro Arg Leu Gly Pro Leu Pro Ala Gly Ala Arg Phe Phe Lys Cys Phe Gly Leu Ala Ala Pro Val Arg His Pro Leu Glu 155 Leu Gly Thr Gly Ala Gln Ser Arg Pro Tyr Asp Leu Gln Tyr Ile Gly 165 Ser Asn Trp Trp Arg Trp Glu Pro Met Thr Glu Met Val Glu Ala Ala 185 Ala Ala Arg Pro Pro Leu Arg Arg Leu Arg Val Cys Gly Arg Trp Trp Asp Gly Gly Ser Cys Ala Gly Phe Glu Glu Ala Thr Leu Ser Glu Pro Gly Trp Leu Arg Ala Arg Gly Val Glu Val His Pro Pro Val Pro 230 235 Phe Gly His Val Val Glu Gln Met Gly Arg Ser Leu Ile Ser Pro Val 245 Leu Val Arg Pro Leu Val Thr Ser Thr Gly Leu Leu Thr Pro Arg Met 265 Phe Glu Thr Leu Ala Ser Gly Ser Leu Pro Val Leu Pro Val Ala Ala Lys Phe Leu Ala Pro Val Tyr Gly Asp Glu Ala Glu His Leu Met Leu 295 300 Gly Asp Asp Pro Ala Gly Thr Leu Ser Arg Leu Ser Ala Glu His Glu 310 315 Arg Tyr Gly Arg Leu Val Gly Glu Ile Gln Asp Arg Leu Arg Val Glu

Tyr Gly Tyr Pro Arg Val Leu Arg Asp Leu Leu Asp Leu Leu Ala 340 345 350

<210> 16 <211> 1020 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1020) <220> <223> evdH <400> 16 atg acc ccc ctg cgg atc gcg atg gtc aac ata ccg ttc cgg ttq ccq 48 Met Thr Pro Leu Arg Ile Ala Met Val Asn Ile Pro Phe Arg Leu Pro age gae gag egg eag tgg ate aeg gte eeg eeg eag ggg tae gge ggg 96 Ser Asp Glu Arg Gln Trp Ile Thr Val Pro Pro Gln Gly Tyr Gly Gly atc cag tgg atc gtg gcc aac aag atc aag ggc ctg ctc gaa ctc ggg 144 Ile Gln Trp Ile Val Ala Asn Lys Ile Lys Gly Leu Leu Glu Leu Gly 40 cac gag gtg ttc ctg ctc ggt gcc ccg ggc agt ccg cgt acg cat cca 192 His Glu Val Phe Leu Leu Gly Ala Pro Gly Ser Pro Arg Thr His Pro 55 ege etg ace gtg gtg eeg geg gge gag eee gag gae ate egg gea tgg 240 Arg Leu Thr Val Val Pro Ala Gly Glu Pro Glu Asp Ile Arg Ala Trp ttg aag tee get eeg gtg gae gte gte aac gae tae age tge gge aag 288 Leu Lys Ser Ala Pro Val Asp Val Val Asn Asp Tyr Ser Cys Gly Lys 85 gtg gat ccg atc gag ctg ccc ccg ggg gtc ggc ctg gtg gcc tcg cac 336 Val Asp Pro Ile Glu Leu Pro Pro Gly Val Gly Leu Val Ala Ser His 100 cac atg acc acc cgc ccg tcc tat ccg gcc ggc tgc gtg tac gcc tcg 384 His Met Thr Thr Arg Pro Ser Tyr Pro Ala Gly Cys Val Tyr Ala Ser 115 aag gcg cag cgg gag cag tgc ggc ggc gcg gac gcc ccg gtc atc 432 Lys Ala Gln Arg Glu Gln Cys Gly Gly Gly Ala Asp Ala Pro Val Ile ccg atc ggg gtg gat ccg tcg ctc tac cgc ccc ggc gac cgc aag gac 480 Pro Ile Gly Val Asp Pro Ser Leu Tyr Arg Pro Gly Asp Arg Lys Asp gac ttc ctg ctc ttc atg ggc cgg atc tcc ccg ttc aag ggc gcg ctg 528 Asp Phe Leu Leu Phe Met Gly Arg Ile Ser Pro Phe Lys Gly Ala Leu 576 Glu Ala Ala Ala Phe Ala Arg Ala Ala Gly Arg Arg Leu Leu Met Ala 180

										cgg Arg						624
ggc Gly	gac Asp 210	cac His	gtc Val	acc Thr	ctc Leu	gtc Val 215	ggc Gly	gag Glu	gtg Val	Gly 999	ggt Gly 220	cag Gln	gaa Glu	cgt Arg	atg Met	672
										gtg Val 235						720
										ccg Pro						768
										gtc Val						816
										gag Glu						864
										gtg Val						912
_		_				_	_			cgg Arg 315	-					960
										cgc Arg						1008
	cgc Arg															1020
<21 <21	0> 13 1> 34 2> PI 3> Mi	10 RT	nonos	spora	a cai	cbona	acea									
<22 <22	0> 3> ev	/dH														
	0> 13 Thr		Leu	Arg 5	Ile	Ala	Met	Val	Asn 10	Ile	Pro	Phe	Arg	Leu 15	Pro	
Ser	Asp	Glu	Arg 20	Gln	Trp	Ile	Thr	Val 25	Pro	Pro	Gln	Gly	Tyr 30	Gly	Gly	
Ile	Gln	Trp 35	Ile	Val	Ala	Asn	Lys 40	Ile	Lys	Gly	Leu	Leu 45	Glu	Leu	Gly	
His	Glu 50	Val	Phe	Leu	Leu	Gly 55	Ala	Pro	Gly	Ser	Pro 60	Arg	Thr	His	Pro	

Arg Leu Thr Val Val Pro Ala Gly Glu Pro Glu Asp Ile Arg Ala Trp

65 70 75 80

Leu Lys Ser Ala Pro Val Asp Val Val Asn Asp Tyr Ser Cys Gly Lys
85 90 95

Val Asp Pro Ile Glu Leu Pro Pro Gly Val Gly Leu Val Ala Ser His 100 105 110

His Met Thr Thr Arg Pro Ser Tyr Pro Ala Gly Cys Val Tyr Ala Ser 115 120 125

Lys Ala Gln Arg Glu Gln Cys Gly Gly Gly Ala Asp Ala Pro Val Ile 130 135 140

Pro Ile Gly Val Asp Pro Ser Leu Tyr Arg Pro Gly Asp Arg Lys Asp 145 150 155 160

Asp Phe Leu Leu Phe Met Gly Arg Ile Ser Pro Phe Lys Gly Ala Leu 165 170 175

Glu Ala Ala Ala Phe Ala Arg Ala Ala Gly Arg Arg Leu Leu Met Ala 180 185 190

Gly Pro Ala Trp Glu Pro Glu Tyr Leu Asp Arg Ile Met Gly Glu Tyr 195 200 205

Gly Asp His Val Thr Leu Val Gly Glu Val Gly Gly Gln Glu Arg Met 210 215 220

Asp Leu Leu Ala Thr Ala Ala Ala Ile Leu Val Leu Ser Gln Pro Val 225 230 235 240

Pro Gly Pro Trp Gly Gly Thr Trp Cys Glu Pro Gly Ala Thr Val Val 245 250 255

Ser Glu Ala Ala Ser Gly Thr Pro Val Val Gly Thr Ser Asn Gly 260 265 270

Cys Leu Ala Glu Ile Val Pro Ala Val Gly Glu Val Val Gly Phe Gly 275 280 285

Thr Gly Phe Asp Glu Arg Glu Ala Arg Ala Val Leu Ser Arg Leu Pro 290 295 300

Ser Pro Ala Gln Ala Arg Lys Ala Ala Ile Arg Cys Trp Gly His Val 305 310 315 320

Glu Ile Ala Arg Arg Tyr Glu Ala Val Tyr Arg Asp Val Leu Ala Gly
325 330 335

Ala Arg Trp Ser

<210> 18

<211> 759

<212> DNA

<213> Micromonospora carbonacea

<220>

<221> CDS

<222> (1)..(759)

<220>

<223> evdI

		_														
atg	0> 18 gcc Ala	gtg														48
_	tac Tyr		_	-						_	_		_	_	_	96
_	gag Glu	_	_				_	_		_				_	_	144
	gcg Ala 50	_		_			_			_		_		_		192
	gac Asp															240
	ctg Leu															288
atc Ile	gcc Ala	tcc Ser	gct Ala 100	ttc Phe	ctc Leu	gac Asp	atc Ile	ccc Pro 105	gag Glu	gac Asp	gaa Glu	ctc Leu	gac Asp 110	ttc Phe	tac Tyr	336
	cac His															384
	cag Gln 130															432
	atc Ile															480
	tac Tyr															528
	aac Asn															576
	acg Thr															624
	gac Asp 210															672
	cgc Arg															720
	gac Asp															759

<210> 19

<211> 253

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evdI

<400> 19

Met Ala Val Gly Thr Val Gly Ala Glu Val Val Asp Arg Arg Leu Glu 1 5 10 15

Ala Tyr Arg Arg Asp Gly Phe Val Thr Leu Pro Gln Leu Ala Asp Asp 20 25 30

Ala Glu Val Ala Trp Leu Arg Ala Ala Tyr Asp Arg Leu Phe Ala Asp 35 40 45

His Ala Ser Pro Asp Thr Gly Asp Tyr Arg Asp Ile Ala Gly Arg Gly 50 55 60

Asp Asp Ala Ala Pro Ala Arg Leu Pro Gln Ile Val Arg Pro Glu Lys 65 70 75 80

Tyr Leu Pro Glu Leu Val Glu Thr Ala His Phe Ala Arg Cys Arg Ala 85 90 95

Ile Ala Ser Ala Phe Leu Asp Ile Pro Glu Asp Glu Leu Asp Phe Tyr 100 105 110

Gly His Ala Ile Leu Lys Pro Pro Arg Tyr Gly Ala Pro Thr Pro Trp 115 120 125

His Gln Asp Glu Ala Tyr Met Asp Pro Arg Trp Ser Arg Arg Gly Leu 130 135 140

Ser Ile Trp Thr Pro Leu Asp Glu Ala Thr Val Ser Ser Gly Cys Leu 145 150 155 160

Gln Tyr Leu Pro Gly Leu His Arg Gly Gly Val Leu Pro His His His 165 170 175

Ile Asn His Asp Asp Arg Ile Glu Gly Leu Met Thr Asp Glu Val Asp 180 185 190

Asp Thr Asp Ser Val Ala Cys Pro Leu Arg Pro Gly Glu Ala Val Met 195 200 205

His Asp Phe Arg Ala Pro His Tyr Ala Gly Pro Asn Glu Thr Asp Gln 210 215 220

Pro Arg Arg Ala Tyr Val Leu Val Phe Met Ser Gln Pro Val Glu Val 225 230 235 240

Thr Asp Pro Glu Pro Arg Pro Trp Leu His Asp Arg Ser 245 250

<210> 20

<211> 750

<212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(750)
<220>
<223> evdJ
<400> 20
atg acc ggg cac agc gcc gtc gcg ctg gac gtc ggc ggg gtc gtc tac
                                                                   48
Met Thr Gly His Ser Ala Val Ala Leu Asp Val Gly Val Val Tyr
tac gac gag ccg ttc gag ctg gcc tgg ctc cag gac acc ttc gac cgc
                                                                   96
Tyr Asp Glu Pro Phe Glu Leu Ala Trp Leu Gln Asp Thr Phe Asp Arg
ctc cag gcc acc gac ccg acg ctc gac ctg cgt gcg ttt ctg gag cac
                                                                   144
Leu Gln Ala Thr Asp Pro Thr Leu Asp Leu Arg Ala Phe Leu Glu His
gtc gag egg ttc tac cac tac ggc gag ggc gac cca acc ggc egg acc
                                                                   192
Val Glu Arg Phe Tyr His Tyr Gly Glu Gly Asp Pro Thr Gly Arg Thr
tgg ctc cac tcg gag gcc gcc gcg ctg agc tgg tcg cgg gtc cgg cag
                                                                   240
Trp Leu His Ser Glu Ala Ala Ala Leu Ser Trp Ser Arg Val Arg Gln
tcc tgg ggc gag ctg gcc cag gag att ccc ggt gcc gtt cgc gcg gtc
                                                                   288
Ser Trp Gly Glu Leu Ala Gln Glu Ile Pro Gly Ala Val Arg Ala Val
acc agg ctg gcc agg gaa cta ccc gtc gtg atc gtc gcc aac cag ccc
                                                                   336
Thr Arg Leu Ala Arg Glu Leu Pro Val Val Ile Val Ala Asn Gln Pro
ccc gag tgc gcg gac gta ctg gcc cgg tgg cag gtc agc cag gtc tgc
Pro Glu Cys Ala Asp Val Leu Ala Arg Trp Gln Val Ser Gln Val Cys
        115
                                                 125
egg gag gtg etc etc gac tec etc gte ggg gtg gee aag eec gae eeg
Arg Glu Val Leu Leu Asp Ser Leu Val Gly Val Ala Lys Pro Asp Pro
    130
                        135
gcc ctg ctc ggg ctc gcc ctg cgg ctg gcg atc ccg ccc gcc gag
                                                                   480
Ala Leu Leu Gly Leu Ala Leu Arg Arg Leu Ala Ile Pro Pro Ala Glu
145
                    150
                                        155
                                                             160
ttg ctg gtg gtg ggc aac cgg acg gat cac gac gtc ctg ccc gcg ctc
Leu Leu Val Val Gly Asn Arg Thr Asp His Asp Val Leu Pro Ala Leu
                165
ggg ctc ggt tgc ccg gtg gcg ttc gtg ctc ccc gat ccg gcg tac cgc
Gly Leu Gly Cys Pro Val Ala Phe Val Leu Pro Asp Pro Ala Tyr Arg
            180
                                185
egg eeg eeg gge gte eat eeg gae etg gte egg gte tae aeg gag etg
                                                                   624
Arg Pro Pro Gly Val His Pro Asp Leu Val Arg Val Tyr Thr Glu Leu
                            200
                                                205
agg gcg ttc cgc acc ggc tcc ccg ccc gcg gac gcc cgg gtc acc acc
                                                                   672
Arg Ala Phe Arg Thr Gly Ser Pro Pro Ala Asp Ala Arg Val Thr Thr
```

220

750

gtg gcg tcc ctg gcg gcc ctg gcc gac tct ccc ctg acg agt gcc acc Val Ala Ser Leu Ala Ala Leu Ala Asp Ser Pro Leu Thr Ser Ala Thr 230 235 ccg cgt tcg aac gcc ggc acc ggc gga ctt Pro Arg Ser Asn Ala Gly Thr Gly Gly Leu 245 <210> 21 <211> 250 <212> PRT <213> Micromonospora carbonacea <220> <223> evdJ <400> 21 Met Thr Gly His Ser Ala Val Ala Leu Asp Val Gly Gly Val Val Tyr Tyr Asp Glu Pro Phe Glu Leu Ala Trp Leu Gln Asp Thr Phe Asp Arg Leu Gln Ala Thr Asp Pro Thr Leu Asp Leu Arg Ala Phe Leu Glu His Val Glu Arg Phe Tyr His Tyr Gly Glu Gly Asp Pro Thr Gly Arg Thr Trp Leu His Ser Glu Ala Ala Ala Leu Ser Trp Ser Arg Val Arg Gln Ser Trp Gly Glu Leu Ala Gln Glu Ile Pro Gly Ala Val Arg Ala Val Thr Arg Leu Ala Arg Glu Leu Pro Val Val Ile Val Ala Asn Gln Pro 105 Pro Glu Cys Ala Asp Val Leu Ala Arg Trp Gln Val Ser Gln Val Cys 120 Arg Glu Val Leu Leu Asp Ser Leu Val Gly Val Ala Lys Pro Asp Pro 135 Ala Leu Leu Gly Leu Ala Leu Arg Arg Leu Ala Ile Pro Pro Ala Glu 150 Leu Leu Val Val Gly Asn Arg Thr Asp His Asp Val Leu Pro Ala Leu Gly Leu Gly Cys Pro Val Ala Phe Val Leu Pro Asp Pro Ala Tyr Arg 185 Arg Pro Pro Gly Val His Pro Asp Leu Val Arg Val Tyr Thr Glu Leu 200 205 Arg Ala Phe Arg Thr Gly Ser Pro Pro Ala Asp Ala Arg Val Thr Thr Val Ala Ser Leu Ala Ala Leu Ala Asp Ser Pro Leu Thr Ser Ala Thr 235

Pro Arg Ser Asn Ala Gly Thr Gly Gly Leu

```
<210> 22
<211> 1245
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1245)
<220>
<223> evdK
<400> 22
gtg gtc ggc gcc acc ggc ttc atc ggc tca cgc ctc gtc tcc cgc ctg
                                                                   48
Val Val Gly Ala Thr Gly Phe Ile Gly Ser Arg Leu Val Ser Arg Leu
gcc gag gcc ggg cat ccg gtg gcg cgc ttc agc cgt gcc gcc cca ccc
                                                                   96
Ala Glu Ala Gly His Pro Val Ala Arg Phe Ser Arg Ala Ala Pro Pro
             20
                                 2.5
gtc gtc gac ggc cgg ccc gcg ccg ggg ctc cgc gag gcg cag gtc gtc
                                                                   144
Val Val Asp Gly Arg Pro Ala Pro Gly Leu Arg Glu Ala Gln Val Val
                             40
tac ttc ctc gcc gcc cgg ctg agc ccg gcg ctg gcg gag cag caa ccg
                                                                   192
Tyr Phe Leu Ala Ala Arg Leu Ser Pro Ala Leu Ala Glu Gln Gln Pro
                         55
gaa cgg gtc gtc cgg gaa cgc gag ttg ttg ctg gac gtg cta agt gcg
                                                                   240
Glu Arg Val Val Arg Glu Arg Glu Leu Leu Leu Asp Val Leu Ser Ala
ctg gcg ggg gtg gac cac cgg ccg gtg ttc gtc ctg gcc agc tcg ggc
                                                                   288
Leu Ala Gly Val Asp His Arg Pro Val Phe Val Leu Ala Ser Ser Gly
                 85
ggg gcg gtg tac acg ccg acg gtg tgg ccg ccc tac cac gag cgg tcg
                                                                   336
Gly Ala Val Tyr Thr Pro Thr Val Trp Pro Pro Tyr His Glu Arg Ser
            100
gee ace ggg eee gee teg geg tae gge egg geg aag etg egg etg gaa
                                                                   384
Ala Thr Gly Pro Ala Ser Ala Tyr Gly Arg Ala Lys Leu Arg Leu Glu
        115
cag gag ctg ctg cgc cac acc gac cgg gtg cag ccg gtg gtg acc cgg
                                                                   432
Gln Glu Leu Leu Arg His Thr Asp Arg Val Gln Pro Val Val Thr Arg
    130
                        135
ctg agc aac gtc tac ggt ccg ggg cag cgg ccg acc ccc ggg tac ggt
                                                                   480
Leu Ser Asn Val Tyr Gly Pro Gly Gln Arg Pro Thr Pro Gly Tyr Gly
145
                                         155
gtc ctg tca cac tgg ctg gag gcc acc gtg cgc gga gag ccg atc cgg
                                                                   528
Val Leu Ser His Trp Leu Glu Ala Thr Val Arg Gly Glu Pro Ile Arg
                                     170
ctc ttc ggc gat ccg gcc gtg gtg cgg gac tac gta cac gtc gac gac
                                                                   576
Leu Phe Gly Asp Pro Ala Val Val Arg Asp Tyr Val His Val Asp Asp
                                185
gte ace geg ate atg gag gte ate geg cag egg gee ggt gae gge gae
                                                                   624
```

Val	Thr	Ala 195	Ile	Met	Glu	Val	Ile 200	Ala	Gln	Arg	Ala	Gly 205	Asp	Gly	Asp	
						gtc Val 215										672
						cag Gln										720
						gtc Val										768
						gcc Ala										816
						gtc Val										864
						ggt Gly 295										912
	_					cgg Arg	_	_	_		_	_		_	_	960
cag Gln	ttc Phe	gtg Val	gct Ala	caa Gln 325	ccc Pro	ggc Gly	ggc Gly	ggt Gly	cgc Arg 330	cgc Arg	ggt Gly	gta Val	gcc Ala	gag Glu 335	ggc Gly	1008
						gga Gly										1056
						ccg Pro										1104
						ccg Pro 375										1152
						gac Asp										1200
						ggc Gly										1245

<210> 23

<210> 23 <211> 415

<212> PRT

<213> Micromonospora carbonacea

<220> <223> evdK

<400> 23

Val Val Gly Ala Thr Gly Phe Ile Gly Ser Arg Leu Val Ser Arg Leu Ala Glu Ala Gly His Pro Val Ala Arg Phe Ser Arg Ala Ala Pro Pro Val Val Asp Gly Arg Pro Ala Pro Gly Leu Arg Glu Ala Gln Val Val Tyr Phe Leu Ala Ala Arg Leu Ser Pro Ala Leu Ala Glu Gln Gln Pro Glu Arg Val Val Arg Glu Arg Glu Leu Leu Leu Asp Val Leu Ser Ala Leu Ala Gly Val Asp His Arg Pro Val Phe Val Leu Ala Ser Ser Gly Gly Ala Val Tyr Thr Pro Thr Val Trp Pro Pro Tyr His Glu Arg Ser Ala Thr Gly Pro Ala Ser Ala Tyr Gly Arg Ala Lys Leu Arg Leu Glu Gln Glu Leu Leu Arg His Thr Asp Arg Val Gln Pro Val Val Thr Arg Leu Ser Asn Val Tyr Gly Pro Gly Gln Arg Pro Thr Pro Gly Tyr Gly 155 Val Leu Ser His Trp Leu Glu Ala Thr Val Arg Gly Glu Pro Ile Arg 165 Leu Phe Gly Asp Pro Ala Val Val Arg Asp Tyr Val His Val Asp Asp 185 Val Thr Ala Ile Met Glu Val Ile Ala Gln Arg Ala Gly Asp Gly Asp Arg Asp Arg Leu Pro Thr Val Val Asn Val Gly Ser Gly Leu Pro Thr 215 Ser Leu Ala Glu Leu Leu Gln Thr Met Ser Thr Val Ala Gly Arg Glu 230 Leu Glu Val Ile Arg Asp Val Arg Arg Gln Phe Asp His Arg Gly Asn Trp Leu Asp Thr Thr Leu Ala Arg Glu Thr Leu Gly Trp Gln Ala Arg 265 Ile Ser Leu Pro Asp Gly Val Arg Gln Cys Trp Glu Ala Val Leu Thr Arg Ala Gly Gly Pro Gly Gly Ser Pro Ala Arg Pro Ser Ala Arg Leu 295 Gly Arg Ala Ser Arg Gly Arg Glu Pro Pro Gln Pro Arg Pro Ser Gln 315 Gln Phe Val Ala Gln Pro Gly Gly Gly Arg Arg Gly Val Ala Glu Gly Gln Trp Gln Gly Glu Pro Gly Phe Arg Gly Arg Thr Val Pro Val Pro 340 345

Phe Leu Ala Gln Ala Gly Pro Cys Leu Val Pro Ser Gly Leu Ala Pro 360 Pro Leu Pro Val Arg Pro Pro Gln Gln Val Pro Gly Gln Pro Ala 375 Arg Val Asp Val Met Gly Asp Arg Val Val Arg Glu Gln Leu Leu Ala Gly Ala Gly Gly Leu His Gly Ala Asp Glu Gly Val Leu Pro 410 <210> 24 <211> 912 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(912) <220> <223> evdL <400> 24 atg ccg aac aac gcc tct gtg gtc agc cgc gat ccg tcc gac cac ccg 48 Met Pro Asn Asn Ala Ser Val Val Ser Arg Asp Pro Ser Asp His Pro atg gtg gtg gcg atc tgc gcg ttc cgg gtg gag aac gtc agg aaa cac 96 Met Val Val Ala Ile Cys Ala Phe Arg Val Glu Asn Val Arg Lys His 20 ctc gcg cac aac atg gcc cag ctc tcc ggc gac gag tac tac gtc ctg 144 Leu Ala His Asn Met Ala Gln Leu Ser Gly Asp Glu Tyr Tyr Val Leu ctg gac cgg ccc gtc acg gcc gag gcg gag gag gtc gcc gag gag gtc Leu Asp Arg Pro Val Thr Ala Glu Ala Glu Val Ala Glu Val 192 55 egg gee gee gge gge ace atg ege ate ete ggt gee ace aat gge etg 240 Arg Ala Ala Gly Gly Thr Met Arg Ile Leu Gly Ala Thr Asn Gly Leu teg gee tee ege aac geg atg ete gee ege tgg eeg eac eac eat etg 288 Ser Ala Ser Arg Asn Ala Met Leu Ala Arg Trp Pro His His Leu 85 atg ttc gtc gac gac gtg cgg ctc gac gcc gct gcc gtc gac gcc 336 Met Phe Val Asp Asp Val Arg Leu Asp Ala Ala Val Asp Ala 105 gtc cgc aag agc ctg cgc gac ggc gcg cac gtg gtc ggc acc cgg ctg Val Arg Lys Ser Leu Arg Asp Gly Ala His Val Val Gly Thr Arg Leu 115 120 125 gcc cgc ccc gcg ctg cgt ctg ccq tgq tac qtc acc tcc qqc caq ttc Ala Arg Pro Ala Leu Arg Leu Pro Trp Tyr Val Thr Ser Gly Gln Phe 130 135 cac ctg gtc ggc tgg cac cgt gac cag gga aac atc aag atc tgg qqc

His Leu Val Gly Trp His Arg Asp Gln Gly Asn Ile Lys Ile Trp Gly

145	150	155 160	
		cac gcc cac ggg ttg gat His Ala His Gly Leu Asp 175	528
ttc gac ctg gcc ctc Phe Asp Leu Ala Leu 180	agc cgt acc ggg ggc Ser Arg Thr Gly Gly 185	aac ctc cag tca ggg gag Asn Leu Gln Ser Gly Glu 190	576
		gcc ggc gcc cgc gag caa Ala Gly Ala Arg Glu Gln 205	624
		atc gac ccg ggc cgg ctg Ile Asp Pro Gly Arg Leu 220	672
		tgg cag ggg cgg tgc gag Trp Gln Gly Arg Cys Glu 235 240	720
		cgc aag gaa tgg gac cgg Arg Lys Glu Trp Asp Arg 255	768
		ctg cca ctg gcc ctc ggc Leu Pro Leu Ala Leu Gly 270	816
tac acc gcg gcg acc Tyr Thr Ala Ala Thr 275	gcc gcc ggg ttg agc Ala Ala Gly Leu Ser 280	cac gaa ctg ctg cga agg His Glu Leu Leu Arg Arg 285	864
		cgc tct ccc gag ccg ggc Arg Ser Pro Glu Pro Gly 300	912
<210> 25 <211> 304 <212> PRT <213> Micromonospora	a carbonacea		
<220> <223> evdL			
<400> 25 Met Pro Asn Asn Ala 1 5	Ser Val Val Ser Arg	Asp Pro Ser Asp His Pro 15	
Met Val Val Ala Ile 20	Cys Ala Phe Arg Val 25	Glu Asn Val Arg Lys His 30	
Leu Ala His Asn Met 35	Ala Gln Leu Ser Gly	Asp Glu Tyr Tyr Val Leu 45	
Leu Asp Arg Pro Val	Thr Ala Glu Ala Glu 55	Glu Val Ala Glu Glu Val 60	
Arg Ala Ala Gly Gly 65	Thr Met Arg Ile Leu	Gly Ala Thr Asn Gly Leu 75 80	
Ser Ala Ser Arg Asn 85	Ala Met Leu Ala Arg 90	Trp Pro His His His Leu 95	

```
Met Phe Val Asp Asp Asp Val Arg Leu Asp Ala Ala Val Asp Ala
Val Arg Lys Ser Leu Arg Asp Gly Ala His Val Val Gly Thr Arg Leu
                            120
Ala Arg Pro Ala Leu Arg Leu Pro Trp Tyr Val Thr Ser Gly Gln Phe
His Leu Val Gly Trp His Arg Asp Gln Gly Asn Ile Lys Ile Trp Gly
Ala Cys Met Gly Val Asp Ser Ala Phe Ala His Ala His Gly Leu Asp
                165
Phe Asp Leu Ala Leu Ser Arg Thr Gly Gly Asn Leu Gln Ser Gly Glu
Asp Thr Ser Phe Ile Ser Ala Met Lys Ala Ala Gly Ala Arg Glu Gln
Leu Leu Pro Asp His Ala Val Thr His Asp Ile Asp Pro Gly Arg Leu
    210
                        215
Thr Pro Arg Tyr Leu Leu Arg Arg Ala Tyr Trp Gln Gly Arg Cys Glu
Ala Gly Arg Asn Gln Ala Arg Ala Gly Leu Arg Lys Glu Trp Asp Arg
His Arg Thr Ala Pro Glu Ser Arg Leu Ala Leu Pro Leu Ala Leu Gly
                                265
Tyr Thr Ala Ala Thr Ala Ala Gly Leu Ser His Glu Leu Leu Arg Arg
        275
                            280
                                                285
Ala Arg Leu Arg Arg Phe Pro Pro Pro Arg Arg Ser Pro Glu Pro Gly
    290
                        295
                                            300
<210> 26
<211> 951
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(951)
<220>
<223> evrA
<400> 26
atg ggc gcg cgg cgt gtc gtg gtc ggt ggt acg ggc ttc gtc ggg
                                                                  48
Met Gly Ala Arg Arg Val Val Val Gly Gly Thr Gly Phe Val Gly
egt cae gtg age gee geg ett gee gee egg gge gae gae gte ete gtg
Arg His Val Ser Ala Ala Leu Ala Ala Arg Gly Asp Asp Val Leu Val
ttg gcc cgc cgc gtc ccg tcg gcg ggg ctg ccg tac cgg gcc cgg gcg
```

Leu	Ala	Arg 35	Arg	Val	Pro	Ser	Ala 40	Gly	Leu	Pro	Tyr	Arg 45	Ala	Arg	Ala	
ctg Leu	gac Asp 50	gtc Val	gcc Ala	acc Thr	ctg Leu	gag Glu 55	ccc Pro	gcc Ala	gcg Ala	ctg Leu	gcc Ala 60	gcc Ala	gtg Val	ttc Phe	gac Asp	192
												ggc Gly				240
_	_	_	_		_	_	_	_	_	_		ccg Pro	_		_	288
gtc Val	acc Thr	gcg Ala	gcg Ala 100	ctg Leu	gag Glu	cgc Arg	acc Thr	cgt Arg 105	tgc Cys	cgg Arg	ccc Pro	agg Arg	ctg Leu 110	gtg Val	cac His	336
												999 Gly 125				384
												ggc Gly				432
												gcc Ala				480
												ccg Pro				528
												gtc Val				576
												ttg Leu 205				624
												gtg Val				672
acg Thr 225	cgg Arg	gag Glu	tcc Ser	gtc Val	acc Thr 230	Gly 999	cgg Arg	gtg Val	atc Ile	ggc Gly 235	gtg Val	Gly ggg	cgg Arg	Gly ggg	gag Glu 240	720
												gag Glu				768
gtg Val	ccg Pro	acc Thr	gag Glu 260	gtg Val	gtg Val	gag Glu	ttg Leu	ccg Pro 265	gat Asp	cgg Arg	ccc Pro	ggc Gly	tcg Ser 270	gtg Val	gag Glu	816
												cgt Arg 285				864
												ggc Gly				912

290 295 300

gac gag gcc gcg agt cgg ctt ccc gat cgg tcc cgg cgc Asp Glu Ala Ala Ser Arg Leu Pro Asp Arg Ser Arg Arg 305 310 315 951

<210> 27

<211> 317

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrA

<400> 27

Met Gly Ala Arg Arg Val Val Val Gly Gly Thr Gly Phe Val Gly
1 5 10 15

Arg His Val Ser Ala Ala Leu Ala Ala Arg Gly Asp Asp Val Leu Val 20 25 30

Leu Ala Arg Arg Val Pro Ser Ala Gly Leu Pro Tyr Arg Ala Arg Ala 35 40 45

Leu Asp Val Ala Thr Leu Glu Pro Ala Ala Leu Ala Ala Val Phe Asp
50 55 60

Ala Glu Gln Pro Asp Ala Val Val Asn Ala Thr Gly Gly Lys Trp Asn 65 70 75 80

Leu Thr Asp Ala Glu Leu Pro Ser Ser Cys Thr Ile Pro Thr Trp Ser 85 90 95

Val Thr Ala Ala Leu Glu Arg Thr Arg Cys Arg Pro Arg Leu Val His
100 105 110

Leu Gly Ser Val Leu Glu Arg Val Gln Glu Pro Pro Gly Ala Pro Ala 115 120 125

Gly Ala Thr Val Pro Thr Gln Pro Glu Ser Met Tyr Gly Arg Ala Lys 130 135 140

Leu Ala Ala Thr Gln Ala Val Leu Ala Ala Thr Arg Ala Gly Ser Val
145 150 155 160

Asp Ala Thr Val Leu Arg Leu Ala Asn Val Val Gly Pro Gly Val Pro 165 170 175

Pro Asp Ser Leu Leu Gly Arg Val Val Arg Leu Val Asp Ala Ala 180 185 190

Gly Arg Asp Arg Ser Ala Arg Val Glu Leu Ser Pro Leu Arg Ala His 195 200 205

Arg Asp Tyr Val Asp Val Arg Asp Val Ala Glu Ala Val Val Ser Ala 210 215 220

Thr Arg Glu Ser Val Thr Gly Arg Val Ile Gly Val Gly Arg Gly Glu 225 230 235 240

Ala Val Pro Val Arg Ser Leu Val Glu Met Leu Ile Glu Val Ser Gly 245 250 255

Val Pro Thr Glu Val Val Glu Leu Pro Asp Arg Pro Gly Ser Val Glu

265

260

Val Val Asp Trp Ala Arg Val Asp Pro Gly Pro Ala Arg Asp Leu Leu Gly Trp Arg Pro Arg Arg Ser Leu Arg Asp Ala Val Gly Gly Leu Trp 290 295 Asp Glu Ala Ala Ser Arg Leu Pro Asp Arg Ser Arg Arg 310 <210> 28 <211> 1032 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1032) <220> <223> evrB <400> 28 atg gcg gag atg acg gtc cgc atc ggg gtt ctc ggc tgc gcc gac atc 48 Met Ala Glu Met Thr Val Arg Ile Gly Val Leu Gly Cys Ala Asp Ile gcg cgc cgt gcc ctg ccg gcg atc agg cgg gtc ccg gag gcg gag 96 Ala Arg Arg Arg Ala Leu Pro Ala Ile Arg Arg Val Pro Glu Ala Glu 25 ctc gtg gtg gtc gcg gcg cgg gaa ctg gcc aag gcg cgc gcc ttc gcc 144 Leu Val Val Ala Ala Arg Glu Leu Ala Lys Ala Arg Ala Phe Ala geg gag ttc ggg tgc gcc gcc gag ggc tac cag tcc gtt ctc gac 192 Ala Glu Phe Gly Cys Ala Ala Ala Glu Gly Tyr Gln Ser Val Leu Asp 50 ege eeg gae ate gat gee gte tae att eeg etg eeg ace ggg etg eac Arg Pro Asp Ile Asp Ala Val Tyr Ile Pro Leu Pro Thr Gly Leu His cac acc tgg atc gaa cgc gcc ctg gcc gcg ggc aaa cac gtg ctg gtg His Thr Trp Ile Glu Arg Ala Leu Ala Ala Gly Lys His Val Leu Val 85 gag aag ccg ctg acc acc cgg ctg gtc gac acc gcg gcg gtg ctg acc 336 Glu Lys Pro Leu Thr Thr Arg Leu Val Asp Thr Ala Ala Val Leu Thr 100 cag gcc cgg tcg cgt ggg ctc gtg ttg atg gac aac ctc acc ttc ctc 384 Gln Ala Arg Ser Arg Gly Leu Val Leu Met Asp Asn Leu Thr Phe Leu 120 cga cat ggg gtg cac cac ttc gtg cgc cgg atg gtc gcg gcc ggc gag 432 Arg His Gly Val His His Phe Val Arg Arg Met Val Ala Ala Gly Glu 135 480

155

cct go Pro Al	g ggc a Gly	gac Asp	atc Ile 165	cgt Arg	tac Tyr	cga Arg	ccc Pro	gag Glu 170	ctg Leu	ggt Gly	ggc Gly	gga Gly	gcg Ala 175	ctg Leu	528
ctg ga Leu As	ıt ctg p Leu	ggc Gly 180	gtc Val	tac Tyr	ccg Pro	ttg Leu	ggc Gly 185	gcg Ala	gcc Ala	cgg Arg	ttc Phe	ttc Phe 190	ctg Leu	ccg Pro	576
gag ga Glu Gl	ıg ccg .u Pro 195	gag Glu	gtg Val	gtg Val	gcg Ala	gcc Ala 200	acc Thr	ctc Leu	cgg Arg	gag Glu	gac Asp 205	ccc Pro	gat Asp	cgc Arg	624
ggc gt Gly Va 21	l Asp														672
acc go Thr Al 225															720
cag ct Gln Le															768
cca co Pro Pr															816
acg cg Thr Ar		Leu													864
cga ga Arg Gl	u Phe														912
acg go Thr Al 305	g atc a Ile	cgc Arg	gcc Ala	cgg Arg 310	gcc Ala	cgg Arg	ctg Leu	ctg Leu	gac Asp 315	gag Glu	gtt Val	cgc Arg	gac Asp	cgg Arg 320	960
gcc ag Ala Ar															1008
ctg ga Leu As															1032
<210><211><211><212><213>	344 PRT	mono	spora	a cai	cbona	acea									
<220> <223>	evrB														
<400> Met Al		Met	Thr 5	Val	Arg	Ile	Gly	Val 10	Leu	Gly	Cys	Ala	Asp 15	Ile	

Ala Arg Arg Ala Leu Pro Ala Ile Arg Arg Val Pro Glu Ala Glu 20 25 30

Leu Val Val Ala Ala Arg Glu Leu Ala Lys Ala Arg Ala Phe Ala 35 40 45

Ala Glu Phe Gly Cys Ala Ala Ala Glu Gly Tyr Gln Ser Val Leu Asp 50 55 60

Arg Pro Asp Ile Asp Ala Val Tyr Ile Pro Leu Pro Thr Gly Leu His 65 70 75 80

His Thr Trp Ile Glu Arg Ala Leu Ala Ala Gly Lys His Val Leu Val 85 90 95

Glu Lys Pro Leu Thr Thr Arg Leu Val Asp Thr Ala Ala Val Leu Thr
100 105 110

Gln Ala Arg Ser Arg Gly Leu Val Leu Met Asp Asn Leu Thr Phe Leu 115 120 125

Arg His Gly Val His His Phe Val Arg Arg Met Val Ala Ala Gly Glu 130 135 140

Ile Gly Glu Leu Arg Met Val Ser Gly Val Phe Gly Phe Pro Pro Leu 145 150 155 160

Pro Ala Gly Asp Ile Arg Tyr Arg Pro Glu Leu Gly Gly Ala Leu 165 170 175

Leu Asp Leu Gly Val Tyr Pro Leu Gly Ala Ala Arg Phe Phe Leu Pro 180 185 190

Glu Glu Pro Glu Val Val Ala Ala Thr Leu Arg Glu Asp Pro Asp Arg 195 200 205

Gly Val Asp Val Ser Gly Ala Ala Leu Leu Cys Thr Pro Asp Gly Arg 210 215 220

Thr Ala Gln Ile Ala Phe Gly Phe Glu His Ser Tyr Arg Cys Glu Tyr 225 230 235 240

Gln Leu Trp Gly Ser Ala Gly Arg Ile Val Val Asp Arg Ala Tyr Thr 245 250 255

Pro Pro Pro Ala Trp His Pro Val Val Arg Val Glu Arg Gln Asp Glu 260 265 270

Thr Arg Glu Leu Thr Phe Pro Ala Glu Asp Gln Phe Val Asn Thr Met 275 280 285

Arg Glu Phe Val Arg Ala Val Thr Ala Gly Gln Pro Ala Glu Glu Val 290 295 300

Thr Ala Ile Arg Ala Arg Ala Arg Leu Leu Asp Glu Val Arg Asp Arg 305 310 315 320

Ala Arg Val Leu Arg Ala Pro Val Thr Cys Gln Gly Pro Gly Gly Arg 325 330 335

Leu Asp Ala Ala Gly Ala Arg Asp 340

<210> 30

<211> 1452

<212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1452)
<220>
<223> evrC
<400> 30
gtg age gat teg teg eee gae eeg aag gte ege gee gae ggg eeg ttg
                                                                      48
Val Ser Asp Ser Ser Pro Asp Pro Lys Val Arg Ala Asp Gly Pro Leu
ctg acc cgg gac gcg ggc ccg cac cgg ccc ggc ccg gtc gac ggc ggc
                                                                      96
Leu Thr Arg Asp Ala Gly Pro His Arg Pro Gly Pro Val Asp Gly Gly
teg tgg teg geg ttg cac gee gag ggg gte egg eeg gae tte ete tee
                                                                     144
Ser Trp Ser Ala Leu His Ala Glu Gly Val Arg Pro Asp Phe Leu Ser
tgg ttc gcc gag cgg acc cgg tcg acc tac tgc cgg gtg gac cgc gtg
                                                                     192
Trp Phe Ala Glu Arg Thr Arg Ser Thr Tyr Cys Arg Val Asp Arg Val
ccg ctg gac cgg ctg ccc ggg tgg gcg ttc gac ccg gtg acc ggc aac
                                                                     240
Pro Leu Asp Arg Leu Pro Gly Trp Ala Phe Asp Pro Val Thr Gly Asn
ctc ggg cac gag agc ggc cgg ttc ttc gtg atc gag ggg ctg cac gtc Leu Gly His Glu Ser Gly Arg Phe Phe Val Ile Glu Gly Leu His Val
                                                                     288
                  85
                                       90
cag acc acc tac ggc gcg gtg cgc gaa tgg cac cag ccg atc atc aac
                                                                     336
Gln Thr Thr Tyr Gly Ala Val Arg Glu Trp His Gln Pro Ile Ile Asn
            100
                                 105
cag ccg gag atc ggc atc ctc ggc atg ctc gtc aag gtc gtc gac ggg
                                                                     384
Gln Pro Glu Ile Gly Ile Leu Gly Met Leu Val Lys Val Val Asp Gly
        115
                             120
aca ccg tac tgc ctg ctc cag gcc aag gtg gag ccc ggc aac atc aac
                                                                     432
Thr Pro Tyr Cys Leu Leu Gln Ala Lys Val Glu Pro Gly Asn Ile Asn
    130
                         135
gtc atg cag ctc tcg ccg acg gtg cag gcc acc cgg agc aac tac acc
                                                                     480
Val Met Gln Leu Ser Pro Thr Val Gln Ala Thr Arg Ser Asn Tyr Thr
145
                     150
                                          155
cgg gtg cac cgt ggc ggc acg aag tac ctc gac tac ttc acc cgc
                                                                     528
Arg Val His Arg Gly Gly Thr Lys Tyr Leu Asp Tyr Phe Thr Arg
ccg ggg gcc ggt cgg gtg ctg gtt gac gtc ctg cag tcg gag cag ggc
                                                                     576
Pro Gly Ala Gly Arg Val Leu Val Asp Val Leu Gln Ser Glu Gln Gly
            180
                                 185
                                                       190
tcc tgg ttc ctg cgc aag cgc aac cgg aac atg gtg gtc cag gtc gac
                                                                     624
Ser Trp Phe Leu Arg Lys Arg Asn Arg Asn Met Val Val Gln Val Asp
                             200
                                                  205
gag gac gtg ccg gcc ggc gac tac cac cgg tgg ctc ccg ctg cgc gaa
                                                                     672
Glu Asp Val Pro Ala Gly Asp Tyr His Arg Trp Leu Pro Leu Arg Glu
    210
```

ctg Leu 225	ctc Leu	gcg Ala	ctg Leu	ctg Leu	cgg Arg 230	gtg Val	gac Asp	ggc Gly	ctg Leu	gtc Val 235	aac Asn	atg Met	gac Asp	acg Thr	cgt Arg 240	720
					ctg Leu											768
					tcg Ser											816
					cgc Arg											864
					cgg Arg											912
					tgg Trp 310											960
					tcc Ser											1008
_					tgg Trp	_	_	_	_	_		_				1056
					ctg Leu											1104
					tac Tyr											1152
					tgc Cys 390											1200
					gtg Val											1248
gac Asp	acc Thr	gtg Val	ctc Leu 420	acc Thr	gag Glu	gag Glu	ggc Gly	999 Gly 425	cga Arg	ttc Phe	tac Tyr	cgg Arg	tcg Ser 430	gag Glu	aac Asn	1296
					gac Asp											1344
					gtg Val											1392
					aac Asn 470											1440

cgc agc ctg tgg 1452

Arg Ser Leu Trp

<210> 31

<211> 484 <212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrC

<400> 31

Val Ser Asp Ser Ser Pro Asp Pro Lys Val Arg Ala Asp Gly Pro Leu

1 5 10 15

Leu Thr Arg Asp Ala Gly Pro His Arg Pro Gly Pro Val Asp Gly Gly 20 25 30

Ser Trp Ser Ala Leu His Ala Glu Gly Val Arg Pro Asp Phe Leu Ser 35 40 45

Trp Phe Ala Glu Arg Thr Arg Ser Thr Tyr Cys Arg Val Asp Arg Val 50 55 60

Pro Leu Asp Arg Leu Pro Gly Trp Ala Phe Asp Pro Val Thr Gly Asn 65 70 75 80

Leu Gly His Glu Ser Gly Arg Phe Phe Val Ile Glu Gly Leu His Val 85 90 95

Gln Thr Thr Tyr Gly Ala Val Arg Glu Trp His Gln Pro Ile Ile Asn 100 105 110

Gln Pro Glu Ile Gly Ile Leu Gly Met Leu Val Lys Val Val Asp Gly
115 120 125

Thr Pro Tyr Cys Leu Leu Gln Ala Lys Val Glu Pro Gly Asn Ile Asn 130 135 140

Val Met Gln Leu Ser Pro Thr Val Gln Ala Thr Arg Ser Asn Tyr Thr 145 150 155 160

Arg Val His Arg Gly Gly Gly Thr Lys Tyr Leu Asp Tyr Phe Thr Arg 165 170 175

Pro Gly Ala Gly Arg Val Leu Val Asp Val Leu Gln Ser Glu Gln Gly 180 185 190

Ser Trp Phe Leu Arg Lys Arg Asn Arg Asn Met Val Val Gln Val Asp

Glu Asp Val Pro Ala Gly Asp Tyr His Arg Trp Leu Pro Leu Arg Glu 210 215 220

Leu Leu Ala Leu Leu Arg Val Asp Gly Leu Val Asn Met Asp Thr Arg 225 230 235 240

Thr Val Leu Ser Cys Leu Pro Ser Ala Phe Tyr Ala Ala Ala Gln Glu 245 250 255

Thr Glu Ala Pro Ser Ser Pro Ala Val Ala Ala Ile Val Arg Ser Ala 260 265 270

Ala Gly Ala Pro Gly Arg His Asp Leu Val Ser Val Leu Ser Trp Phe

275 280 285 Thr Gly Ala Lys Gly Arg His Glu Met Thr Val Arg Arg Val Pro Leu 295 Arg Gly Leu Pro Asp Trp Arg His Thr Ala Asp Gly Ile Ala Arg Asp 305 310 315 Asp Gly Arg His Phe Ser Val Val Gly Val Thr Val Arg Ile Asp Asn Arg Glu Val Thr Gly Trp Ser Gln Pro Leu Leu Tyr Pro Arg His Arg Gly Val Val Ala Phe Leu Val Lys Glu Ile Asp Gly Val Ala His Leu 360 Leu Val His Ala Arg Tyr Gln Ala Gly Leu Leu Asp Ala Met Glu Met 375 Gly Pro Thr Val Gln Cys Ile Pro Asp Asn Gln Pro Gly Pro Arg Pro Leu Phe Leu Ala Glu Val Leu Glu Ala Ala Pro Glu Arg Val Leu Tyr Asp Thr Val Leu Thr Glu Glu Gly Gly Arg Phe Tyr Arg Ser Glu Asn 425 Arg Tyr Leu Leu Val Asp Ala Gly Asp Asp Phe Pro Thr Glu Val Pro Asp Glu Phe Cys Trp Val Thr Val Arg Gln Leu Glu Ala Leu Leu Arg 455 His Gly Tyr Tyr Leu Asn Ile Glu Ala Arg Ser Leu Leu Ala Cys Leu 475 Arg Ser Leu Trp <210> 32 <211> 1062 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1062) <220> <223> evrD gtg gct tca cgg ctg gag act acc ctg aca cgg cgg gcg ctg atc act Val Ala Ser Arg Leu Glu Thr Thr Leu Thr Arg Arg Ala Leu Ile Thr gga att acc ggc cag gac ggc acg tat ctc gcg gag cac ctg ctt cag Gly Ile Thr Gly Gln Asp Gly Thr Tyr Leu Ala Glu His Leu Leu Gln

tcc gga tac gag gta ttt gga ttg gtg cgc ggg cag acc gcg ccc tcg

Ser	Gly	Tyr 35	Glu	Val	Phe	Gly	Leu 40	Val	Arg	Gly	Gln	Thr 45	Ala	Pro	Ser	
					caa Gln											192
gac Asp 65	ctt Leu	ctg Leu	gat Asp	cag Gln	acg Thr 70	agc Ser	ctg Leu	gtg Val	gcg Ala	gcg Ala 75	atc Ile	gaa Glu	cgc Arg	gcg Ala	gcg Ala 80	240
					aac Asn											288
					acg Thr											336
					ttg Leu											384
					cag Gln											432
					cgg Arg 150											480
					tac Tyr											528
					gag Glu											576
					tca Ser											624
aag Lys	gtg Val 210	tcg Ser	ctg Leu	ggc Gly	gtg Val	gcg Ala 215	gcg Ala	gtg Val	aag Lys	ctg Leu	ggc Gly 220	att Ile	cgc Arg	agc Ser	tcg Ser	672
	_	_			ctc Leu 230	_	_			_						720
					atg Met											768
					acg Thr											816
					cac His											864
					atc Ile											912

290 295 300 gat ccg acg aag gcc cgc cag cgg ctc ggc tgg aaa ccc tcc gtc tcc 960 Asp Pro Thr Lys Ala Arg Gln Arg Leu Gly Trp Lys Pro Ser Val Ser 305 310 315 ttc gag gag atg gtc gcc atg atg gtc gac agc gat ctg cgc ctg ttg 1008 Phe Glu Glu Met Val Ala Met Met Val Asp Ser Asp Leu Arg Leu Leu 325 330 geg gac acg gac ggg tet tee cac gee ttt tee gee gaa etg gee gag 1056 Ala Asp Thr Asp Gly Ser Ser His Ala Phe Ser Ala Glu Leu Ala Glu 345 ctg tgg 1062 Leu Trp <210> 33 <211> 354 <212> PRT <213> Micromonospora carbonacea <220> <223> evrD <400> 33 Val Ala Ser Arg Leu Glu Thr Thr Leu Thr Arg Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Thr Tyr Leu Ala Glu His Leu Leu Gln Ser Gly Tyr Glu Val Phe Gly Leu Val Arg Gly Gln Thr Ala Pro Ser Val Arg Ser Leu Arg Gln Pro Asp Pro Ala Val Lys Leu Ile Ser Gly Asp Leu Leu Asp Gln Thr Ser Leu Val Ala Ala Ile Glu Arg Ala Ala 65 70 Pro Asp Glu Val Tyr Asn Leu Gly Ala Leu Ser Tyr Val Pro Val Ser Trp Arg Gln Ser Thr Thr Ala Glu Val Thr Gly Met Gly Val Leu Arg Met Leu Glu Ala Leu Arg Ile Val Gly Gly Leu Ser Asp Ser Arg 120 Ser Pro Ala Ala Gly Gln Pro Arg Phe Tyr Gln Ala Ser Ser Ser Glu Met Phe Gly Lys Val Arg Glu Pro Val Gln Asn Glu Leu Thr Pro Phe His Pro Arg Ser Pro Tyr Gly Ala Ala Lys Ala Phe Gly His Tyr Met 165 Val Gln Asn Tyr Arg Glu Ser Tyr Gly Met Tyr Ala Val Ser Gly Ile 180 Leu Phe Asn His Glu Ser Pro Val Arg Gly Pro Glu Phe Val Thr Arg

200

```
Lys Val Ser Leu Gly Val Ala Ala Val Lys Leu Gly Ile Arg Ser Ser
                          215
Leu Arg Leu Gly Asn Leu Ser Ala Glu Arg Asp Trp Gly Phe Ala Gly
                     230
                                           235
Asp Tyr Val Arg Gly Met Val Leu Met Leu Ala Gln Asp Glu Pro Glu
Asp Tyr Val Leu Gly Thr Gly Val Thr His Ser Val Arg Glu Leu Val
                                  265
Glu Ala Ala Phe Ala His Val Gly Leu Asn Trp Arg Asp His Val Val
        275
                              280
Val Asp Glu Ser Leu Ile Arg Pro Ala Glu Val Glu Leu Leu Cys Ala
Asp Pro Thr Lys Ala Arg Gln Arg Leu Gly Trp Lys Pro Ser Val Ser
Phe Glu Glu Met Val Ala Met Wat Val Asp Ser Asp Leu Arg Leu Leu
                 325
                                      330
Ala Asp Thr Asp Gly Ser Ser His Ala Phe Ser Ala Glu Leu Ala Glu
             340
                                  345
Leu Trp
<210> 34
<211> 1530
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1530)
<220>
<223> evrE
<400> 34
atg gtc gcg ttg gtc gcg gtg atg atc ccg atg gtg ctg gcc acc ctc
Met Val Ala Leu Val Ala Val Met Ile Pro Met Val Leu Ala Thr Leu
                  5
                                       10
gac aac acc atc atc ggc acc gca ctg ccc acc gtg gtc ggc gag ttg
                                                                      96
Asp Asn Thr Ile Ile Gly Thr Ala Leu Pro Thr Val Val Gly Glu Leu
             20
ggc ggc ctc agc acg ctc tcc tgg gtg atc acc tcg tac acg ctg gcc
                                                                      144
Gly Gly Leu Ser Thr Leu Ser Trp Val Ile Thr Ser Tyr Thr Leu Ala
acg gcc gcc tcc acg ccg gtc tgg ggc aag ctc gcc gac atg tac ggc
                                                                      192
Thr Ala Ala Ser Thr Pro Val Trp Gly Lys Leu Ala Asp Met Tyr Gly
                          55
ggc aag gtg gtc ttc gtg gcc acg ctg gtc gtg ttc ctg gcc ggg tcg
Gly Lys Val Val Phe Val Ala Thr Leu Val Val Phe Leu Ala Gly Ser
                                                                      240
```

	atg gcg Met Ala 85						288
	ctc ggc Leu Gly						336
	gtt ctc Val Leu		y Pro				384
	acc atg Thr Met						432
	acc gat Thr Asp 150	Glu Le					480
	ggg gcg Gly Ala 165						528
	cga cac Arg His						576
	gtg gtc Val Val		r Cys				624
	tac ccc Tyr Pro						672
	ctg acc Leu Thr 230	Cys Al					720
	ttg gtg Leu Val 245						768
	ctc atc Leu Ile						816
	ctg gcc Leu Ala		e Gln				864
	ggc ctg Gly Leu						912
	gtc ggg Val Gly 310	Gly Ar					960
	ctc gcc Leu Ala 325						1008

		_	_	_	-				_		acg Thr	_				1056
											ctc Leu					1104
											aac Asn 380					1152
											ggg Gly					1200
											cag Gln					1248
gat Asp	cgg Arg	Gly 999	gtc Val 420	gcc Ala	gac Asp	gtg Val	gct Ala	gac Asp 425	ctc Leu	ctc Leu	ggc Gly	cac His	tcc Ser 430	gcg Ala	cgg Arg	1296
											gcc Ala					1344
											gcc Ala 460					1392
											tgg Trp					1440
											gaa Glu					1488
_	-			_	-	_	_		_		ccg Pro					1530
<21:	0 > 35 1 > 55 2 > PI 3 > M:	10 RT	monos	spora	a cai	rbona	acea									
<22 <22	0> 3> e ⁷	vrE														

<400> 35

Met Val Ala Leu Val Ala Val Met Ile Pro Met Val Leu Ala Thr Leu

Asp Asn Thr Ile Ile Gly Thr Ala Leu Pro Thr Val Val Gly Glu Leu 20 25

Gly Gly Leu Ser Thr Leu Ser Trp Val Ile Thr Ser Tyr Thr Leu Ala 35 40 45

Thr Ala Ala Ser Thr Pro Val Trp Gly Lys Leu Ala Asp Met Tyr Gly

Gly Lys Val Val Phe Val Ala Thr Leu Val Val Phe Leu Ala Gly Ser Leu Leu Ser Gly Met Ala Gln Ser Ile Thr Gln Leu Thr Val Phe Arg Ala Val His Gly Leu Gly Ala Gly Gly Leu Met Val Cys Ala Phe Ala Ile Met Val Glu Val Leu Ala Gly Pro Asp Leu Pro Lys Tyr Gln Gly Ile Met Ser Ala Thr Met Gly Leu Thr Met Val Ala Gly Pro Leu Val 135 Gly Gly Leu Ile Thr Asp Glu Leu Gly Trp Arg Trp Cys Phe Tyr Ile Asn Leu Pro Ile Gly Ala Val Ala Leu Leu Ile Val Val Leu Met Met 170 His Leu Pro Arg Arg His Thr Lys Ala Arg Ile Asp Tyr Ala Gly Ala 180 185 Ala Leu Leu Thr Val Val Ser Ser Cys Val Val Leu Val Thr Thr Trp Gly Gly Ile Thr Tyr Pro Trp Ala Ser Pro Met Ile Leu Gly Leu Val 215 Ala Leu Gly Val Leu Thr Cys Ala Leu Phe Val Val Val Glu Arg Arg 230 235 Val Ala Glu Pro Leu Val Pro Leu Ala Met Phe Arg Ser Leu Asn Phe Thr Leu Ser Thr Leu Ile Ala Phe Leu Val Gly Phe Ala Leu Ile Ala 265 Gly Leu Thr Phe Leu Ala Leu Phe Gln Gln Ala Val Gln Gly Ala Ser 280 Ala Ser Asp Ser Gly Leu Leu Leu Pro Leu Leu Leu Ser Met Ala 295 Ala Val Asn Val Val Gly Gly Arg Leu Met Ser Gly Gly Arg Ser Tyr Arg Leu Leu Met Leu Ala Gly Ala Ala Leu Met Thr Leu Ser Leu Leu 325 330 Leu Phe Ala Leu Met Asp Val Gly Thr Ser Arg Thr Val Thr Ala Ile 345 Pro Met Val Gly Phe Gly Ala Gly Leu Gly Leu Met Gln Thr Ser Leu Met Val Ala Leu Ser Ser Val Glu Met Arg Asn Leu Gly Val Ala Ala Ser Thr Ser Thr Leu Phe Arg Thr Ile Gly Gly Ala Val Gly Ala 390 Ser Ala Thr Val Ser Leu Phe Ser Val Arg Val Gln Ser Ala Leu Ala

405 410 415 Asp Arg Gly Val Ala Asp Val Ala Asp Leu Leu Gly His Ser Ala Arg 425 Leu Asp Ala Ala Gly Leu Ala Gln Leu Pro Arg Ala Val Arg Val His 435 Phe Met His Ala Val Ala Ser Gly Thr Arg Trp Ala Phe Leu Met Thr Val Leu Ala Gly Leu Ile Cys Val Ala Ala Ala Trp Phe Leu Arg Arg 470 475 Val Thr Pro Leu Thr Ser Ala Pro Val Ala Pro Glu Pro Ala Arg Asp 485 490 Val Ala Ala Pro Ala Ala Ser Ser Gly Arg Ala Pro Asn Tyr 505 <210> 36 <211> 1476 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1476) <220> <223> evrF <400> 36 atg tee age aag ate eta gte ate ggt gga ggt eeg gee gga tee aeg Met Ser Ser Lys Ile Leu Val Ile Gly Gly Pro Ala Gly Ser Thr gcc gcc gcg ctg ctc gcc cga tcg ggg ctg tcg gtg acg ctc ctg gaa Ala Ala Leu Leu Ala Arg Ser Gly Leu Ser Val Thr Leu Leu Glu aag gag acg ttc ccg cga tac cac atc ggc gag tcg atc gcg tcc tcg 144 Lys Glu Thr Phe Pro Arg Tyr His Ile Gly Glu Ser Ile Ala Ser Ser 40 tgc cgc acc atc gtc gat ttc gtg ggc gct ctc gac gag gtc gac tcg Cys Arg Thr Ile Val Asp Phe Val Gly Ala Leu Asp Glu Val Asp Ser 192 55 egg ggc tac eeg cag aag aac ggg gte etg etg ege tgg gge aac gag 240 Arg Gly Tyr Pro Gln Lys Asn Gly Val Leu Leu Arg Trp Gly Asn Glu gac tgg gcc atc gac tgg gcc aag atc ttc ggt ccg ggc gtg cgg tcc 288 Asp Trp Ala Ile Asp Trp Ala Lys Ile Phe Gly Pro Gly Val Arg Ser 85 90 95 tgg cag gtc gac cgg gac gac ttc gac cac gtc ctg ctc aac aac gcc 336 Trp Gln Val Asp Arg Asp Asp Phe Asp His Val Leu Leu Asn Asn Ala 100

ggc aag cag ggc gcc aag atc atc cag ggc gcg gct gtc aag cgg gtg

Gly Lys Gln Gly Ala Lys Ile Ile Gln Gly Ala Ala Val Lys Arg Val

115 120 125 ttg ttc gac ggt gag cgg gcc acc gcc gcc gag tgg ttc gac ccc gag 432 Leu Phe Asp Gly Glu Arg Ala Thr Ala Ala Glu Trp Phe Asp Pro Glu 130 135 teg ggt gag gte ege ace ate gat tte gae tae gtg gte gae geg tee 480 Ser Gly Glu Val Arg Thr Ile Asp Phe Asp Tyr Val Val Asp Ala Ser ggc cgg gcc ggg ctg atc ccg tcc cag cac ttc aag cac cgg cgc ccc 528 Gly Arg Ala Gly Leu Ile Pro Ser Gln His Phe Lys His Arg Arg Pro acc gag acg ttc aag aac gtg gcc atc tgg ggc tac tgg cag ggt ggc 576 Thr Glu Thr Phe Lys Asn Val Ala Ile Trp Gly Tyr Trp Gln Gly Gly 185 tog ctg ctg ccg aac tot ccc tcc ggc ggg atc aac gtc atc tcc gcg 624 Ser Leu Leu Pro Asn Ser Pro Ser Gly Gly Ile Asn Val Ile Ser Ala ecc gac ggc tgg tac tgg gtc att ccg ctg cgc ggc gac cgg tac agc 672 Pro Asp Gly Trp Tyr Trp Val Ile Pro Leu Arg Gly Asp Arg Tyr Ser 215 220 ate gge tte gte tge cae cag age ege tte etg gag egg ege aag gag 720 Ile Gly Phe Val Cys His Gln Ser Arg Phe Leu Glu Arg Arg Lys Glu 230 235 cac gcc tcg ctg gag gac atg ctc gcc gca ctg gta cag gag tcc ccg 768 His Ala Ser Leu Glu Asp Met Leu Ala Ala Leu Val Gln Glu Ser Pro 245 250 ace gtg ege etg acg geg aac ggg acg tac cag eeg qqe qtq eqq 816 Thr Val Arg Gly Leu Thr Ala Asn Gly Thr Tyr Gln Pro Gly Val Arg 260 265 gtg gag cag gac ttc tcg tac atc tcc gac agc ttc tgc ggg ccc ggc 864 Val Glu Gln Asp Phe Ser Tyr Ile Ser Asp Ser Phe Cys Gly Pro Gly 275 280 tac ttc gcg gcc ggc gac tcc gcc tgc ttc ctg gac cca ctg ctg tcc 912 Tyr Phe Ala Ala Gly Asp Ser Ala Cys Phe Leu Asp Pro Leu Leu Ser 290 acc ggc gtg cac ctc gcc ctc tac agc ggc atg ctc gcc tcg gcg tcc 960 Thr Gly Val His Leu Ala Leu Tyr Ser Gly Met Leu Ala Ser Ala Ser 305 310 315 320 atc ctg gcc acc atc cac ggt gac gtc acc gag gag gag gcg cgg gcg 1008 Ile Leu Ala Thr Ile His Gly Asp Val Thr Glu Glu Glu Ala Arg Ala 325 tto tac gag tcc ctc tac cgc aac gcc tac cag cgc ctg ttc acc ctc 1056 Phe Tyr Glu Ser Leu Tyr Arg Asn Ala Tyr Gln Arg Leu Phe Thr Leu 340 345 gtc gcc ggc gtc tac cag cag cag gcc ggc aag agg gca tac ttc ggc 1104 Val Ala Gly Val Tyr Gln Gln Gln Ala Gly Lys Arg Ala Tyr Phe Gly 360 ctg gcc gac gcg ctg gtg cac gac agc ggc gaa ccc gag tac gag aag 1152 Leu Ala Asp Ala Leu Val His Asp Ser Gly Glu Pro Glu Tyr Glu Lys 375 380

gta g																
Val A 385																1200
ctg g Leu A																1248
ccg g Pro A																1296
gag g Glu A																1344
gag g Glu A 4																1392
ggc c Gly L 465																1440
ccg g Pro A																1476
<210> 37 <211> 492 <212> PRT <213> Micromonospora carbonacea																
<211><212>	> 49 > PR	92 PT	nonos	spora	a car	cbona	acea									
<211><212>	> 49 > PR > Mi	2 RT .cron	nonos	spora	a car	cbona	acea									
<211><212><213>	> 49 > PR > Mi > ev > 37	22 CT .cron			-			Gly	Gly 10	Gly	Pro	Ala	Gly	Ser 15	Thr	
<211><212><213><220><223><400>Met S	> 49 > PR > Mi > ev > 37 Ser	22 CT CCTOM VTF Ser	Lys	Ile 5	Leu	Val	Ile		10	_			_	15		
<211><212><213> <td>> 49 > PR > Mi > ev > 37 Ser</td> <td>22 RT .Cron YrF Ser</td> <td>Lys Leu 20</td> <td>Ile 5 Leu</td> <td>Leu Ala</td> <td>Val Arg</td> <td>Ile Ser</td> <td>Gly 25</td> <td>10 Leu</td> <td>Ser</td> <td>Val</td> <td>Thr</td> <td>Leu 30</td> <td>15 Leu</td> <td>Glu</td> <td></td>	> 49 > PR > Mi > ev > 37 Ser	22 RT .Cron YrF Ser	Lys Leu 20	Ile 5 Leu	Leu Ala	Val Arg	Ile Ser	Gly 25	10 Leu	Ser	Val	Thr	Leu 30	15 Leu	Glu	
<211><212><213> <td>> 49 > PR > Mi > ev > 37 Ser</td> <td>22 RT Crom</td> <td>Lys Leu 20 Phe</td> <td>Ile 5 Leu Pro</td> <td>Leu Ala Arg</td> <td>Val Arg Tyr</td> <td>Ile Ser His 40</td> <td>Gly 25 Ile</td> <td>10 Leu Gly</td> <td>Ser</td> <td>Val Ser</td> <td>Thr Ile 45</td> <td>Leu 30 Ala</td> <td>15 Leu Ser</td> <td>Glu Ser</td> <td></td>	> 49 > PR > Mi > ev > 37 Ser	22 RT Crom	Lys Leu 20 Phe	Ile 5 Leu Pro	Leu Ala Arg	Val Arg Tyr	Ile Ser His 40	Gly 25 Ile	10 Leu Gly	Ser	Val Ser	Thr Ile 45	Leu 30 Ala	15 Leu Ser	Glu Ser	
<211><212><213> <td>> 49 > PR > Mi > ev > 37 Ger Ala</td> <td>22 RT Cron FF Ser Ala Thr 35</td> <td>Lys Leu 20 Phe Ile</td> <td>Ile 5 Leu Pro</td> <td>Leu Ala Arg Asp</td> <td>Val Arg Tyr Phe 55</td> <td>Ile Ser His 40 Val</td> <td>Gly 25 Ile Gly</td> <td>10 Leu Gly Ala</td> <td>Ser Glu Leu</td> <td>Val Ser Asp 60</td> <td>Thr Ile 45 Glu</td> <td>Leu 30 Ala Val</td> <td>15 Leu Ser Asp</td> <td>Glu Ser Ser</td> <td></td>	> 49 > PR > Mi > ev > 37 Ger Ala	22 RT Cron FF Ser Ala Thr 35	Lys Leu 20 Phe Ile	Ile 5 Leu Pro	Leu Ala Arg Asp	Val Arg Tyr Phe 55	Ile Ser His 40 Val	Gly 25 Ile Gly	10 Leu Gly Ala	Ser Glu Leu	Val Ser Asp 60	Thr Ile 45 Glu	Leu 30 Ala Val	15 Leu Ser Asp	Glu Ser Ser	
<211><212><213> <220><223> <400>Met S 1 Ala A Lys G Cys A Arg G	<pre>4 4 9 PR PR PR AT AT B AT B B AT B B B B B B B B B B B</pre>	22 TT.cron VrF Ser Ala Thr 35 Thr	Lys Leu 20 Phe Ile Pro	Ile 5 Leu Pro Val	Leu Ala Arg Asp Lys	Val Arg Tyr Phe 55 Asn	Ile Ser His 40 Val	Gly 25 Ile Gly Val	10 Leu Gly Ala Leu	Ser Glu Leu Leu 75	Val Ser Asp 60 Arg	Thr Ile 45 Glu Trp	Leu 30 Ala Val Gly	15 Leu Ser Asp	Glu Ser Ser Glu 80	
<211><212><213> 220 223 400 Met S 1 Ala A Lys G Cys A Arg G 65	<pre>4 9 9 PR P</pre>	22 T.cron vrF Ser Ala Thr 35 Thr	Lys Leu 20 Phe Ile Pro	Ile 5 Leu Pro Val Gln Asp	Leu Ala Arg Asp Lys 70	Val Arg Tyr Phe 55 Asn Ala	Ile Ser His 40 Val Gly Lys	Gly 25 Ile Gly Val	Leu Gly Ala Leu Phe 90	Ser Glu Leu Leu 75	Val Ser Asp 60 Arg	Thr Ile 45 Glu Trp Gly	Leu 30 Ala Val Gly	Leu Ser Asp Asn Arg	Glu Ser Ser Glu 80 Ser	

Leu Phe Asp Gly Glu Arg Ala Thr Ala Ala Glu Trp Phe Asp Pro Glu 130 135 140

Ser Gly Glu Val Arg Thr Ile Asp Phe Asp Tyr Val Val Asp Ala Ser Gly Arg Ala Gly Leu Ile Pro Ser Gln His Phe Lys His Arg Arg Pro 165 170 Thr Glu Thr Phe Lys Asn Val Ala Ile Trp Gly Tyr Trp Gln Gly Gly Ser Leu Leu Pro Asn Ser Pro Ser Gly Gly Ile Asn Val Ile Ser Ala 200 Pro Asp Gly Trp Tyr Trp Val Ile Pro Leu Arg Gly Asp Arg Tyr Ser 215 Ile Gly Phe Val Cys His Gln Ser Arg Phe Leu Glu Arg Arg Lys Glu His Ala Ser Leu Glu Asp Met Leu Ala Ala Leu Val Gln Glu Ser Pro Thr Val Arg Gly Leu Thr Ala Asn Gly Thr Tyr Gln Pro Gly Val Arg 260 265 Val Glu Gln Asp Phe Ser Tyr Ile Ser Asp Ser Phe Cys Gly Pro Gly Tyr Phe Ala Ala Gly Asp Ser Ala Cys Phe Leu Asp Pro Leu Leu Ser Thr Gly Val His Leu Ala Leu Tyr Ser Gly Met Leu Ala Ser Ala Ser 310 315 Ile Leu Ala Thr Ile His Gly Asp Val Thr Glu Glu Glu Ala Arg Ala Phe Tyr Glu Ser Leu Tyr Arg Asn Ala Tyr Gln Arg Leu Phe Thr Leu Val Ala Gly Val Tyr Gln Gln Gln Ala Gly Lys Arg Ala Tyr Phe Gly 360 Leu Ala Asp Ala Leu Val His Asp Ser Gly Glu Pro Glu Tyr Glu Lys Val Asp Gly Ala Arg Ala Phe Ala Gln Leu Val Ala Gly Leu Ala Asp Leu Asp Asp Ala Ala Glu Gly Arg His Asp Ser Thr Ala Ala Ala Ala 405 Pro Ala Glu Gln Asp Asn Ser Val Arg Gln Leu Phe Leu Ala Ala Glu 425 Glu Ala Arg Arg Met Ala Asp Ala Arg Thr Pro Ser Ala Pro Val Ser Glu Ala Pro Gly Lys Leu Asp Ser His Asp Leu Phe Asp Ser Ala Thr Gly Leu Tyr Leu Val Thr Thr Pro Arg Leu Gly Ile Arg Arg Ala Lys 470 Pro Ala Asp Thr Gln Ala Ala Ala Glu Gln Ser Ala

```
<210> 38
<211> 1422
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1422)
<220>
<223> evrG
<400> 38
atg tea ege tee etc aga egg gae geg eag gee eag geg gea eeg
Met Ser Arg Ser Leu Arg Arg Asp Ala Gln Ala Gln Ala Ala Pro
geg teg eec gec aac eeg eac gec ggg eac gec eeg gtg eec age
Ala Ser Pro Ala Asn Pro His Ala Gly His Ala Ala Pro Val Pro Ser
             20
cgg gtc agc acg acc acg gtc gcg gtc acc ccg ttc acc gag ccg atg
                                                                  144
Arg Val Ser Thr Thr Val Ala Val Thr Pro Phe Thr Glu Pro Met
                             40
ccc gtc ccg ccg cgg ctg acc ccg gtc tcc cgc cgc gac ggc atc gac
                                                                  192
Pro Val Pro Pro Arg Leu Thr Pro Val Ser Arg Arg Asp Gly Ile Asp
     50
                         55
gtc tac gag atc ccc atc cgg ccg gcg cag gtg cag atc ctg ccc ggc
                                                                  240
Val Tyr Glu Ile Pro Ile Arg Pro Ala Gln Val Gln Ile Leu Pro Gly
ctg ctc acg ccc gcc tac acc tac gcc ggt tcc ttc gtc ggc ccc acc
                                                                  288
Leu Leu Thr Pro Ala Tyr Thr Tyr Ala Gly Ser Phe Val Gly Pro Thr
                 85
ate egg gee ege aeg gge egg eee gtg egg ate aee tae aee gag
                                                                  336
Ile Arg Ala Arg Thr Gly Arg Pro Val Arg Ile Thr Tyr Thr Asn Gly
            100
                                105
ctc gac acc cac gcc aac gtg cac ctg cac ggc ggg cac gtg ccg gcc
                                                                  384
Leu Asp Thr His Ala Asn Val His Leu His Gly Gly His Val Pro Ala
        115
                            120
                                                125
ace age gac ggt cae ceg atg gac etg ate ceg eeg gge gge teg aag
                                                                  432
Thr Ser Asp Gly His Pro Met Asp Leu Ile Pro Pro Gly Gly Ser Lys
gtc tac gac tac ccg aac ctt cag cgc ggc gcg acg ctc tgg tac cac
                                                                  480
Val Tyr Asp Tyr Pro Asn Leu Gln Arg Gly Ala Thr Leu Trp Tyr His
145
gac cac acc cac gcc tac gag gcc gac cac gtc tac cgc gga ctg cac
                                                                  528
Asp His Thr His Ala Tyr Glu Ala Asp His Val Tyr Arg Gly Leu His
ggc ttc tat ctg atc gac gac ccg gcc gag cat cac ctg cgc ctg ccc
                                                                  576
Gly Phe Tyr Leu Ile Asp Asp Pro Ala Glu His His Leu Arg Leu Pro
            180
```

	ggc Gly															624
	tcc Ser 210															672
	gcg Ala															720
	cgg Arg															768
	ctg Leu															816
	ccc Pro															864
	gtc Val 290															912
_	tac Tyr			_		_		_		_	_		_		_	960
tcc Ser	cgg Arg	gcg Ala	gtc Val	acc Thr 325	gac Asp	ccc Pro	agc Ser	cgg Arg	gtg Val 330	ccg Pro	gtc Val	acc Thr	ctg Leu	cgc Arg 335	gca Ala	1008
	ccc Pro															1056
	gac Asp															1104
ttc Phe	gac Asp 370	cct Pro	ctc Leu	cgg Arg	gtg Val	gac Asp 375	gta Val	cag Gln	gtc Val	aag Lys	cgg Arg 380	ggc Gly	agc Ser	acc Thr	gag Glu	1152
	tgg Trp															1200
	ttc Phe															1248
	ccg Pro															1296
	ccc Pro															1344
ctc	999	cag	tac	gtc	tac	cac	tgc	cac	tac	ctg	gag	cac	tcg	tcg	ctg	1392

Leu Gly Gln Tyr Val Tyr His Cys His Tyr Leu Glu His Ser Ser Leu 455 ggg atg atg gcc cag ctg gag gtt gtg ccc Gly Met Met Ala Gln Leu Glu Val Val Pro 465 470 <210> 39 <211> 474 <212> PRT <213> Micromonospora carbonacea <220> <223> evrG <400> 39 Met Ser Arg Ser Leu Arg Arg Asp Ala Gln Ala Ala Gln Ala Ala Pro Ala Ser Pro Ala Asn Pro His Ala Gly His Ala Ala Pro Val Pro Ser Arg Val Ser Thr Thr Thr Val Ala Val Thr Pro Phe Thr Glu Pro Met Pro Val Pro Pro Arg Leu Thr Pro Val Ser Arg Arg Asp Gly Ile Asp Val Tyr Glu Ile Pro Ile Arg Pro Ala Gln Val Gln Ile Leu Pro Gly Leu Leu Thr Pro Ala Tyr Thr Tyr Ala Gly Ser Phe Val Gly Pro Thr Ile Arg Ala Arg Thr Gly Arg Pro Val Arg Ile Thr Tyr Thr Asn Gly Leu Asp Thr His Ala Asn Val His Leu His Gly Gly His Val Pro Ala 120 Thr Ser Asp Gly His Pro Met Asp Leu Ile Pro Pro Gly Gly Ser Lys Val Tyr Asp Tyr Pro Asn Leu Gln Arg Gly Ala Thr Leu Trp Tyr His 150 155 Asp His Thr His Ala Tyr Glu Ala Asp His Val Tyr Arg Gly Leu His 165 Gly Phe Tyr Leu Ile Asp Asp Pro Ala Glu His His Leu Arg Leu Pro Ala Gly Lys Tyr Asp Val Pro Ile Met Leu Arg Asn Ala Gln Phe Asp Asp Ser Gly Ala Leu Val Phe Gly His Pro Asp Asp Arg Val Thr Ile 215 220

Leu Ala Asn Gly Lys Ala Gln Pro Tyr Phe Glu Val Ala Pro Arg Arg

Tyr Arg Phe Arg Leu Leu Asn Ala Ala Leu Lys His Val Phe Arg Leu

Asn Leu Gly Gly Glu Pro Leu Thr Arg Ile Ala Thr Asp Gly Gly Leu 265 Leu Pro Ala Pro Thr Ser His Thr Glu Leu Ala Leu Ser Ser Gly Glu Arg Val Glu Ile Val Ile Asp Phe Ala Glu His Ala Gly Gly Pro 295 Val Tyr Leu Tyr Asp Gly Asp Asn Pro Ile Leu Arg Phe Asp Val Ser Ser Arg Ala Val Thr Asp Pro Ser Arg Val Pro Val Thr Leu Arg Ala Leu Pro Pro Met Gly Thr Pro Thr Val Glu Arg Thr Val Ser Met Ser 345 Phe Asp Met Ser Ala Arg Pro Pro Ile Ala Leu Met Asp Gly Lys Pro Phe Asp Pro Leu Arg Val Asp Val Gln Val Lys Arg Gly Ser Thr Glu 375 Ile Trp Asn Val Val Asn Ala Asp Thr Asp Pro Phe Pro Phe Asp His 395 Pro Phe His Leu His Leu Val Thr Phe Arg Val Leu Gly Arg Asp Gly 410 Gly Pro Pro Ala Pro Glu Asp Ala Gly Leu Lys Asp Thr Val Tyr Val Ser Pro Lys Gly Ser Val Lys Ile Gln Val Thr Phe Ala Thr Pro Tyr 440 Leu Gly Gln Tyr Val Tyr His Cys His Tyr Leu Glu His Ser Ser Leu Gly Met Met Ala Gln Leu Glu Val Val Pro 465 470 <210> 40 <211> 1044 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1044) <220> <223> evrH atg gca cgg acc ctg cga ggg ctg gag gtg gcc gcc cag gag atc 48 Met Ala Arg Thr Leu Arg Gly Leu Glu Glu Val Ala Ala Gln Glu Ile gag gag cgg ggc ctc ggc cgg gtc gag cac cgc cgg cac cgc gag gtg 96 Glu Glu Arg Gly Leu Gly Arg Val Glu His Arg Arg His Arg Glu Val

tgg Trp	ttc Phe	tcc Ser 35	gcc Ala	gcc Ala	agc Ser	gcg Ala	gag Glu 40	ccg Pro	cgc Arg	ctg Leu	ctg Leu	gat Asp 45	ctg Leu	cgt Arg	acc Thr	144
gtc Val	gac Asp 50	gac Asp	ctg Leu	ttc Phe	ctg Leu	ctc Leu 55	gtc Val	gcc Ala	gtc Val	gcc Ala	gac Asp 60	ggc Gly	gtc Val	ggc Gly	cac His	192
		gcg Ala														240
		gcg Ala														288
ccg Pro	gcg Ala	acc Thr	gtg Val 100	gac Asp	gtc Val	gcc Ala	gcc Ala	tcc Ser 105	ttc Phe	ctc Leu	ggc Gly	cgc Arg	cgc Arg 110	aac Asn	tac Tyr	336
		tac Tyr 115														384
		ttg Leu														432
		ctg Leu														480
		cgg Arg														528
		acg Thr														576
		gcc Ala 195														624
ggc Gly	acc Thr 210	ggc Gly	acg Thr	atc Ile	ccc Pro	gtg Val 215	gag Glu	gca Ala	gcc Ala	gly ggg	ctg Leu 220	gca Ala	ccg Pro	gly ggg	gcg Ala	672
		ttc Phe														720
		tcg Ser														768
		cga Arg														816
		ccc Pro 275														864
gat	tcc	ggc	cgc	ctc	ttc	gcg	gag	ctg	cgc	cgg	gtg	acg	gtc	gac	ggc	912

Asp Ser Gly 290	Arg Lei		la Glu 95	Leu	Arg	Arg	Val 300	Thr	Val	Asp	Gly
ggg cgg gcg Gly Arg Ala 305											
gcc cgc gcc Ala Arg Ala		Phe G									
ttc ggc gcc Phe Gly Ala											
<210> 41 <211> 348 <212> PRT <213> Micron	monospoi	a carb	onacea								
<220> <223> evrH											
<400> 41 Met Ala Arg 1	Thr Lev	_	ly Leu	Glu	Glu 10	Val	Ala	Ala	Gln	Glu 15	Ile
Glu Glu Arg	Gly Let 20	Gly A	rg Val	Glu 25	His	Arg	Arg	His	Arg 30	Glu	Val
Trp Phe Ser	Ala Ala	a Ser A	la Glu 40	Pro	Arg	Leu	Leu	Asp 45	Leu	Arg	Thr
Val Asp Asp 50	Leu Phe		eu Val 55	Ala	Val	Ala	Asp 60	Gly	Val	Gly	His
Thr Lys Ala 65	Asp Let	ı Ala A 70	la Phe	Thr	Arg	Leu 75	Ala	Arg	Ala	Ala	Ala 80
Leu Pro Ala	Val Let 85		la Arg	Ala	Ala 90	Cys	Gly	Val	Pro	Gly 95	Arg
Pro Ala Thr	Val Ası 100	Val A	la Ala	Ser 105	Phe	Leu	Gly	Arg	Arg 110	Asn	Tyr
Asn Arg Tyr 115	Asp Ile	e Glu A	sp Ala 120	Val	Gly	Arg	His	Ala 125	Val	Ala	Ala
Leu Gly Leu 130	Arg Ty		er Arg .35	Arg	Gly	Gly	Glu 140	Ala	Pro	Pro	Glu
Gly Gly Leu 145	Ser Le	Arg V 150	al Thr	Val	Glu	Gly 155	Thr	Gln	Ala	Thr	Leu 160
Ala Val Arg	Val Ala	_	rg Pro	Leu	His 170	Arg	Arg	Ala	Tyr	Lys 175	Arg
Ser Ser Thr	Pro Gly 180	Thr L	eu His	Pro 185	Pro	Leu	Ala	Ala	Ala 190	Leu	Ala
Trp Leu Ala 195	Gly Ile	e Arg P	ro Gly 200	Met	Leu	Val	Ala	Asp 205	Pro	Сув	Cys

Gly Thr Gly Thr Ile Pro Val Glu Ala Ala Gly Leu Ala Pro Gly Ala

	210					215					220					
Va 22	l Leu 5	Phe	Gly	Ser	Asp 230	His	Asp	Pro	Glu	Thr 235	Val	Gly	Ala	Ala	Val 240	
Al	a Asn	Ser	Ala	Ala 245	Ser	Gly	Ala	Arg	Val 250	Thr	Trp	Ala	Val	Ala 255	Asp	
Al	a Gly	Arg	Leu 260	Pro	Leu	Arg	Thr	Gly 265	Arg	Val	Asp	Arg	Val 270	Val	Ser	
As	n Pro	Pro 275	Trp	Asp	Arg	Gln	Val 280	Gln	Ala	Arg	Gly	Val 285	Leu	Ala	Gly	
As	p Ser 290	Gly	Arg	Leu	Phe	Ala 295	Glu	Leu	Arg	Arg	Val 300	Thr	Val	Asp	Gly	
G1 30	y Arg 5	Ala	Val	Leu	Leu 310	Leu	His	Glu	Phe	Ala 315	Asp	Gln	Ala	Asp	Leu 320	
Al	a Arg	Ala	Ala	Gly 325	Phe	Gly	Val	Gly	Asp 330	Val	Arg	Pro	Val	Ser 335	Leu	٠
Ph	e Gly	Ala	His 340	Pro	Ser	Ile	Val	Asp 345	Leu	His	Gly					
<2 <2 <2 <2 <2	11> 1 12> D: 13> M 20> 21> C: 22> (NA icro DS		_	a ca	rbona	acea									
<2	23> e [.] 00> 4															
at Me	g ccg t Pro 1	cac	ggg Gly	ccc Pro 5	gtg Val	cgc Arg	cga Arg	aat Asn	cgt Arg 10	gga Gly	gat Asp	tgc Cys	gca Ala	gtg Val 15	cgt Arg	48
	a ccg r Pro															96
	g agc l Ser															144
	g gag 1 Glu 50															192
	g ccg a Pro 5															240
	ggc Gly															288

					ggc Gly											336
					ctg Leu											384
					ttc Phe											432
					gcc Ala 150											480
					tgg Trp											528
					atc Ile											576
					aag Lys											624
					ttc Phe											672
					atc Ile 230											720
					gac Asp											768
					gcg Ala											816
					tcc Ser											864
					atg Met											912
			_		gcg Ala 310	_	_		_	_	_	_	_		_	960
					ctc Leu											1008
acc Thr	gcg Ala	ccg Pro	ggc Gly 340	gtg Val	gtg Val	gtg Val	tcg Ser	tgc Cys 345	gcg Ala	atc Ile	gtc Val	cag Gln	gtg Val 350	atc Ile	gag Glu	1056
tcg	ccg	acg	tgg	cgg	gag											1074

Ser Pro Thr Trp Arg Glu 355

<210> 43

<211> 358

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrI

<400> 43

Met Pro His Gly Pro Val Arg Arg Asn Arg Gly Asp Cys Ala Val Arg 1 5 10 15

Thr Pro Asp Leu Phe Ile Gly Ala Val Gly Ala Phe Val Pro Pro Thr 20 25 30

Val Ser Val Glu Trp Ala Ile Asp Arg Gly Leu Tyr Ser Arg Glu Gln 35 40

Val Glu Leu His Glu Leu Ala Gly Thr Ala Ile Ala Gly Asp Leu Pro 50 55 60

Ala Pro Glu Met Ala Leu Arg Ala Ala Gln Gln Ala Val Lys Arg Trp 65 70 75 80

Gly Gly Ser Pro Thr Glu Phe Asp Leu Leu Leu Tyr Ala Ser Thr Trp 85 90 95

His Gln Gly Pro Asp Gly Trp Pro Pro His Ser Tyr Leu Gln Arg His 100 105 110

Leu Val Gly Gly Asp Leu Leu Ala Leu Glu Ile Arg Gln Gly Cys Asn 115 120 125

Gly Met Phe Ser Ala Phe Glu Leu Ala Ala Ser His Leu Gln Ala Val 130 135 140

Pro Glu Arg Thr Ser Ala Leu Leu Val Ala Ala Asp Asn Tyr Gly Thr 145 150 155 160

Pro Met Val Asp Arg Trp Arg Met Gly Pro Gly Phe Ile Gly Gly Asp 165 170 175

Ala Gly Ser Ala Leu Ile Leu Thr Lys Arg Pro Gly Phe Ala Arg Leu 180 185 190

Arg Ser Val Cys Thr Lys Ser Val Pro Glu Ala Glu Arg Leu His Arg 195 200 205

Gly Asp Glu Pro Leu Phe Pro Pro Ser Val Leu Thr Gly Arg Glu Leu 210 215 220

Asn Phe Thr Ala Arg Ile Asp Gln Gln Phe Ala Ala Arg Ser Pro Ala 225 230 235 240

Ser Ile Ala Met Ala Asp Val Gly Asp His Ile Glu Glu Val Val Gly
245 250 255

Arg Ala Leu Ala Glu Ala Glu Ile Glu Val Gly Asp Leu Ala Arg Val 260 265 270

Ala Phe Met Asn Phe Ser Arg Glu Ile Met Glu Gln Arg Cys Leu Ala

275 280 Asn Trp Gly Leu Pro Met Ser Arg Ser Thr Phe Asp Phe Gly Arg Arg 295 Ile Gly His Cys Gly Ala Ser Asp Pro Leu Leu Ala Leu Glu His Leu 315 305 310 Ala Arg Thr Gly Gly Leu Gly Pro Gly Asp His Leu Leu Thr Leu Gly Thr Ala Pro Gly Val Val Val Ser Cys Ala Ile Val Gln Val Ile Glu Ser Pro Thr Trp Arg Glu 355 <210> 44 <211> 3792 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(3792) <220> <223> evrJ <400> 44 gtg gaa gca gag aag gac cgg ttg cgt ccg gtg gcg tcc gag gcg gtc 48 Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val gcc gtg gtg ggg atc ggc tgc cgg ttc ccg ggc gac gtc aac tcg ccc 96 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro gac gag ttc tgg gac ctg ctc acc ggg ggt cgc aac acc acc ggg acg 144 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr gtg eee gag gag ege tgg age geg tae ege gae etg ggt eeg geg tte 192 Val Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe gag tee geg ete egg teg gee ace egg geg gge aae tte etg gee gae 240 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp ate tee gge tte gae geg gae tte tte gge ate tee eeg ege gag gee 288 Ile Ser Gly Phe Asp Ala Asp Phe Phe Gly Ile Ser Pro Arg Glu Ala gag ctg atg gac ccg cag cag ctc atg ctg gag gtg acc tgg cag 336 Glu Leu Met Asp Pro Gln Gln Arg Leu Met Leu Glu Val Thr Trp Gln 100 gcg ctg gag gac gcc ggg atc ccg ccc cgc acc ctg gcc ggc acc gac 384 Ala Leu Glu Asp Ala Gly Ile Pro Pro Arg Thr Leu Ala Gly Thr Asp

gtc Val	ggc Gly 130	gtc Val	ttc Phe	gcc Ala	ggc Gly	gtg Val 135	tgc Cys	acc Thr	tac Tyr	gac Asp	tac Tyr 140	ggc Gly	ggc Gly	cac His	cag Gln	432
											ggc Gly					480
	_	_	_	_			_				ctc Leu	_	_	_		528
											tcg Ser					576
											agc Ser					624
											cag Gln 220					672 ·
											agc Ser					720
											tgc Cys					768
											gac Asp					816
											cgg Arg					864
											atg Met 300					912
											tac Tyr					960
											gcc Ala					1008
tcg Ser	gtc Val	tac Tyr	ggg Gly 340	cag Gln	gac Asp	cgc Arg	ccg Pro	gac Asp 345	gac Asp	gag Glu	ccc Pro	tgc Cys	ctg Leu 350	atc Ile	ggt Gly	1056
											gcg Ala					1104
											gcc Ala 380					1152
acc	ctg	ctg	gtc	acc	gag	gtc	aac	ccg	gac	atc	gag	tgg	aag	cgg	ctg	1200

Thr 385	Leu	Leu	Val	Thr	Glu 390	Val	Asn	Pro	Asp	Ile 395	Glu	Trp	Lys	Arg	Leu 400	
				gtc Val 405												1248
				gga Gly												1296
				gaa Glu												1344
				gag Glu												1392
				cgg Arg												1440
				ctc Leu 485												1488
				gtg Val												1536
				ctc Leu												1584
				gcg Ala												1632
				tgg Trp												1680
				gac Asp 565												1728
				tca Ser												1776
				acc Thr												1824
				cga Arg												1872
				gag Glu												1920
				gca Ala												1968

645 650 655 gag gtc gcc ggc cag ggc gcg atg gcc ctg gtg acg ctg ccc ttc gag 2016 Glu Val Ala Gly Gln Gly Ala Met Ala Leu Val Thr Leu Pro Phe Glu 660 gag gtc gcg gcc agg ctg gcc ggc cgc gtc gac gtg gtc gcc gcg atc 2064 Glu Val Ala Ala Arg Leu Ala Gly Arg Val Asp Val Val Ala Ala Ile ged ted ted edd teg acc gtg gtd ted ggd gad deg ged geg dtg 2112 Ala Ser Ser Pro Ser Ser Thr Val Val Ser Gly Asp Pro Ala Ala Leu 695 gac gcg ctg gtc gcc gag tgg acc gag gag ggc ctg ggc gta cgc cgg 2160 Asp Ala Leu Val Ala Glu Trp Thr Glu Glu Gly Leu Gly Val Arg Arg gtc gcc tcc gac gtg gcc ttc cac agc ccg cac atg gat ccg ctg ctc 2208 Val Ala Ser Asp Val Ala Phe His Ser Pro His Met Asp Pro Leu Leu gac egg etg ege gee gee gte gac tte ace gee ege gea eee egg gtg 2256 Asp Arg Leu Arg Ala Ala Val Asp Phe Thr Ala Arg Ala Pro Arg Val ceg atc tac age acg geg ctg gec gac ceg egg gec ceg atc acc gec 2304 Pro Ile Tyr Ser Thr Ala Leu Ala Asp Pro Arg Ala Pro Ile Thr Ala 760 gac ggc gag tac tgg gcc gcg aat ctg cgc aac ccg gtc cgg ctc gcc 2352 Asp Gly Glu Tyr Trp Ala Ala Asn Leu Arg Asn Pro Val Arg Leu Ala gca gcg gtg gcc gcc gcc gtc tcc gac gga cac cgg gcc ttc atc gag 2400 Ala Ala Val Ala Ala Val Ser Asp Gly His Arg Ala Phe Ile Glu gtc tcc ccg cac ccg gtg gtg acc cac tcg atc cac gag acg ctg gcc Val Ser Pro His Pro Val Val Thr His Ser Ile His Glu Thr Leu Ala 2448 805 815 gga age ete gae gae gag gte tte gte gge gge ace etg ege ege gae 2496 Gly Ser Leu Asp Asp Glu Val Phe Val Gly Gly Thr Leu Arg Arg Asp 820 acc ccg gag gcg cag gcc ttc ctg tcc agc ctg ggg gcc gcg cac tgc 2544 Thr Pro Glu Ala Gln Ala Phe Leu Ser Ser Leu Gly Ala Ala His Cys 835 840 cac ggg gtc gcg gtc gac tgg ggc cgg gtg cat ccg tcc ggg ccg ctg 2592 His Gly Val Ala Val Asp Trp Gly Arg Val His Pro Ser Gly Pro Leu 855 gtc acc ctg ccc ggc tac ccc tgg cgg cac cgg agt cac tgg cac tgg 2640 Val Thr Leu Pro Gly Tyr Pro Trp Arg His Arg Ser His Trp His Trp 875 ceg acg ceg gee gee acg gge egg gge cae gae eee geg teg cae 2688 Pro Thr Pro Ala Ala Ala Thr Gly Arg Gly His Asp Pro Ala Ser His 885 890 acc ctg ctc ggc gcg gtc gac aac gtg gcg ggc agc gac gtg cgg gtg 2736 Thr Leu Leu Gly Ala Val Asp Asn Val Ala Gly Ser Asp Val Arg Val 900 905 910

Trp Arg Thr Ala 915	ctc gac gac Leu Asp Asp	gcc agc cgc Ala Ser Arg 920	ccg tac ccg Pro Tyr Pro 925	ggc agc cac Gly Ser His	2784
gcc ctc aac ggc Ala Leu Asn Gly 930		Val Pro Ala			2832
ctc atg gct gcc Leu Met Ala Ala 945					2880
ttg tcg atg cgg Leu Ser Met Arg					
gtg gtg cgg gac Val Val Arg Asp 980					2976
gcg gag gcc gac Ala Glu Ala Asp 995	Pro Ser Arg				3024
gtg gcc gac gcc Val Ala Asp Ala 1010					3072
ccc gac gac cac Pro Asp Asp His 1025		Pro Gly Asp	5 55	_	3120
cgg ctc gcc gag Arg Leu Ala Glu					3168
gag gag ctg ctc Glu Glu Leu Leu 1060			Arg Ala Arg		3216
Glu Glu Leu Leu	ser Gly Tyr acc tgg gcg Thr Trp Ala	Gly Val Leu 1065 ccg gtg ctg	gac gcc gtc	Val Arg Ser 1070 atg tcg gtc	3216 3264
Glu Glu Leu Leu 1060 gcc gac tcg tcc Ala Asp Ser Ser	ser Gly Tyr acc tgg gcg Thr Trp Ala ttc ccc ggc	Gly Val Leu 1065 ccg gtg ctg Pro Val Leu 1080 gtg ccg cag	gac gcc gtc Asp Ala Val 1085 cta cgc atg	Val Arg Ser 1070 atg tcg gtc Met Ser Val gtg gtg tac	
Glu Glu Leu Leu 1060 gcc gac tcg tcc Ala Asp Ser Ser 1075 gcc ccc gcc gtc Ala Pro Ala Val	ser Gly Tyr acc tgg gcg Thr Trp Ala ttc ccc ggc Phe Pro Gly 1095 ctg ctc acc	CCG gtg ctg Pro Val Leu 1080 gtg ccg cag Val Pro Gln ggc gag cca Gly Glu Pro	gac gcc gtc Asp Ala Val 1085 cta cgc atg Leu Arg Met 1100 ccg gag gtg	Val Arg Ser 1070 atg tcg gtc Met Ser Val gtg gtg tac Val Val Tyr acg ctg atc	3264
Glu Glu Leu Leu 1060 gcc gac tcg tcc Ala Asp Ser Ser 1075 gcc ccc gcc gtc Ala Pro Ala Val 1090 gtc gac gag gtg Val Asp Glu Val 1105 gag gtc gcc ctc Glu Val Ala Leu	ser Gly Tyr acc tgg gcg Thr Trp Ala ttc ccc ggc Phe Pro Gly	CCG gtg ctg Pro Val Leu 1080 gtg ccg cag Val Pro Gln ggc gag cca Gly Glu Pro cgg ccc gac	gac gcc gtc Asp Ala Val 1085 cta cgc atg Leu Arg Met 1100 ccg gag gtg Pro Glu Val 1115 acg gcg aac	Val Arg Ser 1070 atg tcg gtc Met Ser Val gtg gtg tac Val Val Tyr acg ctg atc Thr Leu Ile 1120 gcg ctg gtc	3264 3312
Glu Glu Leu Leu 1060 gcc gac tcg tcc Ala Asp Ser Ser 1075 gcc ccc gcc gtc Ala Pro Ala Val 1090 gtc gac gag gtg Val Asp Glu Val 1105 gag gtc gcc ctc Glu Val Ala Leu	ser Gly Tyr acc tgg gcg Thr Trp Ala ttc ccc ggc Phe Pro Gly 1095 ctg ctc acc Leu Leu Thr 1110 gac cca gac Asp Pro Asp 1125 ggc cgg gtc	CCG GTG CCG CAG VAl Pro Gln GGG GAG CCA Gly Glu Pro CGG CCC GAC Arg Pro Asp 1130 GTG GCC AGC	gac gcc gtc Asp Ala Val 1085 cta cgc atg Leu Arg Met 1100 ccg gag gtg Pro Glu Val 1115 acg gcg aac Thr Ala Asn ctt ccc ggg Leu Pro Gly	Val Arg Ser 1070 atg tcg gtc Met Ser Val gtg gtg tac Val Val Tyr acg ctg atc Thr Leu Ile 1120 gcg ctg gtc Ala Leu Val 1135 ctg cgc tac	3264 3312 3360

gtg gag gag gtg tcc ttc gcc ggc ctg tcc gac gag gaa ctg cac Val Glu Glu Ala Val Ser Phe Ala Gly Leu Ser Asp Glu Glu Leu His 1170 1175 1180	3552
gag cgg gtg ttc gac gag gtg cgc cgg cag atc gcc ggg gag atg cga Glu Arg Val Phe Asp Glu Val Arg Arg Gln Ile Ala Gly Glu Met Arg 1185 1190 1195 1200	3600
ctc gac gcc gac gac ctg cat ccc cgc cgg ccg ctg gcc gag cag ggc Leu Asp Ala Asp Asp Leu His Pro Arg Arg Pro Leu Ala Glu Gln Gly 1205 1210 1215	648
ctc gac tcg gtg atg acg gtg gtg atc cgg cga cgc ctg gag aag cgc Leu Asp Ser Val Met Thr Val Val Ile Arg Arg Arg Leu Glu Lys Arg 1220 1225 1230	696
acc ggg cgg agc ctc tcc ccg acc gtc ttc tgg cag cgg ccc acc gtc Thr Gly Arg Ser Leu Ser Pro Thr Val Phe Trp Gln Arg Pro Thr Val 1235 1240 1245	744
gcc gcc atc gcc gac cac ctg gtg gag ctg ttg agc acc ccg cag gag Ala Ala Ile Ala Asp His Leu Val Glu Leu Leu Ser Thr Pro Gln Glu 1250 1260	792
<210> 45 <211> 1264 <212> PRT <213> Micromonospora carbonacea	
<220> <223> evrJ	
<400> 45 Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1 5 10 15	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1 5 10 15 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1 S Pro Glu Ala Val Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro 20 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr 35 Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe 50 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 15 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro 25 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr 45 Val Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe 50 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp 80 Ile Ser Gly Phe Asp Ala Asp Phe Phe Gly Ile Ser Pro Arg Glu Ala	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 15 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro 30 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr 35 Val Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe 50 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp 80 Ile Ser Gly Phe Asp Ala Asp Phe Phe Gly Ile Ser Pro Arg Glu Ala 95 Glu Leu Met Asp Pro Gln Gln Arg Leu Met Leu Glu Val Thr Trp Gln	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 15 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro 25 Pro 30 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr 45 Val Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe 50 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp 80 Ile Ser Gly Phe Asp Ala Asp Phe Phe Gly Ile Ser Pro Arg Glu Ala 95 Glu Leu Met Asp Pro Gln Gln Arg Leu Met Leu Glu Val Thr Trp Gln 100 Ala Leu Glu Asp Ala Gly Ile Pro Pro Arg Thr Leu Ala Gly Thr Asp	
Val Glu Ala Glu Lys Asp Arg Leu Arg Pro Val Ala Ser Glu Ala Val 1 15 Ala Val Val Gly Ile Gly Cys Arg Phe Pro Gly Asp Val Asn Ser Pro 25 Asp Glu Phe Trp Asp Leu Leu Thr Gly Gly Arg Asn Thr Thr Gly Thr 45 Val Pro Glu Glu Arg Trp Ser Ala Tyr Arg Asp Leu Gly Pro Ala Phe 50 Glu Ser Ala Leu Arg Ser Ala Thr Arg Ala Gly Asn Phe Leu Ala Asp 65 Glu Ser Gly Phe Asp Ala Asp Phe Phe Gly Ile Ser Pro Arg Glu Ala 95 Glu Leu Met Asp Pro Gln Gln Arg Leu Met Leu Glu Val Thr Trp Gln 100 Ala Leu Glu Asp Ala Gly Ile Pro Pro Arg Thr Leu Ala Gly Thr Asp 115 Val Gly Val Phe Ala Gly Val Cys Thr Tyr Asp Tyr Gly Gly His Gln	

165 170 175 Pro Ser Leu Ser Ile Asp Thr Ala Cys Ser Ala Ser Leu Val Ala Leu 185 His Leu Ala Ala Gln Ser Leu Arg Leu Gly Glu Ser Thr Leu Ala Leu 195 200 205 Ala Gly Gly Val Asn Leu Ile Val Thr Pro Gly Gln Ser Ile Thr Leu Gly Ser Ala Gly Ala Leu Ala Pro Asp Gly Arg Ser Lys Ser Phe Asp Ala Thr Ala Asp Gly Tyr Gly Arg Gly Glu Gly Cys Gly Val Leu Val Leu Lys Leu Ser Asp Ala Gln Arg Asp Gly Asp Arg Val Leu Ala 265 Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Arg Thr Asn Gly Ile Met Ala Pro Cys Gly Gln Ala Gln Glu His Val Met Val Arg Ala Leu 295 Arg Ser Ala Gly Ile Glu Ala Gly Ser Val Asp Tyr Ile Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Met Glu Ala Ala Ile Gly 330 Ser Val Tyr Gly Gln Asp Arg Pro Asp Asp Glu Pro Cys Leu Ile Gly Ser Val Lys Ser Asn Ile Gly His Leu Glu Gly Ala Ala Gly Val Ala Gly Val Ile Lys Ala Val Leu Ala Leu Asn Arg Ala Glu Val Pro Ala 375 Thr Leu Leu Val Thr Glu Val Asn Pro Asp Ile Glu Trp Lys Arg Leu 395 Arg Leu Arg Leu Val Thr Arg Asn Gln Pro Trp Pro Asp Arg Pro Gly 410 Pro Arg Arg Ala Gly Val Ser Gly Phe Gly Tyr Gly Gly Thr Val Ala 420 425 His Val Val Leu Glu Gln Ala Pro Pro Val Ala Ala Glu Pro Ala Pro Ala Leu Thr Gly Glu Thr Leu Phe Pro Ile Ser Ala Gly Ser Ala His Ser Leu Arg Glu Arg Ala Arg Ala Leu Ala Gly Ile Val Pro Asp Val 475 Asp Leu Ala Ala Leu Gly His Thr Leu Ala Arg Arg Arg Ser His Leu 490 Thr His Arg Ala Val Ala Val Ala Gly Arg Asp Asp Leu Val Ala

Ala Phe Ala Ala Leu Ala Asp Asp Arg Pro His Asp Arg Val Arg Thr 520 Gly Ser Pro Val Ala Glu Pro Pro Arg Thr Val Trp Val Phe Ser Gly 535 His Gly Ser Gln Trp Thr Gly Met Gly Arg Glu Leu Leu Ala Thr Glu 555 Pro Ala Phe Ala Asp Ala Ile Asp Arg Ile Glu Gln Ile Phe Leu Asp 565 Glu Ile Gly Phe Ser Pro Arg Gln Ala Ile Leu Asp Gly Asp Tyr Glu 585 Ala Val Asp Arg Thr Gln Thr Met Ile Phe Ala Met Gln Leu Gly Leu 600 Ala Glu Met Trp Arg Ala Arg Gly Val Glu Pro Asp Ala Val Ile Gly His Ser Val Gly Glu Ile Ala Ala Ala Val Thr Ala Gly Ile Leu Thr 630 635 Val Ala Asp Gly Ala Arg Leu Ile Cys Arg Arg Ser Leu Leu Leu Arg Glu Val Ala Gly Gln Gly Ala Met Ala Leu Val Thr Leu Pro Phe Glu 665 Glu Val Ala Ala Arg Leu Ala Gly Arg Val Asp Val Val Ala Ala Ile Ala Ser Ser Pro Ser Ser Thr Val Val Ser Gly Asp Pro Ala Ala Leu 695 Asp Ala Leu Val Ala Glu Trp Thr Glu Glu Gly Leu Gly Val Arg Arg Val Ala Ser Asp Val Ala Phe His Ser Pro His Met Asp Pro Leu Leu 725 730 Asp Arg Leu Arg Ala Ala Val Asp Phe Thr Ala Arg Ala Pro Arg Val 745 Pro Ile Tyr Ser Thr Ala Leu Ala Asp Pro Arg Ala Pro Ile Thr Ala Asp Gly Glu Tyr Trp Ala Ala Asn Leu Arg Asn Pro Val Arg Leu Ala 775 Ala Ala Val Ala Ala Val Ser Asp Gly His Arg Ala Phe Ile Glu Val Ser Pro His Pro Val Val Thr His Ser Ile His Glu Thr Leu Ala 805 Gly Ser Leu Asp Asp Glu Val Phe Val Gly Gly Thr Leu Arg Arg Asp 825 Thr Pro Glu Ala Gln Ala Phe Leu Ser Ser Leu Gly Ala Ala His Cys 835 His Gly Val Ala Val Asp Trp Gly Arg Val His Pro Ser Gly Pro Leu 850 855 860

- Val Thr Leu Pro Gly Tyr Pro Trp Arg His Arg Ser His Trp His Trp 865 870 875 880
- Pro Thr Pro Ala Ala Ala Thr Gly Arg Gly His Asp Pro Ala Ser His 885 890 895
- Thr Leu Leu Gly Ala Val Asp Asn Val Ala Gly Ser Asp Val Arg Val
 900 905 910
- Trp Arg Thr Ala Leu Asp Asp Ala Ser Arg Pro Tyr Pro Gly Ser His 915 920 925
- Ala Leu Asn Gly Val Glu Ile Val Pro Ala Ala Val Leu Val Glu Thr 930 935 940
- Leu Met Ala Ala Ala Gly Arg Gly Asp Gly Arg Pro Leu Leu Thr Gly 945 950 955 960
- Leu Ser Met Arg Tyr Pro Leu Met Thr Ala Gly Leu His Glu Val Gln
 965 970 975
- Val Val Arg Asp Gly Ala Glu Val Arg Leu Ala Ser Arg Ser Val Asp 980 985 990
- Ala Glu Ala Asp Pro Ser Arg Asp Trp Leu Ile His Thr Asp Ala Thr 995 1000 1005
- Val Ala Asp Ala Asp Ala Thr Val Leu Ala Ala Arg Ala Leu Ala Asp 1010 1015 1020
- Pro Asp Asp His Arg Met Glu Pro Gly Asp Pro Gly Ser Ile His Arg 1025 1030 1035 1040
- Arg Leu Ala Glu Val Gly Val Pro Ser Thr Gly Phe Asp Trp Ser Val 1045 1050 1055
- Glu Glu Leu Leu Ser Gly Tyr Gly Val Leu Arg Ala Arg Val Arg Ser 1060 1065 1070
- Ala Asp Ser Ser Thr Trp Ala Pro Val Leu Asp Ala Val Met Ser Val 1075 1080 1085
- Ala Pro Ala Val Phe Pro Gly Val Pro Gln Leu Arg Met Val Val Tyr 1090 1095 1100
- Val Asp Glu Val Leu Leu Thr Gly Glu Pro Pro Glu Val Thr Leu Ile 1105 1110 1115 1120
- Glu Val Ala Leu Asp Pro Asp Arg Pro Asp Thr Ala Asn Ala Leu Val 1125 1130 1135
- Ala Asp Ala Gln Gly Arg Val Val Ala Ser Leu Pro Gly Leu Arg Tyr
 1140 1145 1150
- Pro Val Ile Asp Gln Pro Val Ala Pro Ala Gln Asp Ser Ser Gly Glu 1155 1160 1165
- Val Glu Glu Ala Val Ser Phe Ala Gly Leu Ser Asp Glu Glu Leu His 1170 1175 1180
- Glu Arg Val Phe Asp Glu Val Arg Arg Gln Ile Ala Gly Glu Met Arg 1185 1190 1195 1200
- Leu Asp Ala Asp Asp Leu His Pro Arg Pro Leu Ala Glu Gln Gly

1205 1210 1215 Leu Asp Ser Val Met Thr Val Val Ile Arg Arg Arg Leu Glu Lys Arg Thr Gly Arg Ser Leu Ser Pro Thr Val Phe Trp Gln Arg Pro Thr Val 1235 Ala Ile Ala Asp His Leu Val Glu Leu Leu Ser Thr Pro Gln Glu 1255 <210> 46 <211> 1317 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1317) <220> <223> evrK <400> 46 gtg eec eeg etg gge tee eac eag eta etg etg tte etg etc eag gtg Val Pro Pro Leu Gly Ser His Gln Leu Leu Leu Phe Leu Leu Gln Val ggc ctg ctg ctg ctc gcc gtc gtc ctg gga cgg gtg gcg caa cgc Gly Leu Leu Leu Leu Ala Val Val Leu Gly Arg Val Ala Gln Arg 96 tte gge etg eeg geg gte ggt gag etg etg ace ggg gtg etg ete 144 Phe Gly Leu Pro Ala Val Val Gly Glu Leu Leu Thr Gly Val Leu Leu gge eec teg gtg etg ggg gee etg gea eec gae ate gga egg tgg etg 192 Gly Pro Ser Val Leu Gly Ala Leu Ala Pro Asp Ile Gly Arg Trp Leu 50 ctg ccc gcc gac ccc gac cag gtc cac ctg ctc gac gcc atc ggt cag 240 Leu Pro Ala Asp Pro Asp Gln Val His Leu Leu Asp Ala Ile Gly Gln 65 ttc ggc gtc gta ctg ctg gtc gcc gtg gcc ggt ctg cac ctg gac ctg 288 Phe Gly Val Val Leu Leu Val Ala Val Ala Gly Leu His Leu Asp Leu 85 90 egg etg gte egg egg gee gge aeg ate gge geg gtg gee gte gge 336 Arg Leu Val Arg Arg Ala Gly Thr Ile Gly Ala Val Ala Val Gly 100 ggc ctc gcg gtg ccc ctc ggc ctg ggc atc gcc gcc ggc ctg ctg gcc 384 Gly Leu Ala Val Pro Leu Gly Leu Gly Ile Ala Ala Gly Leu Leu Ala 115 120 125 ceg geg geg ett ete geg gee ggg cag gag egg act gte tte geg etg 432

Pro Ala Ala Leu Leu Ala Ala Gly Gln Glu Arg Thr Val Phe Ala Leu

ttc gtc ggc gtg gcg atg gcg gtc agc gcc gtg ccg gtg atc gcg aag

Phe Val Gly Val Ala Met Ala Val Ser Ala Val Pro Val Ile Ala Lys

155

480

135

	ctc Leu															528
ctg Leu	gct Ala	gcg Ala	gcg Ala 180	tcg Ser	ctg Leu	gag Glu	gac Asp	gct Ala 185	gcg Ala	gcc Ala	tgg Trp	ttc Phe	ctg Leu 190	ctg Leu	tcg Ser	576
	atc Ile															624
	gcc Ala 210															672
	cgg Arg															720
	ggc Gly															768
	gcg Ala															816
	gcg Ala															864
	gca Ala 290															912
	gcc Ala															960
	gtg Val															1008
	tac Tyr															1056
	gag Glu															1104
	atc Ile 370															1152
	tca Ser															1200
	ccg Pro															1248

gag gag acc ctg cgg gag agc cgc cac ctg gag tgg gcc gcc acc cct 1296 Glu Glu Thr Leu Arg Glu Ser Arg His Leu Glu Trp Ala Ala Thr Pro gcg gtg gac cag cgg ccg ggc 1317 Ala Val Asp Gln Arg Pro Gly 435 <210> 47 <21.1.> 439 <212> PRT <213> Micromonospora carbonacea <220> <223> evrK <400> 47 Val Pro Pro Leu Gly Ser His Gln Leu Leu Leu Phe Leu Leu Gln Val Gly Leu Leu Leu Leu Ala Val Val Leu Gly Arg Val Ala Gln Arg Phe Gly Leu Pro Ala Val Val Gly Glu Leu Leu Thr Gly Val Leu Leu Gly Pro Ser Val Leu Gly Ala Leu Ala Pro Asp Ile Gly Arg Trp Leu Leu Pro Ala Asp Pro Asp Gln Val His Leu Leu Asp Ala Ile Gly Gln Phe Gly Val Val Leu Leu Val Ala Val Ala Gly Leu His Leu Asp Leu Arg Leu Val Arg Arg Ala Gly Thr Ile Gly Ala Val Ala Val Gly Gly Leu Ala Val Pro Leu Gly Leu Gly Ile Ala Ala Gly Leu Leu Ala 115 125 Pro Ala Ala Leu Leu Ala Ala Gly Gln Glu Arg Thr Val Phe Ala Leu Phe Val Gly Val Ala Met Ala Val Ser Ala Val Pro Val Ile Ala Lys Thr Leu Thr Asp Met Arg Leu Leu His Arg Asp Val Gly Gln Ile Ile 170 Leu Ala Ala Ser Leu Glu Asp Ala Ala Ala Trp Phe Leu Leu Ser Leu Ile Ser Ser Val Ala Val Ser Thr Leu Thr Ala Gly Gln Val Val 195 Thr Ala Leu Leu Tyr Leu Val Ala Tyr Leu Ala Val Ala Val Leu Val 215 Gly Arg Pro Val Thr Arg Arg Ala Met Arg Trp Ala Asn Ala Gln Pro 225 235 Asp Gly Gly Ala Ala Ser Ala Val Ala Val Ile Val Leu Ala Phe

250

Ala Ala Gly Ala His Ala Leu Gly Leu Glu Ala Ile Phe Gly Ala Leu Val Ala Gly Val Leu Ile Gly Leu Pro Gly Asn Gly Glu Pro Ala Arg 280 Leu Ala Pro Leu Arg Thr Val Val Leu Ser Val Leu Ala Pro Ile Phe Leu Ala Ser Ala Gly Leu Arg Val Asp Leu Arg Ala Leu Ala Asp Pro 315 Glu Val Leu Ala Ala Gly Ala Val Ile Leu Ala Leu Ala Val Leu Gly Lys Tyr Thr Gly Ala Tyr Leu Gly Ala Arg Leu Ala Arg Gln Ser His Trp Glu Gly Val Ala Leu Gly Ala Gly Leu Asn Ala Arg Gly Ala Val Glu Ile Ile Ala Met Val Gly Leu Arg Leu Gly Val Leu Asn Thr 370 375 380 Ala Ser Tyr Thr Ile Val Val Leu Val Ala Val Val Thr Ser Val Met 390 Ala Pro Pro Met Leu Arg Val Ala Met Arg Arg Val Glu Gln Asn Ala 405 Glu Glu Thr Leu Arg Glu Ser Arg His Leu Glu Trp Ala Ala Thr Pro 420 425 Ala Val Asp Gln Arg Pro Gly 435 <210> 48 <211> 939 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(939) <220> <223> evrL atg cgc cgg acc cgg ctg gcg atg ctg gcc ggg gag cgg gtc gac gcc Met Arg Arg Thr Arg Leu Ala Met Leu Ala Gly Glu Arg Val Asp Ala tgc tcc tac tgc tac cac cgc gag gac cac ggc gcg ctg tcg tac cgg 96 Cys Ser Tyr Cys Tyr His Arg Glu Asp His Gly Ala Leu Ser Tyr Arg 20 cag gag atc aac cag cgg ttc cgg gac atc gcc gac ccc gac cgg ctg 144 Gln Glu Ile Asn Gln Arg Phe Arg Asp Ile Ala Asp Pro Asp Arg Leu gee gee ege ace geg eee gae gge ace gte gag gae tte eeg tte tte

Ala Ala Arg Thr Ala Pro Asp Gly Thr Val Glu Asp Phe Pro Phe Phe

50 55 60 ctc gac atc egg ttc ggc aac acc tgc aac etg egg tgc gtg atg tgc 240 Leu Asp Ile Arg Phe Gly Asn Thr Cys Asn Leu Arg Cys Val Met Cys gcg tac ccg gtc agc tcg ggc tgg ggc gcc aag aag cgg ccg gcc tgg 288 Ala Tyr Pro Val Ser Ser Gly Trp Gly Ala Lys Lys Arg Pro Ala Trp tog toe geg gte ate gae gee tae egg gae gae gae gag etg tgg eag 336 Ser Ser Ala Val Ile Asp Ala Tyr Arg Asp Asp Glu Leu Trp Gln ace etg ege gag aac gee eac ete ate egg egg etg tae tte gee ggt 384 Thr Leu Arg Glu Asn Ala His Leu Ile Arg Arg Leu Tyr Phe Ala Gly 115 120 ggg gag ccg ttc atg cag ccg ggc cac ttc gcc ctg ctc gac ctg ctq 432 Gly Glu Pro Phe Met Gln Pro Gly His Phe Ala Leu Leu Asp Leu Leu gtg gag acg ggt aac gcc ggc aac gtc gac gtc gtc tac aac tcc aac 480 Val Glu Thr Gly Asn Ala Gly Asn Val Asp Val Val Tyr Asn Ser Asn 155 ctc acc gtg ttg ccg gag tcg gtc ttc gac cgg ttc cgg cac ttc aag 528 Leu Thr Val Leu Pro Glu Ser Val Phe Asp Arg Phe Arg His Phe Lys 170 age ate gge ate gge gee tee tge gae gge tae gge gag gtg tte gag 576 Ser Ile Gly Ile Gly Ala Ser Cys Asp Gly Tyr Gly Glu Val Phe Glu 180 185 egg ate egg cag gge geg aag tgg gag ace tte ate geg aae gte ege 624 Arg Ile Arg Gln Gly Ala Lys Trp Glu Thr Phe Ile Ala Asn Val Arg cgg gcc cgc tcg gag gtc aac ctc tgg ctc cag gtg gca ccc cag cgg 672 Arg Ala Arg Ser Glu Val Asn Leu Trp Leu Gln Val Ala Pro Gln Arg 210 215 gac aac gtc tgg ggg ctg cgc gac ctg ctg gag ttc gcc cgg gcc gag 720 Asp Asn Val Trp Gly Leu Arg Asp Leu Leu Glu Phe Ala Arg Ala Glu 225 ggg ctc gac gtg gac ctg gcc aac gtg gtg cag tgg ccg gcc gag atg 768 Gly Leu Asp Val Asp Leu Ala Asn Val Val Gln Trp Pro Ala Glu Met 245 250 teg gtg etc age etg ecc gag gag gac aag gtt egg gec acc ggg gag 816 Ser Val Leu Ser Leu Pro Glu Glu Asp Lys Val Arg Ala Thr Gly Glu 260 ctg acc tcc ctc atc gat tgg tgc gcc ggg ctg ggc tgg gag aag ccc 864 Leu Thr Ser Leu Ile Asp Trp Cys Ala Gly Leu Gly Trp Glu Lys Pro 275 280 gcc gcc gac ctg cgg gcc ctg cgg acc ttc atg aac tcg gcc gac ccg 912 Ala Ala Asp Leu Arg Ala Leu Arg Thr Phe Met Asn Ser Ala Asp Pro 295 300 gtg gac ctg ccg ccc gag atc gcg gcc 939 Val Asp Leu Pro Pro Glu Ile Ala Ala 305 310

```
<210> 49
```

<211> 313

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrL

<400> 49

Met Arg Arg Thr Arg Leu Ala Met Leu Ala Gly Glu Arg Val Asp Ala 1 5 10 15

Cys Ser Tyr Cys Tyr His Arg Glu Asp His Gly Ala Leu Ser Tyr Arg 20 25 30

Gln Glu Ile Asn Gln Arg Phe Arg Asp Ile Ala Asp Pro Asp Arg Leu 35 40 45

Ala Ala Arg Thr Ala Pro Asp Gly Thr Val Glu Asp Phe Pro Phe 50 55 60

Leu Asp Ile Arg Phe Gly Asn Thr Cys Asn Leu Arg Cys Val Met Cys 65 70 75 80

Ala Tyr Pro Val Ser Ser Gly Trp Gly Ala Lys Lys Arg Pro Ala Trp 85 90 95

Ser Ser Ala Val Ile Asp Ala Tyr Arg Asp Asp Asp Glu Leu Trp Gln
100 105 110

Thr Leu Arg Glu Asn Ala His Leu Ile Arg Arg Leu Tyr Phe Ala Gly
115 120 125

Gly Glu Pro Phe Met Gln Pro Gly His Phe Ala Leu Leu Asp Leu Leu 130 135 140

Val Glu Thr Gly Asn Ala Gly Asn Val Asp Val Val Tyr Asn Ser Asn 145 150 155 160

Leu Thr Val Leu Pro Glu Ser Val Phe Asp Arg Phe Arg His Phe Lys
165 170 175

Ser Ile Gly Ile Gly Ala Ser Cys Asp Gly Tyr Gly Glu Val Phe Glu 180 185 190

Arg Ile Arg Gln Gly Ala Lys Trp Glu Thr Phe Ile Ala Asn Val Arg 195 200 205

Arg Ala Arg Ser Glu Val Asn Leu Trp Leu Gln Val Ala Pro Gln Arg 210 215 220

Asp Asn Val Trp Gly Leu Arg Asp Leu Leu Glu Phe Ala Arg Ala Glu 225 230 235 240

Gly Leu Asp Val Asp Leu Ala Asn Val Val Gln Trp Pro Ala Glu Met 245 250 255

Ser Val Leu Ser Leu Pro Glu Glu Asp Lys Val Arg Ala Thr Gly Glu 260 265 270

Leu Thr Ser Leu Ile Asp Trp Cys Ala Gly Leu Gly Trp Glu Lys Pro 275 280 285

Ala Ala Asp Leu Arg Ala Leu Arg Thr Phe Met Asn Ser Ala Asp Pro Val Asp Leu Pro Pro Glu Ile Ala Ala 310 <210> 50 <211> 1236 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1) .. (1236) <220> <223> evrM <400> 50 gtg gtc gag cgg acc acc tgc cgg gtg tgt ggc ggg acc ctg cgt acg Val Val Glu Arg Thr Thr Cys Arg Val Cys Gly Gly Thr Leu Arg Thr 10 gtc ctc gac ctc ggt gcc cag tac cta cag ggc agc ttc gtg aag ccc 96 Val Leu Asp Leu Gly Ala Gln Tyr Leu Gln Gly Ser Phe Val Lys Pro ggc gtg tcg gac ccg ccc agg gtg cgc ttc ccc ctg gag ctg acc cgg 144 Gly Val Ser Asp Pro Pro Arg Val Arg Phe Pro Leu Glu Leu Thr Arg 35 40 tge geg gaa ege gae gge ggt gae eeg tge gge etg gtg eag ttg egg 192 Cys Ala Glu Arg Asp Gly Gly Asp Pro Cys Gly Leu Val Gln Leu Arg cac acc ctg ccg ggt ggg ctg ctc tac gac acc tac tgg tac cgc tcg 240 His Thr Leu Pro Gly Gly Leu Leu Tyr Asp Thr Tyr Trp Tyr Arg Ser egg ate aac gae aeg atg ege egg cat ete gee gae gte gtg gae geg 288 Arg Ile Asn Asp Thr Met Arg Arg His Leu Ala Asp Val Val Asp Ala 90 gcg gtc gag gtg ttg ggg gag cgg ccc ggc aag gtg ctc gac atc ggc 336 Ala Val Glu Val Leu Gly Glu Arg Pro Gly Lys Val Leu Asp Ile Gly 100 105 tgc aac gac ggc acc ctg ctg ggc aac ctg acc gac gcg cag cgg tgg 384 Cys Asn Asp Gly Thr Leu Leu Gly Asn Leu Thr Asp Ala Gln Arg Trp ggc atc gac ccc tcc agc gcc gcc gac gcg ccc gac gac ttc aat 432 Gly Ile Asp Pro Ser Ser Ala Ala Asp Asp Ala Pro Asp Asp Phe Asn 130 135 ctg atc cgc gac ttc ttc ccc agc ccc gag ctg gtc ccg cac gcg ggc 480 Leu Ile Arg Asp Phe Phe Pro Ser Pro Glu Leu Val Pro His Ala Gly 145

age tte gae etg gte ace teg ate geg atg tte tae gae gte gag gae

Ser Phe Asp Leu Val Thr Ser Ile Ala Met Phe Tyr Asp Val Glu Asp

							gtc Val									576
							tac Tyr 200									624
							gag Glu									672
							gcg Ala									720
							ggc Gly									768
							gcc Ala									816
							ctg Leu 280									864
							cac His									912
							cgc Arg									960
							cag Gln									1008
							aat Asn									1056
ctc Leu	ggc Gly	acg Thr 355	gac Asp	atc Ile	gaa Glu	atc Ile	atc Ile 360	agc Ser	gag Glu	cag Gln	gag Glu	tcg Ser 365	cgg Arg	gcg Ala	gcc Ala	1104
							ctg Leu									1152
							ctg Leu									1200
ccg Pro	ctg Leu	ccc Pro	cgg Arg	gtc Val 405	gag Glu	acg Thr	gtc Val	ggc Gly	cga Arg 410	ccg Pro	gga Gly					1236

<210> 51 <211> 412 <212> PRT <213> Micromonospora carbonacea

<220> <223> evrM

<400> 51

Val Val Glu Arg Thr Thr Cys Arg Val Cys Gly Gly Thr Leu Arg Thr
1 5 10 15

Val Leu Asp Leu Gly Ala Gln Tyr Leu Gln Gly Ser Phe Val Lys Pro 20 25 30

Gly Val Ser Asp Pro Pro Arg Val Arg Phe Pro Leu Glu Leu Thr Arg
35 40 45

Cys Ala Glu Arg Asp Gly Gly Asp Pro Cys Gly Leu Val Gln Leu Arg
50 55 60

His Thr Leu Pro Gly Gly Leu Leu Tyr Asp Thr Tyr Trp Tyr Arg Ser
65 70 75 80

Arg Ile Asn Asp Thr Met Arg Arg His Leu Ala Asp Val Val Asp Ala 85 90 95

Ala Val Glu Val Leu Gly Glu Arg Pro Gly Lys Val Leu Asp Ile Gly
100 105 110

Cys Asn Asp Gly Thr Leu Leu Gly Asn Leu Thr Asp Ala Gln Arg Trp
115 120 125

Gly Ile Asp Pro Ser Ser Ala Ala Asp Asp Ala Pro Asp Asp Phe Asn 130 135 140

Leu Ile Arg Asp Phe Phe Pro Ser Pro Glu Leu Val Pro His Ala Gly
145 150 155 160

Ser Phe Asp Leu Val Thr Ser Ile Ala Met Phe Tyr Asp Val Glu Asp 165 170 175

Pro Val Glu Phe Ala Arg Gln Val Glu Ala Leu Leu Ala Pro Gly Gly 180 185 190

Val Trp Val Val Glu Val Ala Tyr Leu Pro Ala Met Leu Glu Ile Ala 195 200 205

Gly Tyr Asp Ser Ile Cys His Glu His Leu Ser Tyr Tyr Ser Leu Ala 210 215 220

Thr Leu Ser Arg Ile Leu Gly Ala Ala Gly Leu Glu Ile Val Arg Ala 225 230 235 240

Ser Leu Asn Gly Val Asn Gly Gly Ser Ile Cys Cys Val Val Thr Arg 245 250 255

Ala Gly Glu Val Gly Gly Arg Ala Asp Gly Ser Val Lys Ala Leu Ala 260 265 270

Asp Arg Glu Leu Ala Leu Gly Leu Asp Gly Asp Ala Pro Tyr Gln Arg 275 280 285

Phe Ala Glu Gln Val Arg Gln His Arg Asp Glu Val Ser Ala Leu Leu 290 295 300

Arg Glu Leu Arg Gly Gln Gly Arg Thr Val His Val Tyr Gly Ala Ser 305 310 315 320

Thr Lys Gly Asn Thr Leu Leu Gln Phe Cys Gly Ile Asp Arg Glu Leu 325 330 335	
Ile Arg Tyr Ala Ala Glu Arg Asn Pro Asp Lys Val Gly Ala Arg Thr 340 345 350	
Leu Gly Thr Asp Ile Glu Ile Ile Ser Glu Gln Glu Ser Arg Ala Ala 355 360 . 365	
Arg Pro Asp Tyr Tyr Leu Val Leu Pro Trp His Phe Arg Asp Glu Ile 370 375 380	
Val Ala Arg Glu Ala Glu Met Leu Ala Ser Gly Thr Arg Leu Ile Phe 385 390 395 400	
Pro Leu Pro Arg Val Glu Thr Val Gly Arg Pro Gly 405 410	
<210> 52 <211> 759 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS	
<222> (1)(759)	
<220> <223> evrN <400> 52	
atg gcc gaa cgg ttc cgg gag cgg atc gag ccc cgg ccc ggg gac tgg 48 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp 1 5 10 15	'
gca tac gcc cac ttc ctg gac ctg cgc gac gcg ctg gcg gag gcg gtc 96 Ala Tyr Ala His Phe Leu Asp Leu Arg Asp Ala Leu Ala Glu Ala Val 20 25 30	
cgg gac gcc acg gga gtc tgg ctc gac tac ggc gcg ggc acc tcg cca 14 Arg Asp Ala Thr Gly Val Trp Leu Asp Tyr Gly Ala Gly Thr Ser Pro 35 40 45	4
tac cgg ggc ctg ttc cgc tcc gcc gag ttg cag acc gcc gac atc ccg 19 Tyr Arg Gly Leu Phe Arg Ser Ala Glu Leu Gln Thr Ala Asp Ile Pro 50 55 60	2
ggc ggt gag tcc ctg ccg gcc gac cac gcc ctc gac cgg gac ggg cgc 24 Gly Gly Glu Ser Leu Pro Ala Asp His Ala Leu Asp Arg Asp Gly Arg 65 70 75 80	0
tgc ccg gtg ccg gac ggg acg ttc gac ggg gtg ctc tcc acc cag gtg 28 Cys Pro Val Pro Asp Gly Thr Phe Asp Gly Val Leu Ser Thr Gln Val 85 90 95	8
ctc gaa cac gtc tcg gac gcg gac gcg tac ctg cgg gag gcg tac cgg 33 Leu Glu His Val Ser Asp Ala Asp Ala Tyr Leu Arg Glu Ala Tyr Arg	6
100 105 110	

gag gag cac ggc ggc cag gac ctg tgg cgg tgg acc gcc gac ggg ctg Glu Glu His Gly Gly Gln Asp Leu Trp Arg Trp Thr Ala Asp Gly Leu 130 135 140	432											
gcc cgc cag gcc gag tgg gcc ggc ttc acc gtc gac cgc acc gtc aag Ala Arg Gln Ala Glu Trp Ala Gly Phe Thr Val Asp Arg Thr Val Lys 145 150 155 160	480											
ctg acc tgc ggg ccg cgc ggc ctg ttg ctg ctg c	528											
cgc gag cac ggc tgg ccg tcc ggc ggc ccg gtg ggt ctg gcc ctg cgc Arg Glu His Gly Trp Pro Ser Gly Gly Pro Val Gly Leu Ala Leu Arg 180 185 190	576											
gcc ctg tgg ctg gtg gac cgg ctg cgg ccc cgc gcg ctc gac gag tac Ala Leu Trp Leu Val Asp Arg Leu Arg Pro Arg Ala Leu Asp Glu Tyr 195 200 205	624											
ctc gac cgg gcg ttc cgg cat ctc ggc cgc agc gag ggc ccc gac cag Leu Asp Arg Ala Phe Arg His Leu Gly Arg Ser Glu Gly Pro Asp Gln 210 215 220	672											
ccc ttc tat ctg gac atc ctg ctg gtc gcc agc aaa ccg cac gac gggPro Phe Tyr Leu Asp Ile Leu Leu Val Ala Ser Lys Pro His Asp Gly225230	720											
gcg cct ggt ccc gca cac cgg cac gag acg agg agg acc Ala Pro Gly Pro Ala His Arg His Glu Thr Arg Arg Thr 245 250	759											
<210> 53 <211> 253 <212> PRT <213> Micromonospora carbonacea												
<211> 253 <212> PRT												
<211> 253 <212> PRT												
<211> 253 <212> PRT <213> Micromonospora carbonacea <220>												
<211> 253 <212> PRT <213> Micromonospora carbonacea <220> <223> evrN <400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp												
<pre><211> 253 <212> PRT <213> Micromonospora carbonacea </pre> <pre><220> <223> evrN </pre> <pre><400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp</pre>												
<pre><211> 253 <212> PRT <213> Micromonospora carbonacea <220> <223> evrN <400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp</pre>												
<pre><211> 253 <212> PRT <213> Micromonospora carbonacea <220> <223> evrN <400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp</pre>												
<pre><211> 253 <212> PRT <213> Micromonospora carbonacea <220> <223> evrN <400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp</pre>												
<pre><211> 253 <212> PRT <213> Micromonospora carbonacea <220> <223> evrN <400> 53 Met Ala Glu Arg Phe Arg Glu Arg Ile Glu Pro Arg Pro Gly Asp Trp</pre>												

Glu Glu His Gly Gly Gln Asp Leu Trp Arg Trp Thr Ala Asp Gly Leu 130 Ala Arg Gln Ala Glu Trp Ala Gly Phe Thr Val Asp Arg Thr Val Lys 155 Leu Thr Cys Gly Pro Arg Gly Leu Leu Leu Leu Arg Trp Tyr Gly Arg Glu His Gly Trp Pro Ser Gly Gly Pro Val Gly Leu Ala Leu Arg Ala Leu Trp Leu Val Asp Arg Leu Arg Pro Arg Ala Leu Asp Glu Tyr Leu Asp Arg Ala Phe Arg His Leu Gly Arg Ser Glu Gly Pro Asp Gln Pro Phe Tyr Leu Asp Ile Leu Leu Val Ala Ser Lys Pro His Asp Gly Ala Pro Gly Pro Ala His Arg His Glu Thr Arg Arg Thr <210> 54 <211> 942 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(942) <220> <223> evr0 <400> 54 atg age geg act gtg gae gte ege ace gag eag gee gte eee gag tge 48 Met Ser Ala Thr Val Asp Val Arg Thr Glu Gln Ala Val Pro Glu Cys cac atc cac gag acc ggg ctg ctt ccg gag cac ctg acc gcc ttc cgc 96 His Ile His Glu Thr Gly Leu Leu Pro Glu His Leu Thr Ala Phe Arg cgg cag ggc gcg ctg atc ctg cgc ggg ctg ctg gac ccc gac gag ctg 144 Arg Gln Gly Ala Leu Ile Leu Arg Gly Leu Leu Asp Pro Asp Glu Leu egg tee gtg eag geg gee gae gag etg ate gae gaa gee tgg ege 192 Arg Ser Val Gln Ala Ala Ala Asp Glu Leu Ile Asp Glu Ala Trp Arg acc egg acg atg acc gac acc atc tgg acg etg gaa eeg cac gag eeg 240 Thr Arg Thr Met Thr Asp Thr Ile Trp Thr Leu Glu Pro His Glu Pro gac gcg gcg ccg gtg cgg atc gag tac gtg gtc gac aag tcc ccg gtg 288 Asp Ala Ala Pro Val Arg Ile Glu Tyr Val Val Asp Lys Ser Pro Val

gtc gcc cgg ctc gcc ggc cac ccc ctg ctg ctg cgg gcg atg gag gac

Val	Ala	Arg	Leu 100	Ala	Gly	His	Pro	Leu 105	Leu	Leu	Arg	Ala	Met 110	Glu	Asp	
					ctc Leu											384
					ccc Pro											432
					gtc Val 150											480
					gac Asp											528
					tac Tyr											576
					acc Thr											624
					gac Asp											672
					acc Thr 230											720
					gtc Val											768
					cag Gln											816
					cac His											864
					cgc Arg											912
cgg Arg 305	tac Tyr	ccg Pro	cac His	gag Glu	gag Glu 310	tac Tyr	tgg Trp	cgt Arg	tgg Trp							942

<210> 55 <211> 314

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrO

<400> 55

Met Ser Ala Thr Val Asp Val Arg Thr Glu Gln Ala Val Pro Glu Cys
1 5 10 15

His Ile His Glu Thr Gly Leu Leu Pro Glu His Leu Thr Ala Phe Arg
20 25 30

Arg Gln Gly Ala Leu Ile Leu Arg Gly Leu Leu Asp Pro Asp Glu Leu 35 40 45

Arg Ser Val Gln Ala Ala Ala Asp Glu Leu Ile Asp Glu Ala Trp Arg
50 55 60

Thr Arg Thr Met Thr Asp Thr Ile Trp Thr Leu Glu Pro His Glu Pro 65 70 75 80

Asp Ala Ala Pro Val Arg Ile Glu Tyr Val Val Asp Lys Ser Pro Val 85 90 95

Val Ala Arg Leu Ala Gly His Pro Leu Leu Leu Arg Ala Met Glu Asp 100 105 110

Leu Val Gly Pro Asn Leu Ile Pro Thr Trp Asp Ser Met Val Phe Lys 115 120 125

Thr Glu Ala Gly Ala Pro Arg Leu Pro Trp His Arg Asp Gly Gly Leu 130 135 140

Tyr Pro Glu Asn Ala Val Gly Ile Thr Gly Ala Gly Arg Val Ile Asp 145 150 155 160

Val Gly Ile Tyr Leu Asp Pro Ala Pro Glu Asp Asn Cys Val Trp Cys 165 170 175

Ile Pro Gln Ser Asn Tyr Trp Asp Thr Asp Arg Ala Asn Glu Thr Thr 180 185 190

Thr Arg Met Asn Ala Thr Glu Trp Asp Thr Thr Gly Ala Val Pro Ala 195 200 205

Val Met Asn Pro Gly Asp Val Met Leu His Asn Ile Leu Met Leu His 210 215 220

Ala Ala Pro Ala Val Thr Gly Lys Arg Arg Arg Val Ile Tyr Phe Glu 225 230 235 240

Tyr Arg Pro Ala Glu Val Glu Leu Asp Leu Gly Pro His Val Pro Glu 245 250 255

Tyr Ile Gly Leu Lys Gln Gln Val Leu Leu Ser Cys Leu Ala Gln Arg 260 265 270

Arg Ala Ala Pro Glu His Ala Gly Glu Gln Pro Phe Glu Tyr Arg Pro 275 280 285

Ala Ala Ser Leu Arg Arg Trp Glu Gly Leu Pro Glu Pro Thr Thr Met 290 295 300

Arg Tyr Pro His Glu Glu Tyr Trp Arg Trp 305 310

<210> 56

<211> 726

<212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(726)
<220>
<223> evrP
<400> 56
atg aac gac tgg tac gac cag ctc acc gtg gcg ctg atc gag cag atc
                                                                     48
Met Asn Asp Trp Tyr Asp Gln Leu Thr Val Ala Leu Ile Glu Gln Ile
tgc gaa ccg gac gcc aac acc gtg gac atc ggg gcc ggc gcc ggc gac
                                                                     96
Cys Glu Pro Asp Ala Asn Thr Val Asp Ile Gly Ala Gly Ala Gly Asp
atc ctg cgt cac ctg ctg cgg gtc gcc ccc cgt ggc cgg cac gtg gcc
                                                                     144
Ile Leu Arg His Leu Leu Arg Val Ala Pro Arg Gly Arg His Val Ala
gtc gag gcg ctg ccg tcg tac gcc gag ggg ctg cgc cgg gac ttc ccc
                                                                     192
Val Glu Ala Leu Pro Ser Tyr Ala Glu Gly Leu Arg Arg Asp Phe Pro
gge gtg aeg gtg gtg gee gee gee gee gag ege aee gge egg gae
                                                                     240
Gly Val Thr Val Val Ala Ala Ala Ala Glu Arg Thr Gly Arg Asp
age tte gte cae gtg gte tee aac eee gge tae age ggg etg ege egg
Ser Phe Val His Val Val Ser Asn Pro Gly Tyr Ser Gly Leu Arg Arg
                                                                     288
                                      90
cgt ccc tac gac cgc ccg gac gag acc ctg cgg gag ctg acg gtc gac
                                                                     336
Arg Pro Tyr Asp Arg Pro Asp Glu Thr Leu Arg Glu Leu Thr Val Asp
            100
                                 105
acc gtc cgc ctg gac gac gtg ctc ccc ggt gac cgc cgg atc gac ctg
                                                                     384
Thr Val Arg Leu Asp Asp Val Leu Pro Gly Asp Arg Ile Asp Leu
        115
                             120
                                                  125
gtc aag gtg gac acc gag ggc ggc gag gtg ctc gcc ctg cgc ggt gcc
                                                                     432
Val Lys Val Asp Thr Glu Gly Gly Glu Val Leu Ala Leu Arg Gly Ala
    130
gtg gag ctg ctc cgc cgc tgg cgg ccg gtg atc gtc ttc gag cac ggc
                                                                     480
Val Glu Leu Leu Arg Arg Trp Arg Pro Val Ile Val Phe Glu His Gly
145
                     150
                                          155
                                                               160
ggc gac cac gcc atg cgg gag tac ggc acc acc agc gcc gac ctg tgg
                                                                     528
Gly Asp His Ala Met Arg Glu Tyr Gly Thr Thr Ser Ala Asp Leu Trp
                                     170
gcg ctg ctc gtg acc gag ctg ggt tac gag ctg cgt acc ctg ccc ggg
                                                                     576
Ala Leu Leu Val Thr Glu Leu Gly Tyr Glu Leu Arg Thr Leu Pro Gly
            180
                                 185
ege ege gee ggg eag eeg geg etg gae egg geg ggg tte gee gae geg
                                                                     624
Arg Arg Ala Gly Gln Pro Ala Leu Asp Arg Ala Gly Phe Ala Asp Ala
                             200
ctg cgg gag cac tgg tac ttc gtc gcc gac cga ccg agc ccg ggc ccg
                                                                     672
Leu Arg Glu His Trp Tyr Phe Val Ala Asp Arg Pro Ser Pro Gly Pro
```

220

726

gcc ggc ggc tcc ggg cag cac gaa ccg tcc gcc tgg cag aag gga acc Ala Gly Gly Ser Gly Gln His Glu Pro Ser Ala Trp Gln Lys Gly Thr 230 235 gaa cca Glu Pro <210> 57 <211> 242 <212> PRT <213> Micromonospora carbonacea <220> <223> evrP <400> 57 Met Asn Asp Trp Tyr Asp Gln Leu Thr Val Ala Leu Ile Glu Gln Ile Cys Glu Pro Asp Ala Asn Thr Val Asp Ile Gly Ala Gly Ala Gly Asp Ile Leu Arg His Leu Leu Arg Val Ala Pro Arg Gly Arg His Val Ala Val Glu Ala Leu Pro Ser Tyr Ala Glu Gly Leu Arg Arg Asp Phe Pro Gly Val Thr Val Val Ala Ala Ala Ala Glu Arg Thr Gly Arg Asp 70 Ser Phe Val His Val Val Ser Asn Pro Gly Tyr Ser Gly Leu Arg Arg Arg Pro Tyr Asp Arg Pro Asp Glu Thr Leu Arg Glu Leu Thr Val Asp 105 Thr Val Arg Leu Asp Asp Val Leu Pro Gly Asp Arg Arg Ile Asp Leu 115 125 Val Lys Val Asp Thr Glu Gly Gly Glu Val Leu Ala Leu Arg Gly Ala Val Glu Leu Leu Arg Arg Trp Arg Pro Val Ile Val Phe Glu His Gly Gly Asp His Ala Met Arg Glu Tyr Gly Thr Thr Ser Ala Asp Leu Trp 165 170 Ala Leu Leu Val Thr Glu Leu Gly Tyr Glu Leu Arg Thr Leu Pro Gly Arg Arg Ala Gly Gln Pro Ala Leu Asp Arg Ala Gly Phe Ala Asp Ala Leu Arg Glu His Trp Tyr Phe Val Ala Asp Arg Pro Ser Pro Gly Pro 215 Ala Gly Gly Ser Gly Gln His Glu Pro Ser Ala Trp Gln Lys Gly Thr 230 235

Glu Pro

```
<210> 58
<211> 1026
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1026)
<220>
<223> evr0
<400> 58
gtg cgg cag cgc tgc atc ggt gag cgg ggg ccg ctg gtc tcg gcg ctc
                                                                    48
Val Arg Gln Arg Cys Ile Gly Glu Arg Gly Pro Leu Val Ser Ala Leu
ggc ctg ggc acc tgg gcg ctc ggc ggc cag tgg ggc cgg cgg atc gaa
                                                                    96
Gly Leu Gly Thr Trp Ala Leu Gly Gly Gln Trp Gly Arg Arg Ile Glu
cca ggc gtg cag gcc gtc cgc cgg gcc ttc gac ctg ggc gtc acc ctt
                                                                    144
Pro Gly Val Gln Ala Val Arg Arg Ala Phe Asp Leu Gly Val Thr Leu
tte gae ace tee egg geg tae gge gge gge gee gee gag geg gee ett
                                                                    192
Phe Asp Thr Ser Arg Ala Tyr Gly Gly Gly Ala Ala Glu Ala Ala Leu
ged ege ggg etg ged gad etg ttg ede geg dad egg gad gag atd gtg
                                                                    240
Ala Arg Gly Leu Ala Asp Leu Leu Pro Ala His Arg Asp Glu Ile Val
                     70
ate gee acg gee gge ggg etg gag ace egg eee gge gtg ega egg cae
                                                                    288
Ile Ala Thr Ala Gly Gly Leu Glu Thr Arg Pro Gly Val Arg Arg His
aag ete gae eeg eee gga egg aeg gtg egt aae age gae eee geg tte
                                                                    336
Lys Leu Asp Pro Pro Gly Arg Thr Val Arg Asn Ser Asp Pro Ala Phe
                                 105
ctc cgg gac gag ctg ctg gcc agc ctg cgt cag ctc ggc acg gac cac
                                                                    384
Leu Arg Asp Glu Leu Leu Ala Ser Leu Arg Gln Leu Gly Thr Asp His
                            120
gtc gac gtg tac tcc gtg cac tgg ccc gac ccg acc gtc ccg ctc gcg
                                                                    432
Val Asp Val Tyr Ser Val His Trp Pro Asp Pro Thr Val Pro Leu Ala
                        135
                                             140
gag acc gcc gag gtg ctg gcg ggg ttc gtg cgc gag ggc ctg gcc cgc
                                                                    480
Glu Thr Ala Glu Val Leu Ala Gly Phe Val Arg Glu Gly Leu Ala Arg
                                         155
cat gtc ggc ttc gcc aac gtg acg gcg ggc gac ctg gcc gag ctg gtg
                                                                    528
His Val Gly Phe Ala Asn Val Thr Ala Gly Asp Leu Ala Glu Leu Val
                165
                                     170
                                                         175
ccg acc ggg ctg ctg gac gtc gtc cag gtg ccg ttc aac ctg ctc gac
                                                                   576
Pro Thr Gly Leu Leu Asp Val Val Gln Val Pro Phe Asn Leu Leu Asp
            180
                                 185
                                                     190
egt ggt gee gag aag gag gtg etg eee ege tge eag gag gee gge gte
                                                                   624
Arg Gly Ala Glu Lys Glu Val Leu Pro Arg Cys Gln Glu Ala Gly Val
```

195 200 205 ggg gtg ctg ggc ggc tcc gcg ctc gcc cac ggg ctg ctc acc ggc gcg 672 Gly Val Leu Gly Gly Ser Ala Leu Ala His Gly Leu Leu Thr Gly Ala 210 215 ctg cac cgc gac cag gca ttc gcc ccc gag gac tgg cgg gcc tac tcg 720 Leu His Arg Asp Gln Ala Phe Ala Pro Glu Asp Trp Arg Ala Tyr Ser 225 235 cac gcc ttc cgg ggt gag gac tac gcc caa ctg ctc gac gtg gtc gac 768 His Ala Phe Arg Gly Glu Asp Tyr Ala Gln Leu Leu Asp Val Val Asp 245 250 gge etc gec gec tte gec gec gag egt ggg eac ace gte geg eag gtg 816 Gly Leu Ala Ala Phe Ala Ala Glu Arg Gly His Thr Val Ala Gln Val 260 265 gca ctg gcc tgg gcg ctg cac cac ccg gcc ggg gtg gtg ccg gtg ttc Ala Leu Ala Trp Ala Leu His His Pro Ala Gly Val Val Pro Val Phe 280 ggc gct cag tcg ccc gga gtc gtc gag gag aac gtc cgc gcc gcc ggc 912 Gly Ala Gln Ser Pro Gly Val Val Glu Glu Asn Val Arg Ala Ala Gly 295 300 ctg gag ctg tcc gag atc gag ctg cgg gag ctg gaa ctc ctg gtc cgt 960 Leu Glu Leu Ser Glu Ile Glu Leu Arg Glu Leu Glu Leu Val Arg 310 315 ace gee eeg geg gte gge tee ggg gee gga eeg geg tge egg ace gag 1008 Thr Ala Pro Ala Val Gly Ser Gly Ala Gly Pro Ala Cys Arg Thr Glu 325 330 gag cgt gac gat gtc cac 1026 Glu Arg Asp Asp Val His 340 <210> 59 <211> 342 <212> PRT <213> Micromonospora carbonacea <220> <223> evrQ <400> 59 Val Arg Gln Arg Cys Ile Gly Glu Arg Gly Pro Leu Val Ser Ala Leu Gly Leu Gly Thr Trp Ala Leu Gly Gly Gln Trp Gly Arg Arg Ile Glu Pro Gly Val Gln Ala Val Arg Arg Ala Phe Asp Leu Gly Val Thr Leu Phe Asp Thr Ser Arg Ala Tyr Gly Gly Ala Ala Glu Ala Ala Leu Ala Arg Gly Leu Ala Asp Leu Leu Pro Ala His Arg Asp Glu Ile Val Ile Ala Thr Ala Gly Gly Leu Glu Thr Arg Pro Gly Val Arg Arg His

```
Lys Leu Asp Pro Pro Gly Arg Thr Val Arg Asn Ser Asp Pro Ala Phe
Leu Arg Asp Glu Leu Leu Ala Ser Leu Arg Gln Leu Gly Thr Asp His
                            120
Val Asp Val Tyr Ser Val His Trp Pro Asp Pro Thr Val Pro Leu Ala
Glu Thr Ala Glu Val Leu Ala Gly Phe Val Arg Glu Gly Leu Ala Arg
His Val Gly Phe Ala Asn Val Thr Ala Gly Asp Leu Ala Glu Leu Val
                165
Pro Thr Gly Leu Leu Asp Val Val Gln Val Pro Phe Asn Leu Leu Asp
                                185
Arg Gly Ala Glu Lys Glu Val Leu Pro Arg Cys Gln Glu Ala Gly Val
Gly Val Leu Gly Gly Ser Ala Leu Ala His Gly Leu Leu Thr Gly Ala
                        215
Leu His Arg Asp Gln Ala Phe Ala Pro Glu Asp Trp Arg Ala Tyr Ser
His Ala Phe Arg Gly Glu Asp Tyr Ala Gln Leu Leu Asp Val Val Asp
Gly Leu Ala Ala Phe Ala Ala Glu Arg Gly His Thr Val Ala Gln Val
                                265
Ala Leu Ala Trp Ala Leu His His Pro Ala Gly Val Val Pro Val Phe
Gly Ala Gln Ser Pro Gly Val Val Glu Asn Val Arg Ala Ala Gly
Leu Glu Leu Ser Glu Ile Glu Leu Arg Glu Leu Glu Leu Val Arg
                    310
                                        315
Thr Ala Pro Ala Val Gly Ser Gly Ala Gly Pro Ala Cys Arg Thr Glu
                325
Glu Arg Asp Asp Val His
           340
<210> 60
<211> 492
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(492)
<220>
<223> evrR
```

atg geg gee ggg ete gee gae egg gtg ege gtg ete tge gee gae

Met Al 1	a Ala	a Gly	Leu 5	Ala	Asp	Arg	Val	Arg 10	Ala	Val	Leu	Cys	Ala 15	Asp	
gtc ag Val Se															96
gag aa Glu As		l Ser													144
ccg ac Pro Th 5															192
ctc aa Leu As 65															240
ctg cg Leu Ar															288
aac ac Asn Th															336
aac co Asn Pr		Glu													384
atg ac Met Th 13	r Gly														432
atg at Met Il 145															480
gag co Glu Pr															492
<210><211><211><212><213>	164 PRT	omono	spora	a cai	rbona	acea									
<220> <223>	evrR														
<400> Met Al 1		a Gly	Leu 5	Ala	Asp	Arg	Val	Arg 10	Ala	Val	Leu	Cys	Ala 15	Asp	
Val Se	er Arg	g Ser 20	Phe	Leu	Asp	Lys	Ala 25	Arg	Ala	Thr	Cys	Glu 30	Gly	Arg	
Glu As	n Val		Tyr	His	His	Ile 40	Glu	Asn	Asp	Phe	Leu 45	Glu	Lys	Leu	
Pro Th	r Ala	a Ala	Phe	Asp	Ala 55	Gly	Phe	Ser	Leu	Asn 60	Val	Phe	Ile	His	
Leu As	n Val	l Phe	Glu	Val	Phe	Leu	Tyr	Phe	Arg	Gln	Ile	Arg	Arg	Ile	

75

80

70

65

Leu Arg Pro Gly Gly Leu Phe Cys Phe Asn Phe Leu Asp Leu Gly Asp Asn Thr Arg Gly Phe Phe His Thr Tyr Ala Glu Arg Tyr Arg Asp Ala 100 105 110 Asn Pro Val Glu Phe Lys Gly Phe Leu Asn Trp His Gly Val Glu Leu Met Thr Gly Ile Ala Ala Glu Ala Gly Leu Thr Pro Val Thr Asp Lys Met Ile Asn His Asp Gly Val Val Phe Leu Thr Leu Arg Ser Asp Gly 155 Glu Pro Ala Ala <210> 62 <211> 1269 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1269) <220> <223> evrS <400> 62 atg aag gtt ctg ttc acc gtg tcc aac tgg gcc ggg cac tac atg tgc Met Lys Val Leu Phe Thr Val Ser Asn Trp Ala Gly His Tyr Met Cys atg gtg ccg ctg gcc tgg gcg ctg cgg gcc ggc cac gac gtc aag Met Val Pro Leu Ala Trp Ala Leu Arg Ala Ala Gly His Asp Val Lys gtc gcc tgt tcg ccg tcc cag gtc cgg ggc gtg gcc gcg gcg ggc atg Val Ala Cys Ser Pro Ser Gln Val Arg Gly Val Ala Ala Ala Gly Met 40 atg eec gte teg gtg ete gae gga eec gae atg atg gag age gee egg 192 Met Pro Val Ser Val Leu Asp Gly Pro Asp Met Met Glu Ser Ala Arg 60 ctg ggc ttc tac gtc cag gcc ctc tac acc ccg cag cac atg gtg gag 240 Leu Gly Phe Tyr Val Gln Ala Leu Tyr Thr Pro Gln His Met Val Glu caa ccg ctg ccg ttg aac ccc ttc acg ggc cgg ccg atg gac tcg ctc 288 Gln Pro Leu Pro Leu Asn Pro Phe Thr Gly Arg Pro Met Asp Ser Leu 85 90 gcc gac ttc gac acc gac ctg ctc gcc gac tac tgg aag cgc acg gtc 336 Ala Asp Phe Asp Thr Asp Leu Leu Ala Asp Tyr Trp Lys Arg Thr Val 100 110 acc gcg gtc cag cgc agc tac gac aac gcg gtc gac tac gcc gcc cac 384 Thr Ala Val Gln Arg Ser Tyr Asp Asn Ala Val Asp Tyr Ala Ala His

115 120 125 tac cgg ccc gac ctg gtg gtc cac gac atc atg gcc gtg gag ggc gcg 432 Tyr Arg Pro Asp Leu Val Val His Asp Ile Met Ala Val Glu Gly Ala 130 135 ctg gtc gcc gag ctg cac cac atc ccc agc gtc tac ttc tcg ccc ggg 480 Leu Val Ala Glu Leu His His Ile Pro Ser Val Tyr Phe Ser Pro Gly ttc atc ggc acc atc gag acc gag ccc ggg ctc gac ctg gtc tcc ggc 528 Phe Ile Gly Thr Ile Glu Thr Glu Pro Gly Leu Asp Leu Val Ser Gly 165 gac eeg gtg ace gag tte ege aag tae gge gte gag tgg age egg cae 576 Asp Pro Val Thr Glu Phe Arg Lys Tyr Gly Val Glu Trp Ser Arg His cag atc cgg tac gcc atc gac ccg tcg ccc gac gtg gcg atc ccg ccg 624 Gln Ile Arg Tyr Ala Ile Asp Pro Ser Pro Asp Val Ala Ile Pro Pro atg ggc gac gcg ctg cgg atc ccg atc cgc tac cag ccc tac aac ggc 672 Met Gly Asp Ala Leu Arg Ile Pro Ile Arg Tyr Gln Pro Tyr Asn Gly 215 tcc cag gac gtg gac ccc tgg ctg ctc ggt ccg cgc cgg ggc aag cgg 720 Ser Gln Asp Val Asp Pro Trp Leu Leu Gly Pro Arg Gly Lys Arg 230 235 gtc tgc gtg gtg tgg ggc aac tcc gcc acg ggc gtg ttc ggc gcg cag 768 Val Cys Val Val Trp Gly Asn Ser Ala Thr Gly Val Phe Gly Ala Gln 245 250 gtg ccg gcg ctg cgg cac gcc gtc gac gcc gcc cag cgg ggc gtg 816 Val Pro Ala Leu Arg His Ala Val Asp Ala Ala Ala Gln Arg Gly Val 265 gag gtc gtg atc acc gcc gcc tcc tcc gag gtg gag ggg ctg ggc gcg 864 Glu Val Val Ile Thr Ala Ala Ser Ser Glu Val Glu Gly Leu Gly Ala 275 280 285 ctg ccg ccg aac gtg cgg gtg ctc agc aac tgc ccg ctg gag ctc atc 912 Leu Pro Pro Asn Val Arg Val Leu Ser Asn Cys Pro Leu Glu Leu Ile 290 295 ctc ccc gac tgc gac ttg ctg gtg cac cac ggc agc gcc aac tgc tac 960 Leu Pro Asp Cys Asp Leu Leu Val His His Gly Ser Ala Asn Cys Tyr 305 310 315 320 atg aac ggg ctc gcc atg ggc gtg ccg cag ttg tcg ctg gcg ctc aac 1008 Met Asn Gly Leu Ala Met Gly Val Pro Gln Leu Ser Leu Ala Leu Asn tac gac gcc ctg atc tac ggg cgg cgg ctc gac ccg cag ggc gcg acg 1056 Tyr Asp Ala Leu Ile Tyr Gly Arg Arg Leu Asp Pro Gln Gly Ala Thr 340 aag acg ctg ccc ggc ctg aag gcg tcc cgc gag gag gtc gac gag gcc 1104 Lys Thr Leu Pro Gly Leu Lys Ala Ser Arg Glu Glu Val Asp Glu Ala 360 ctc ggc tcc gtc ctc tac gac cac cga ttc cgg gtg gcg gcg cag cgg 1152 Leu Gly Ser Val Leu Tyr Asp His Arg Phe Arg Val Ala Ala Gln Arg 370 375 380

		Thr Gly Pr	g acc gcc gtc o Thr Ala Val 395		
			c gcg ctg agc y Ala Leu Ser 410		Val
gcc gag ttc Ala Glu Phe					1269
<210> 63 <211> 423 <212> PRT <213> Micro	monospora ca	ırbonacea			
<220> <223> evrS					
<400> 63 Met Lys Val 1	Leu Phe Thi	Val Ser As	n Trp Ala Gly 10	His Tyr Met	-
Met Val Pro	Leu Ala Try 20	Ala Leu Ar 2	g Ala Ala Gly 5	His Asp Val	Lys
Val Ala Cys 35	Ser Pro Sei	Gln Val Ar 40	g Gly Val Ala	Ala Ala Gly 45	Met
Met Pro Val 50	Ser Val Le	ı Asp Gly Pr 55	o Asp Met Met 60		Arg
Leu Gly Phe 65	Tyr Val Glr	_	r Thr Pro Gln 75	His Met Val	Glu 80
Gln Pro Leu	Pro Leu Ası 85	Pro Phe Th	r Gly Arg Pro 90	Met Asp Ser 95	
Ala Asp Phe	Asp Thr Asp	Leu Leu Al 10	a Asp Tyr Trp 5	Lys Arg Thr 110	Val
Thr Ala Val 115	Gln Arg Sei	Tyr Asp As 120	n Ala Val Asp	Tyr Ala Ala 125	His
Tyr Arg Pro 130	Asp Leu Val	Val His As 135	p Ile Met Ala 140	-	Ala
Leu Val Ala 145	Glu Leu His		o Ser Val Tyr 155	Phe Ser Pro	Gly 160
Phe Ile Gly	Thr Ile Glu 165	ı Thr Glu Pr	o Gly Leu Asp 170	Leu Val Ser 175	Gly
Asp Pro Val	Thr Glu Phe	e Arg Lys Ty 18	r Gly Val Glu 5	Trp Ser Arg 190	His
Gln Ile Arg 195	Tyr Ala Ile	Asp Pro Se 200	r Pro Asp Val	Ala Ile Pro 205	Pro
Met Gly Asp 210	Ala Leu Arg	Ile Pro Il 215	e Arg Tyr Gln 220	_	Gly

Ser Gln Asp Val Asp Pro Trp Leu Leu Gly Pro Arg Arg Gly Lys Arg

```
Val Cys Val Val Trp Gly Asn Ser Ala Thr Gly Val Phe Gly Ala Gln
Val Pro Ala Leu Arg His Ala Val Asp Ala Ala Ala Gln Arg Gly Val
                                265
Glu Val Val Ile Thr Ala Ala Ser Ser Glu Val Glu Gly Leu Gly Ala
Leu Pro Pro Asn Val Arg Val Leu Ser Asn Cys Pro Leu Glu Leu Ile
Leu Pro Asp Cys Asp Leu Leu Val His His Gly Ser Ala Asn Cys Tyr
                    310
Met Asn Gly Leu Ala Met Gly Val Pro Gln Leu Ser Leu Ala Leu Asn
Tyr Asp Ala Leu Ile Tyr Gly Arg Arg Leu Asp Pro Gln Gly Ala Thr
Lys Thr Leu Pro Gly Leu Lys Ala Ser Arg Glu Glu Val Asp Glu Ala
Leu Gly Ser Val Leu Tyr Asp His Arg Phe Arg Val Ala Ala Gln Arg
                        375
Met Arg Glu Ser Val Thr Thr Gly Pro Thr Ala Val Gln Val Ala Glu
                    390
                                         395
Leu Leu Ala Arg Leu Ala Asp Thr Gly Ala Leu Ser Pro Glu Asp Val
                                    410
Ala Glu Phe Ala Arg Arg Pro
            420
<210> 64
<211> 672
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(672)
<220>
<223> evrT
<400> 64
atg acc acc atg tcg cgg gag cgc gag gcc gtg gcc agc cgg ttc cgc
                                                                   48
Met Thr Thr Met Ser Arg Glu Arg Glu Ala Val Ala Ser Arg Phe Arg
age gae ggg ate geg cae gte ggg eeg gtg ete gae eee gag gtg etg
                                                                   96
Ser Asp Gly Ile Ala His Val Gly Pro Val Leu Asp Pro Glu Val Leu
gcc cag ctc aag gcc ggc gcg gta agc ctg atc gac cgg ttc gcc ggt
                                                                   144
Ala Gln Leu Lys Ala Gly Ala Val Ser Leu Ile Asp Arg Phe Ala Gly
                             40
                                                 45
```

ccg Pro	gcg Ala 50	cgg Arg	gcc Ala	aac Asn	gcc Ala	gac Asp 55	tac Tyr	tgg Trp	aac Asn	tac Tyr	gag Glu 60	gtc Val	gag Glu	ggc Gly	gcg Ala	192
							cac His									240
							ccg Pro									288
							ccc Pro									336
							gtg Val 120									384
							aac Asn									432
							gag Glu									480
							gcc Ala									528
							gac Asp									576
					_		ccc Pro 200		_	_			_			624
							gcg Ala									672
<213 <212	0> 65 L> 22 2> PF B> Mi	24 ?T	nonos	spora	a car	rbona	acea									
<220 <223)> 3> ev	rT														
)> 65 Thr		Met	Ser 5	Arg	Glu	Arg	Glu	Ala 10	Val	Ala	Ser	Arg	Phe 15	Arg	
Ser	Asp	Gly	Ile 20	Ala	His	Val	Gly	Pro 25	Val	Leu	Asp	Pro	Glu 30	Val	Leu	
Ala	Gln	Leu 35	Lys	Ala	Gly	Ala	Val 40	Ser	Leu	Ile	Asp	Arg 45	Phe	Ala	Gly	

Pro Ala Arg Ala Asn Ala Asp Tyr Trp Asn Tyr Glu Val Glu Gly Ala

50 55 60 Glu Pro Val Leu Tyr Arg Ile His Asn Leu Glu Lys Gln Asp Trp Pro Gln Gly Glu Leu Leu His Arg Pro Glu Ile Ala Ala Val Ala Ala Asp Val Leu Gly Thr Pro Val Val Pro Thr Ala Phe Ala Leu Val Leu Lys 105 Glu Pro Leu Arg Ala Ala Gly Val Pro Trp His Arg Asp Arg Val Asn Val Pro Pro His Ala Val Cys Asn Ile Ser Ile Cys Leu Asp Thr Ala Gly Pro Glu Asn Gly Cys Leu Glu Gly Val Pro Gly Ser His Leu Leu Pro Asp Asp Ala Asp Val Thr Ala Val Arg Asp Ala Gly Pro Arg Val 165 Pro Val Pro Ser Gln Glu Gly Asp Phe Ile Val His Asp Val Arg Leu 185 Val His Gly Ser Gly Pro Asn Pro Ser Asp Gln Trp Arg Arg Thr Ile 195 Val Ile Glu Phe Ala Asp Pro Ala Arg Glu Leu Pro Val Leu Thr Ser 210 215 <210> 66 <211> 687 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(687) <220> <223> evrU gtg aat gga ttc gag cac gac gga gtg cgt tac gcc gag ggc tcc cag 48 Val Asn Gly Phe Glu His Asp Gly Val Arg Tyr Ala Glu Gly Ser Gln cac ggt tat ctg ctg agc cag tcc ccg gcc gac cgg gcc gcg aag ttc His Gly Tyr Leu Leu Ser Gln Ser Pro Ala Asp Arg Ala Ala Lys Phe tto ggt gog ttt coo gao gog ogg ogg ato oto gaa oto ggo goa otg Phe Gly Ala Phe Pro Asp Ala Arg Arg Ile Leu Glu Leu Gly Ala Leu 35 gag ggc gcg gac acg ctt gcc ctc gcc cgg cac ccc gqc acq acq gtg Glu Gly Ala Asp Thr Leu Ala Leu Ala Arg His Pro Gly Thr Thr Val 50 ett gee etg gag gge egt eeg gag aac etg ege ege geg gag etg gtg 240

Leu Ala Leu Glu Gly Arg Pro Glu Asn Leu Arg Arg Ala Glu Leu Val

65	70	75	80
		gtg gag ctg cgc gtc Val Glu Leu Arg Val 90	
		ggc gag ttc gac gcc Gly Glu Phe Asp Ala 105	
		gag ccg tgg acc ctg Glu Pro Trp Thr Leu 125	2 2 2
		tac ctc tcc acc cac Tyr Leu Ser Thr His 140	
		gac ggc tac acg gtc Asp Gly Tyr Thr Val 155	
cgc gag gag cac Arg Glu Glu His	ccc gag ccg cag Pro Glu Pro Gln 165	gcc cgg ggg ctc agc Ala Arg Gly Leu Ser 170	gtc gac gtg 528 Val Asp Val 175
		ttc gcc gcc ctg cac Phe Ala Ala Leu His 185	
		gag cgc cgg tcg ccg Glu Arg Arg Ser Pro 205	
		acc ggc acg cgc cga Thr Gly Thr Arg Arg 220	
ggg gtg agc ctc Gly Val Ser Leu 225	-		687
<210> 67 <211> 229 <212> PRT <213> Micromonos	spora carbonacea		
<220> <223> evrU			
<400> 67 Val Asn Gly Phe 1	Glu His Asp Gly	Val Arg Tyr Ala Glu 10	Gly Ser Gln 15
His Gly Tyr Leu 20	Leu Ser Gln Ser	Pro Ala Asp Arg Ala 25	Ala Lys Phe 30
Phe Gly Ala Phe 35	Pro Asp Ala Arg	Arg Ile Leu Glu Leu 45	Gly Ala Leu
Glu Gly Ala Asp 50	Thr Leu Ala Leu 55	Ala Arg His Pro Gly 60	Thr Thr Val
Leu Ala Leu Glu	Gly Arg Pro Glu	Asn Leu Arg Arg Ala	Glu Leu Val

65					70					75					80	
Met	Glu	Val	Asn	Gly 85	Ile	Thr	Asn	Val	Glu 90	Leu	Arg	Val	Ala	Asp 95	Val	
Glu	Arg	Ile	Asp 100	Phe	Thr	Glu	Leu	Gly 105	Glu	Phe	Asp	Ala	Val 110	Leu	Cys	
Ala	Gly	Leu 115	Leu	Tyr	His	Val	Arg 120	Glu	Pro	Trp	Thr	Leu 125	Leu	Lys	Asp	
Ile	Ala 130	Gly	Val	Ala	Ala	Gly 135	Ile	Tyr	Leu	Ser	Thr 140	His	Tyr	Trp	Gly	
Gly 145	Val	Gly	Asp	Leu	Gln 150	Pro	Ile	Asp	Gly	Tyr 155	Thr	Val	Lys	Gln	Val 160	
Arg	Glu	Glu	His	Pro 165	Glu	Pro	Gln	Ala	Arg 170	Gly	Leu	Ser	Val	Asp 175	Val	
Arg	Trp	Leu	Asp 180	Arg	Glu	Ser	Leu	Phe 185	Ala	Ala	Leu	His	Asn 190	Ala	Gly	
Phe	Ala	Glu 195	Val	Glu	Val	Leu	His 200	Glu	Arg	Arg	Ser	Pro 205	Glu	Val	Cys	
Asp	Ile 210	Ile	Ala	Val	Gly	Arg 215	Arg	Thr	Gly	Thr	Arg 220	Arg	Pro	Thr	Glu	
Gly 225	Val	Ser	Leu	Arg												
<21: <21: <21: <22: <22:	0 > 68 1 > 10 2 > DN 3 > Mi 0 > 1 > CI 2 > (1	026 NA icror OS		-	a cai	rbona	acea									
<22 <22	0> 3> ev	vrV														
atg	0> 68 gtt Val	cgt														48
	gtg Val															96
	ctc Leu															144
	gtc Val 50															192
	aac Asn															240

65					70					75					80	
gcg Ala	atc Ile	agc Ser	cat His	tcg Ser 85	gtg Val	aag Lys	cag Gln	ctc Leu	aac Asn 90	tac Tyr	ggc Gly	acc Thr	aat Asn	gtg Val 95	atg Met	288
				ctg Leu												336
ttc Phe	tgt Cys	ttc Phe 115	gcc Ala	tcc Ser	tcc Ser	gtg Val	gcg Ala 120	gtc Val	tac Tyr	ggc Gly	cac His	ggc Gly 125	gag Glu	acg Thr	ccg Pro	384
atg Met	cgc Arg 130	gag Glu	tcc Ser	gtc Val	gtc Val	ccc Pro 135	gtc Val	ccc Pro	gcg Ala	gac Asp	agc Ser 140	tac Tyr	ggc Gly	ctg Leu	gcc Ala	432
aag Lys 145	tac Tyr	ctg Leu	gtc Val	gag Glu	cgc Arg 150	gag Glu	ctg Leu	gag Glu	gtg Val	acg Thr 155	atg Met	cgg Arg	acc Thr	cag Gln	999 Gly 160	480
				gcc Ala 165												528
aac Asn	atg Met	cgg Arg	gac Asp 180	ccg Pro	tac Tyr	cgc Arg	aac Asn	gcg Ala 185	gtc Val	gcc Ala	atc Ile	ttc Phe	ttc Phe 190	aac Asn	cag Gln	576
				gag Glu												624
				tac Tyr												672
				gcc Ala												720
				gtg Val 245												768
				cat His												816
				acc Thr												864
tgg Trp	acg Thr 290	gac Asp	acc Thr	ccg Pro	ctg Leu	gcc Ala 295	gag Glu	gga Gly	ctg Leu	gcc Ala	cgc Arg 300	acc Thr	gcc Ala	agg Arg	tgg Trp	912
				Gly ggg												960
				cgg Arg 325												1008

ctc agc acg gcg agc cgc Leu Ser Thr Ala Ser Arg

340 <210> 69 <211> 342 <212> PRT <213> Micromonospora carbonacea <220> <223> evrV <400> 69 Met Val Arg Cys Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Glu Ser Leu Val Arg Asn Gly His Arg Val Thr Val Leu Asp Asp Leu Ser Gly Gly Ser Arg Gln Arg Val Pro Ala Gly Val Asp Leu Ala Val Gly Ser Val Thr Asp Val Asp Phe Val Asp Ser Leu Phe Ala Glu Asn Arg Phe Glu Arg Val Phe His Phe Ala Ala Phe Ala Ala Glu Ala Ile Ser His Ser Val Lys Gln Leu Asn Tyr Gly Thr Asn Val Met 90 Gly Ser Ile Asn Leu Ile Asn Ala Ser Leu Arg Thr Gly Val Arg Phe 105 Phe Cys Phe Ala Ser Ser Val Ala Val Tyr Gly His Gly Glu Thr Pro Met Arg Glu Ser Val Val Pro Val Pro Ala Asp Ser Tyr Gly Leu Ala 135 Lys Tyr Leu Val Glu Arg Glu Leu Glu Val Thr Met Arg Thr Gln Gly Leu Pro Phe Thr Ala Phe Arg Met His Asn Val Tyr Gly Glu Trp Gln Asn Met Arg Asp Pro Tyr Arg Asn Ala Val Ala Ile Phe Phe Asn Gln 185 Ile Leu Arg Gly Glu Pro Ile Thr Val Tyr Gly Asp Gly Gly Val Arg Ala Phe Thr Tyr Val Gly Asp Val Val Asn Val Val Ser Arg Ala 215 Ala Glu Thr Glu Ala Ala Trp Gly Arg Ala Phe Asn Val Gly Ser Ser 235 Ser Thr Asn Thr Val Leu Glu Leu Ala Gln Ala Val Arg Ser Ala Ala 245 Gly Val Pro Glu His Pro Ile Ala His Leu Pro Ser Arg Asp Glu Val 260 265 270

Arg Thr Ala Tyr Thr Ala Thr Glu Leu Ala Arg Ser Val Phe Gly Asp

Trp Thr Asp Thr Pro Leu Ala Glu Gly Leu Ala Arg Thr Ala Arg Trp 295 Ala Ala Asp Ala Gly Pro Ala Glu Leu Gln Ser Ser Phe Asp Ile Glu Ile Gly Gly Asp Arg Ile Pro Glu Trp Ala Arg Leu Val Asn Glu Arg Leu Ser Thr Ala Ser Arg 340 <210> 70 <211> 987 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(987) <220> <223> evrW <400> 70 atg cgt cgc gtc ctg gtc acc ggc ggt gcc ggt ttc atc ggc tcg cag 48 Met Arg Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln tac gtc cgc gac ctg gcc acc ggt gcc tac ccc gac acg gcg cag gcc 96 Tyr Val Arg Asp Leu Ala Thr Gly Ala Tyr Pro Asp Thr Ala Gln Ala cgg gtg acg gtg ctg gac aag ctg acg tac gcg ggc aac ctc gcc aac 144 Arg Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Leu Ala Asn ctc gaa ccg gtc cag gac cgg atc acc ttc gtc cag ggc gac gtc tgc 192 Leu Glu Pro Val Gln Asp Arg Ile Thr Phe Val Gln Gly Asp Val Cys gac acg gcg ctg ctg gcc gag gtg ctg ccc ggg cac gac gtg gtg gtc 240 Asp Thr Ala Leu Leu Ala Glu Val Leu Pro Gly His Asp Val Val Val 70 aac ttc gcc gcc gag tcg cac gtc gac cgg tcc atc gcc gac tcg gcg 288 Asn Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Ala Asp Ser Ala gag ttc gtc cgc acc aac gtg cag ggc gtc cag acg ctc atg cag gcg 336 Glu Phe Val Arg Thr Asn Val Gln Gly Val Gln Thr Leu Met Gln Ala 100 105 110 tgt ete gae gee ggg gte gee egg gtg gte eag gte tee ace gae gag Cys Leu Asp Ala Gly Val Ala Arg Val Val Gln Val Ser Thr Asp Glu 115 gtc tac ggc agc atc gac gag ggt tcc tgg gcc gag gac acc ccc ctg

Val Tyr Gly Ser Ile Asp Glu Gly Ser Trp Ala Glu Asp Thr Pro Leu

130	135	140	
gcg ccg aac tcc cc Ala Pro Asn Ser Pr 145	g tac gcg gcg g o Tyr Ala Ala A 150	cg aag gcc ggc la Lys Ala Gly 155	ggg gac ctg atc 480 Gly Asp Leu Ile 160
gcc ctg gcc tac gc Ala Leu Ala Tyr Al 16	a Arg Thr His G	gg ctg ccg gtc ly Leu Pro Val 170	tgc ctc acc cgg 528 Cys Leu Thr Arg 175
tgc ggc aac aac ta Cys Gly Asn Asn Ty 180	r Gly Pro Tyr G		
ctg ttc gtc acc ga Leu Phe Val Thr Gl 195			
gac ggc ggg aac gt Asp Gly Gly Asn Va 210			
ggc atc cag acc gt Gly Ile Gln Thr Va 225			
atc gcc ggc acg gc Ile Ala Gly Thr Al 24	a Glu Leu Ser A		
ctg gac gcc ttg gg Leu Asp Ala Leu Gl 260	y Ala Gly Trp A		
cgc aag ggc cac ga Arg Lys Gly His As 275			
gcg ctc ggc tac cg Ala Leu Gly Tyr Ar 290			
acg atc gac tgg ta Thr Ile Asp Trp Ty 305			
aag cag gcc gac cg Lys Gln Ala Asp Ar 32	g Ser Pro Val P		987
<210> 71 <211> 329 <212> PRT <213> Micromonospo	ra carbonacea		
<220> <223> evrW			
<400> 71 Met Arg Arg Val Le 1	u Val Thr Gly G 5	ly Ala Gly Phe 10	Ile Gly Ser Gln 15
Tyr Val Arg Asp Le		la Tyr Pro Asp 25	Thr Ala Gln Ala 30 .

Arg Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Leu Ala Asn 35 40 45

Leu Glu Pro Val Gln Asp Arg Ile Thr Phe Val Gln Gly Asp Val Cys
50 55 60

Asp Thr Ala Leu Leu Ala Glu Val Leu Pro Gly His Asp Val Val 65 70 75 80

Asn Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Ala Asp Ser Ala 85 90 95

Glu Phe Val Arg Thr Asn Val Gln Gly Val Gln Thr Leu Met Gln Ala 100 105 110

Cys Leu Asp Ala Gly Val Ala Arg Val Val Gln Val Ser Thr Asp Glu 115 120 125

Val Tyr Gly Ser Ile Asp Glu Gly Ser Trp Ala Glu Asp Thr Pro Leu 130 135 140

Ala Pro Asn Ser Pro Tyr Ala Ala Ala Lys Ala Gly Gly Asp Leu Ile 145 150 155 160

Ala Leu Ala Tyr Ala Arg Thr His Gly Leu Pro Val Cys Leu Thr Arg 165 . 170 . 175

Cys Gly Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Leu Ile Pro 180 185 190

Leu Phe Val Thr Glu Leu Leu Asn Gly Arg Arg Val Pro Leu Tyr Gly 195 200 205

Asp Gly Gly Asn Val Arg Asp Trp Ile His Val Thr Asp His Cys Arg 210 215 220

Gly Ile Gln Thr Val Val Asp Arg Gly Val Pro Gly Glu Val Tyr His 225 230 235 240

Ile Ala Gly Thr Ala Glu Leu Ser Asn Met Glu Leu Thr Gly Arg Leu 245 250 255

Leu Asp Ala Leu Gly Ala Gly Trp Asp Arg Val Glu Arg Val Pro Asp 260 265 270

Arg Lys Gly His Asp Arg Arg Tyr Ser Leu Thr Asp Ala Lys Leu Arg 275 280 285

Ala Leu Gly Tyr Arg Pro Glu Val Ala Phe Ala Asp Gly Leu Ala Glu 290 295 300

Thr Ile Asp Trp Tyr Arg Thr His Arg Asp Trp Trp Glu Pro Leu Lys 305 310 315 320

Lys Gln Ala Asp Arg Ser Pro Val Pro 325

<210> 72

<211> 1065

<212> DNA

<213> Micromonospora carbonacea

<220> <221> CDS <222> (1)..(1065) <220> <223> evrX <400> 72 gtg aag gcg ctg gtc ctg gcg gga ggg gtg gga tcg aga ttg cgt ccg 48 Val Lys Ala Leu Val Leu Ala Gly Gly Val Gly Ser Arg Leu Arg Pro ate ace cac acg tee gee aaa caa ete att eee gtg gee aac aag eeg 96 Ile Thr His Thr Ser Ala Lys Gln Leu Ile Pro Val Ala Asn Lys Pro 20 25 gtg ctg ttc tac ggg ctc gag gct att cgt gag ggc ggt atc gag gag 144 Val Leu Phe Tyr Gly Leu Glu Ala Ile Arg Glu Gly Gly Ile Glu Glu gtg ggc atc gtc ggc agc acc gcg ccc gaa att cag cgc gtg gtc 192 Val Gly Ile Val Val Gly Ser Thr Ala Pro Glu Ile Gln Arg Val Val 55 ggc gat ggt tcc cag ttc ggc ctc cag gtg acc tac ctt ccg cag gag 240 Gly Asp Gly Ser Gln Phe Gly Leu Gln Val Thr Tyr Leu Pro Gln Glu 70 75 288 get eee egg ggg etg geg eae gee gtg ete ate tee ege gae tae ete Ala Pro Arg Gly Leu Ala His Ala Val Leu Ile Ser Arg Asp Tyr Leu 85 90 ggc gac gac gac ttc gtc atg tac ctc ggc gac aac ttc atc gtc ggc 336 Gly Asp Asp Phe Val Met Tyr Leu Gly Asp Asn Phe Ile Val Gly 100 ggg atc aag gac atc gtc gag cgc ttc cgg cag gag cga ccg cac gcg 384 Gly Ile Lys Asp Ile Val Glu Arg Phe Arg Gln Glu Arg Pro His Ala 115 cag atc atg ctg acc cgg gtc gcc gac ccg cac gcc ttc ggc gtc gcc 432 Gln Ile Met Leu Thr Arg Val Ala Asp Pro His Ala Phe Gly Val Ala gag atg ggc gcg gac ggc cgg gtg atc ggg gtg gag gag aag ccc gag 480 Glu Met Gly Ala Asp Gly Arg Val Ile Gly Val Glu Glu Lys Pro Glu cac ccc aag agc gac ctg gcc ctg gtc ggg gtc tac gtc ttc agc ccg 528 His Pro Lys Ser Asp Leu Ala Leu Val Gly Val Tyr Val Phe Ser Pro 165 gtg gtc cac gat gcc gtg gcc gag ctg aag ccg tcc tgg cgc aac gag 576 Val Val His Asp Ala Val Ala Glu Leu Lys Pro Ser Trp Arg Asn Glu ctg gag atc acc gac gcg gtg cag tgg atg atc gac cgc ggc cac cgg Leu Glu Ile Thr Asp Ala Val Gln Trp Met Ile Asp Arg Gly His Arg 624 200 gto gao too acc atg atc acg ggo tac tgg aag gac acc ggo aac cto 672 Val Asp Ser Thr Met Ile Thr Gly Tyr Trp Lys Asp Thr Gly Asn Leu 215 gcc gac atg ctg gag atg aac cgg ttc gtc ctc ggc agc gtc gag cct 720

A1a 225	Asp	Met	Leu	Glu	Met 230	Asn	Arg	Phe	Val	Leu 235	Gly	Ser	Val	Glu	Pro 240	
ttg Leu			ggc Gly													768
gtg Val			gcc Ala 260													816
gtg Val																864
			atc Ile													912
cac His 305			gtg Val													960
gag Glu																1008
gtg Val																1056
gtg		_														1065
Val	GIA	Val 355														
<210 <211 <212	> 73 > 35 > PF	355 355 355 RT	nonos	spora	a car	rbona	acea									
<210 <211 <212	73 > 35 > PF > Mi	355 355 RT Icron	nonos	spora	a car	rbona	ıcea									
<210 <211 <212 <213	73 > 35 > PF > Mi	355 355 RT icron						Gly	Val 10	Gly	Ser	Arg	Leu	Arg 15	Pro	
<210 <211 <212 <213 <220 <223 <400 Val	73 > 35 > PF > Mi > ev > 73 Lys	355 S5 RT CCTON YTX Ala		Val 5	Leu	Ala	Gly		10	_				15		
<210 <211 <212 <213 <220 <223 <400 Val	2> 73 3 9 PF 5> Mi 5> ev 1> 73 Lys	355 ST CCTON YTX Ala	Leu Thr 20	Val 5 Ser	Leu Ala	Ala Lys	Gly Gln	Leu 25	10 Ile	Pro	Val	Ala	Asn 30	15 Lys	Pro	
<210 <211 <212 <213 <220 <223 <400 Val 1	> 73 > 35 > PF > Mi > ev > 73 Lys	355 SST CCTON YTX Ala His	Leu Thr 20 Tyr	Val 5 Ser Gly	Leu Ala Leu	Ala Lys Glu	Gly Gln Ala 40	Leu 25 Ile	10 Ile Arg	Pro Glu	Val Gly	Ala Gly 45	Asn 30 Ile	15 Lys Glu	Pro Glu	
<210 <211 <212 <213 <220 <223 <400 Val 1 Ile	2> 73 > 35 > PF > Mi > ev > 73 Lys Thr Leu Gly 50	355 ST CT Cron YrX Ala His Phe 35	Leu Thr 20 Tyr	Val 5 Ser Gly Val	Leu Ala Leu Gly	Ala Lys Glu Ser 55	Gly Gln Ala 40 Thr	Leu 25 Ile Ala	10 Ile Arg Pro	Pro Glu Glu	Val Gly Ile 60	Ala Gly 45 Gln	Asn 30 Ile Arg	15 Lys Glu Val	Pro Glu Val	
<210 <211 <212 <213 <220 <223 <400 Val Ile Val Val Gly	2> 73 2> 35 2> PF 2> M3 2> ev 2> 73 Lys Thr Leu Gly 50 Asp	355 ST CT Cron YrX Ala His Phe 35 Ile	Leu Thr 20 Tyr Val	Val 5 Ser Gly Val	Leu Ala Leu Gly Phe 70	Ala Lys Glu Ser 55	Gly Gln Ala 40 Thr	Leu 25 Ile Ala Gln	10 Ile Arg Pro Val	Pro Glu Glu Thr 75	Val Gly Ile 60	Ala Gly 45 Gln Leu	Asn 30 Ile Arg	15 Lys Glu Val	Pro Glu Val Glu 80	

```
Gly Ile Lys Asp Ile Val Glu Arg Phe Arg Gln Glu Arg Pro His Ala
Gln Ile Met Leu Thr Arg Val Ala Asp Pro His Ala Phe Gly Val Ala
                        135
Glu Met Gly Ala Asp Gly Arg Val Ile Gly Val Glu Glu Lys Pro Glu
His Pro Lys Ser Asp Leu Ala Leu Val Gly Val Tyr Val Phe Ser Pro
                                    170
Val Val His Asp Ala Val Ala Glu Leu Lys Pro Ser Trp Arg Asn Glu
                                185
Leu Glu Ile Thr Asp Ala Val Gln Trp Met Ile Asp Arg Gly His Arg
Val Asp Ser Thr Met Ile Thr Gly Tyr Trp Lys Asp Thr Gly Asn Leu
Ala Asp Met Leu Glu Met Asn Arg Phe Val Leu Gly Ser Val Glu Pro
225
                    230
                                        235
Leu Val Glu Gly Lys Val Asp Asp Arg Thr Glu Leu Ile Gly Pro Val
Val Ile Ser Ala Gly Ala Asp Val Ser Gly Ser Arg Ile Val Gly Pro
Val Val Gly Ala Gly Ser Ile Ile Arg Asn Ser Tyr Leu Gly Pro
                            280
Tyr Thr Ser Ile Asp Cys Asp Cys Thr Leu Leu Glu Thr Glu Ile Glu
His Ser Ile Val Leu Arg Gly Ala Tyr Ile Glu Gly Ile Gly Arg Ile
305
Glu Phe Ser Met Ile Gly Arg Glu Ala Arg Val Val Pro Gly Pro Arg
                                    330
Val Pro Lys Thr His Arg Phe Val Leu Gly Asp His Ser Glu Val Arg
Val Gly Val
        355
<210> 74
<211> 744
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(744)
<220>
<223> evrY
```

atg acg acc ccc ctg ccc cgt ccg atc gac gcc gtc ctg ttc gac ttc

Met 1	Thr	Thr	Pro	Leu 5	Pro	Arg	Pro	Ile	Asp 10	Ala	Val	Leu	Phe	Asp 15	Phe	
					gcc Ala											96
					ggc Gly											144
					ctg Leu											192
	_	_	_	_	999 Gly 70		_				_	_		_		240
					cgc Arg											288
					ggc Gly											336
					ctg Leu											384
					ggc Gly											432
tgg Trp 145	gac Asp	ctg Leu	cgg Arg	ccc Pro	acc Thr 150	ttc Phe	gcg Ala	gcg Ala	tac Tyr	999 Gly 155	atg Met	gcg Ala	gag Glu	ctg Leu	gtg Val 160	480
					tcc Ser											528
cgg Arg	atc Ile	ttc Phe	cgc Arg 180	acc Thr	gcc Ala	tgc Cys	gac Asp	gag Glu 185	ctg Leu	aag Lys	gtc Val	gcc Ala	ccg Pro 190	gag Glu	cgg Arg	576
gcg Ala	ctg Leu	atg Met 195	gtg Val	ggc Gly	gac Asp	acc Thr	ctg Leu 200	gcc Ala	gac Asp	ggt Gly	Gly 999	gcg Ala 205	gtg Val	tac Tyr	gcc Ala	624
					ctg Leu											672
					ctc Leu 230											720
					gcg Ala											744

```
<211> 248
```

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evrY

<400> 75

Met Thr Thr Pro Leu Pro Arg Pro Ile Asp Ala Val Leu Phe Asp Phe 1 5 10 15

Ser Gly Thr Leu Phe Ala Val Glu Leu Pro Gln Arg Trp Leu Arg Ala 20 25 30

Ala Ala Thr Val Gly Val Gln Leu Asp Pro Ala Gln Glu Ala 35 40 45

Leu Thr Gly Leu Leu Ala Ala Gly Arg Pro Gly Gly Pro Glu Pro
50 55 60

His Ala Val Pro Pro Gly Leu Ala Glu Val Tyr Ala Arg Arg Asp Leu 65 70 75 80

Ser Pro Glu Thr His Arg Ser Ala Tyr Val Gly Leu Leu Ser Thr Val 85 90 95

Asp Leu Pro His Pro Gly Leu Ala Glu Ala Leu Tyr Asp Arg Leu Phe 100 105 110

Arg Thr Asp Gly Trp Leu Pro Tyr Arg Asp Ala Ala Pro Val Leu Ala 115 120 125

Glu Leu Arg Arg Gly Val Gly Thr Ala Val Val Ser Asn Ile Ala 130 135 140

Trp Asp Leu Arg Pro Thr Phe Ala Ala Tyr Gly Met Ala Glu Leu Val 145 150 155 160

Asp Ala Tyr Val Phe Ser His Glu Val Gly Ala Val Lys Pro Asp Pro 165 170 175

Arg Ile Phe Arg Thr Ala Cys Asp Glu Leu Lys Val Ala Pro Glu Arg 180 185 190

Ala Leu Met Val Gly Asp Thr Leu Ala Asp Gly Gly Ala Val Tyr Ala 195 200 205

Gly Leu Gln Thr Leu Leu Pro Ala Ser Pro Pro Asp Thr Val His 210 215 220

Gly Leu Ala Ala Val Leu Glu Leu Val Gly Gly Pro Ala Arg Pro
225 230 235

Pro Phe Ala Glu Met Ala Asp Ala 245

<210> 76

<213> Micromonospora carbonacea

<220>

<221> CDS

<211> 750

<212> DNA

<222> (1)..(750)

<220>

<220 <223)> }> e1	rZ														
gtg		cgt			acc Thr											48
					gct Ala											96
		_	_		acc Thr				_					_		144
					agc Ser											192
					ggt Gly 70											240
					tac Tyr											288
					atc Ile											336
					gcc Ala											384
	_	-	_		gcc Ala		_		_			_	_			432
					atg Met 150											480
					ggc Gly											528
			_	_	acc Thr		_				_		_			576
					cgc Arg											624
	_	_	_		agc Ser			_		_	_			_	_	672
			_		aac Asn 230	_	_	_						_	_	720

750

acc cgg ctg atc gcg ctg gcg aac aac acc Thr Arg Leu Ile Ala Leu Ala Asn Asn Thr 245 <210> 77 <211> 250 <212> PRT <213> Micromonospora carbonacea <220> <223> evrZ <400> 77 Val Thr Arg Thr Arg Thr Ala Leu Arg Arg Leu Leu Ala Ala Gly Leu Ala Ser Leu Ala Thr Ala Ala Ala Thr Leu Val Ala Thr Ala Gly Pro Ala Ala Ala Thr Thr Pro Gly Ile Asp Val Ser His Tyr Gln Gly Ser Ile Asn Trp Thr Ser Val Arg Asn Ala Gly Ile Gln Phe Ala Phe Ile Lys Ala Thr Glu Gly Thr Ser Tyr Lys Asp Pro Asn Phe Asn Ala Asn Tyr Val Asn Ser Tyr Asn Ala Gly Val Ile Arg Gly Ala Tyr His Phe Ala Arg Pro Asn Ile Ser Ser Gly Ala Thr Gln Ala Asn Tyr Leu Ala Ser Asn Gly Gly Ala Trp Ser Ala Asp Ser Arg Thr Leu Pro Ala 120 Ala Leu Asp Val Glu Ala Asn Pro Tyr Ser Gly Gly Thr Cys Tyr Gly 135 Leu Ser Thr Ser Gly Met Arg Ser Trp Ile Gln Asp Phe Leu Asn Thr

Pro Leu Trp Leu Ala Arg Trp Ser Ser Thr Pro Gly Thr Leu Pro Ala 195 200 205

Tyr Lys Ala Arg Thr Gly Arg Tyr Ala Val Ile Tyr Thr Thr Thr Ser

Trp Trp Asn Gln Cys Thr Gly Ser Trp Thr Gly Pro Trp Ala Asn His 180 185 190

Gly Ala Ser Val Trp Ser Phe Trp Gln Tyr Thr Ala Ser Gly Ser Val 210 215 220

Ser Gly Ile Ser Gly Asn Val Asp Arg Asn Asn Trp Asn Gly Asp Arg 225 230 235 240

Thr Arg Leu Ile Ala Leu Ala Asn Asn Thr 245 250

```
<210> 78
<211> 2076
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(2076)
<220>
<223> evsA
<400> 78
atg ggt cgg gta tgg aag gcg cgc gac gag gtg ctg cac cgg gat gtg
Met Gly Arg Val Trp Lys Ala Arg Asp Glu Val Leu His Arg Asp Val
gcg atc aag gaa ctg gtc ccg ccc agc ctc acc ccg gag gag cqc
Ala Ile Lys Glu Leu Val Pro Pro Pro Ser Leu Thr Pro Glu Glu Arq
cgc gag atg cgg gaa cgc tcg ctg cgg gag gcc cgt gcc atc gcg cga
Arg Glu Met Arg Glu Arg Ser Leu Arg Glu Ala Arg Ala Ile Ala Arg
ctc aac cac gtc aac gtg gtc cgc atc ttc gac gtt ctg cgc acc gac
                                                                   192
Leu Asn His Val Asn Val Val Arg Ile Phe Asp Val Leu Arg Thr Asp
ggc gac ccg tgg atc gtc atg gag tac gtg gcg tcg aag tcc ctt cag
                                                                   240
Gly Asp Pro Trp Ile Val Met Glu Tyr Val Ala Ser Lys Ser Leu Gln
                     70
gac act ctc gcg gag gac ggg ccg gtg tcg ccg gcc aag gcg gtc gaq
                                                                   288
Asp Thr Leu Ala Glu Asp Gly Pro Val Ser Pro Ala Lys Ala Val Glu
atc ggc ctg ggg gtg ctc ggc gcg ctg aag gcg gcg cac aag gcc ggc
                                                                   336
Ile Gly Leu Gly Val Leu Gly Ala Leu Lys Ala Ala His Lys Ala Gly
            100
                                105
gtc atg cac cgg gac atc aag ccg ggc aac gtg ctg ctc ggc acc gac
                                                                   384
Val Met His Arg Asp Ile Lys Pro Gly Asn Val Leu Leu Gly Thr Asp
                            120
ggc cgg gtg gtg ctg acc gat ttc ggc ctg gcg acc atc ccc ggt gac Gly Arg Val Val Leu Thr Asp Phe Gly Leu Ala Thr Ile Pro Gly Asp
                                                                   432
    130
                        135
ccg aac gtg acg cgg acc gga atg gtg ctg ggc tcc ccg gcg tac atc
                                                                   480
Pro Asn Val Thr Arg Thr Gly Met Val Leu Gly Ser Pro Ala Tyr Ile
145
                    150
                                        155
528
Ala Pro Glu Arg Ala Arg Asp Gly Thr Ala Gly Pro Glu Ala Asp Leu
                165
                                    170
tgg tcg ctg ggc gcg acg ctc tac gcg gcg gtg gag ggc aag tcg ccg
                                                                   576
Trp Ser Leu Gly Ala Thr Leu Tyr Ala Ala Val Glu Gly Lys Ser Pro
                                185
tte gee ega eeg teg geg ate gee ace etg geg geg etg gee ace gag
                                                                   624
Phe Ala Arg Pro Ser Ala Ile Ala Thr Leu Ala Ala Leu Ala Thr Glu
        195
                            200
                                                 205
```

						aac Asn 215										672
						ccg Pro										720
						gcc Ala										768
ctg Leu	ctc Leu	gac Asp	ggc Gly 260	gta Val	cgc Arg	cgg Arg	ccg Pro	999 Gly 265	ccg Pro	aac Asn	ggc Gly	ccg Pro	cgc Arg 270	gag Glu	ccg Pro	816
						gca Ala										864
						gca Ala 295										912
						gcc Ala										960
						gac Asp										1008
						ccg Pro										1056
						gcg Ala										1104
						ggc Gly 375										1152
ccg Pro 385	gcg Ala	gac Asp	cgg Arg	gcc Ala	gcc Ala 390	gag Glu	gct Ala	Gly aaa	gac Asp	gaa Glu 395	gly aaa	gcc Ala	gac Asp	Gly aaa	gcc Ala 400	1200
						gac Asp										1248
						ccc Pro										1296
ccc Pro	gcc Ala	gtc Val 435	gcg Ala	ccc Pro	cgc Arg	gag Glu	gag Glu 440	gcc Ala	gcc Ala	ccg Pro	acg Thr	tcg Ser 445	gtg Val	ctg Leu	ccg Pro	1344
						ctc Leu 455										1392

										ggc Gly 475						1440
										gcg Ala						1488
										ggc Gly						1536
										ccg Pro						1584
										ccg Pro						1632
_	_						_		_	gac Asp 555	_				_	1680
										agc Ser						1728
atc Ile	gtc Val	ttc Phe	gac Asp 580	gag Glu	cgc Arg	gac Asp	Gly aaa	gtg Val 585	ggc	gag Glu	ctg Leu	ctg Leu	gtg Val 590	cag Gln	tgg Trp	1776
										gac Asp						1824
										cag Gln						1872
										tgg Trp 635						1920
										cgg Arg						1968
										gtg Val						2016
_			_	_	_		_			gcc Ala	_			_	_	2064
_		gtc Val	_													2076

<210> 79 <211> 692 <212> PRT <213> Micromonospora carbonacea

<220> <223> evsA

<400> 79

Met Gly Arg Val Trp Lys Ala Arg Asp Glu Val Leu His Arg Asp Val 1 5 10 15

Ala Ile Lys Glu Leu Val Pro Pro Pro Ser Leu Thr Pro Glu Glu Arg
20 25 30

Arg Glu Met Arg Glu Arg Ser Leu Arg Glu Ala Arg Ala Ile Ala Arg 35 40 45

Leu Asn His Val Asn Val Val Arg Ile Phe Asp Val Leu Arg Thr Asp
50 55 60

Gly Asp Pro Trp Ile Val Met Glu Tyr Val Ala Ser Lys Ser Leu Gln 65 70 75 80

Asp Thr Leu Ala Glu Asp Gly Pro Val Ser Pro Ala Lys Ala Val Glu 85 90 95

Ile Gly Leu Gly Val Leu Gly Ala Leu Lys Ala Ala His Lys Ala Gly
100 105 110

Val Met His Arg Asp Ile Lys Pro Gly Asn Val Leu Leu Gly Thr Asp 115 120 125

Gly Arg Val Val Leu Thr Asp Phe Gly Leu Ala Thr Ile Pro Gly Asp 130 135 140

Pro Asn Val Thr Arg Thr Gly Met Val Leu Gly Ser Pro Ala Tyr Ile 145 150 155 160

Ala Pro Glu Arg Ala Arg Asp Gly Thr Ala Gly Pro Glu Ala Asp Leu 165 170 175

Trp Ser Leu Gly Ala Thr Leu Tyr Ala Ala Val Glu Gly Lys Ser Pro 180 185 190

Phe Ala Arg Pro Ser Ala Ile Ala Thr Leu Ala Ala Leu Ala Thr Glu 195 200 205

Pro Met Pro Pro Pro Arg Asn Ala Gly Pro Leu Lys Pro Val Leu Asn 210 215 220

Gly Leu Leu Arg Lys Asp Pro Ala Glu Arg Ile Asp Ala Glu Val Ala 225 230 235 240

Glu Arg Leu Leu Arg Arg Ala Ala Gly Arg Arg Ala Lys Thr Ile Ser

Leu Leu Asp Gly Val Arg Arg Pro Gly Pro Asn Gly Pro Arg Glu Pro 260 265 270

Arg Pro Pro Val Val Pro Ala Pro Arg Pro Ala Glu Gln Arg Thr Gly 275 280 285

Arg Pro Ala Ala Pro Pro Ala Pro Arg Thr Pro Glu Gly Gly Leu Ala 290 295 300

Ala Gly Gly Ala Ala Ala Gly Val Gly Gly Asp Ala Thr Ala 305 310 315 320

Lys	Val	Pro	Ala	Gly 325	Val	Asp	Ala	Ala	Pro 330	Thr	Ala	Met	Val	Asp 335	Leu
Pro	Ser	Ala	Asp 340	Ala	Asp	Pro	Thr	Ala 345	Lys	Val	Thr	Asp	Phe 350	Gly	Pro
Gln	Ala	Ala 355	Asp	Pro	Thr	Ala	Lys 360	Ile	Pro	Ala	Pro	Asp 365	Ala	Ala	Thr
Ser	Ala 370	Asp	Glu	Ala	Ala	Gly 375	Thr	Pro	Ala	Gly	Gly 380	Ser	Asp	Gly	Pro
Pro 385	Ala	Asp	Arg	Ala	Ala 390	Glu	Ala	Gly	Asp	Glu 395	Gly	Ala	Asp	Gly	Ala 400
Pro	Ala	Ala	Gly	Arg 405	Ala	Asp	Asp	Thr	Arg 410	Ala	Asp	Asp	Thr	Arg 415	Val
Asp	Pro	Gly	Ala 420	Ala	Val	Pro	Val	Ser 425	Pro	Pro	Ala	Pro	Ala 430	Arg	Glu
Pro	Ala	Val 435	Ala	Pro	Arg	Glu	Glu 440	Ala	Ala	Pro	Thr	Ser 445	Val	Leu	Pro
Ala	Ala 450	Ser	Gly	Pro	Ala	Leu 455	Ser	Ser	Thr	Gly	Arg 460	Ala	Thr	Val	Val
Gly 465	Gly	Thr	Lys	Pro	Glu 470	Arg	Arg	Arg	Arg	Gly 475	Leu	Leu	Val	Gly	Ala 480
Leu	Val	Ala	Val	Leu 485	Leu	Ile	Gly	Leu	Leu 490	Ala	Ala	Val	Pro	Leu 495	Leu
Gly	Arg	Ser	Gly 500	Asp	Asp	Asp	Pro	Gly 505	Pro	Gly	Gly	Asp	Pro 510	Gln	Ala
Gly	Val	Ser 515	Thr	Pro	Thr	Pro	Ser 520	Ala	Ala	Pro	Ala	Thr 525	Ser	Ser	Ala
Ala	Pro 530	Pro	Ser	Pro	Thr	Pro 535	Ser	Ala	Ser	Pro	Ser 540	Val	Asp	Pro	Asn
Ala 545	Leu	Pro	Glu	Gly	Trp 550	Leu	Leu	His	Lys	Asp 555	Pro	Ala	Gly	Phe	Ser 560
Leu	Pro	Leu	Pro	Lys 565	Gly	Trp	Val	Arg	Arg 570	Ser	Val	Gly	Gln	Asn 575	Thr
Ile	Val	Phe	Asp 580	Glu	Arg	Asp	Gly	Val 585	Gly	Glu	Leu	Leu	Val 590	Gln	Trp
Thr	Ser	Thr 595	Pro	Glu	Gly	Asp	Ala 600	Tyr	Ala	Asp	Trp	Lys 605	Glu	Lys	Glu
Pro	Ala 610	Arg	Lys	Asn	Tyr	Val 615	Asn	Gly	Tyr	Gln	Tyr 620	Leu	Ser	Ile	Lys
Arg 625	Cys	Asp	Tyr	Tyr	Lys 630	Thr	Суѕ	Ala	Asp	Trp 635	Glu	Trp	Leu	Glu	Asn 640
Arg	Asp	Gly	Thr	Arg 645	Ile	His	Val	Arg	Asn 650	Arg	Gly	Phe	Val	Thr 655	Ala
Ser	Asn	Arg	Gly 660	Tyr	Ala	Leu	Arg	Trp 665	Glu	Val	Ala	Asn	Lys 670	Asp	Trp

Gln Ala Arg Leu Ala Asp Phe Asp Arg Ile Ala Lys Gly Phe Lys Pro Asp Arg Val Asp 690 <210> 80 <211> 1086 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1086) <220> <223> evsB <400> 80 gtg cgt gcg agt cct gaa acc gat ggt gcc ttg cga ata cgg gct gac Val Arg Ala Ser Pro Glu Thr Asp Gly Ala Leu Arg Ile Arg Ala Asp cag tgg cac ctt aac tac ctg aag gcg gcg gag gct cag aag ctg tca Gln Trp His Leu Asn Tyr Leu Lys Ala Ala Glu Ala Gln Lys Leu Ser ctg gga gaa ggg gtt gta gta gcg gtc ccg gat act ggc gtt gat cca Leu Gly Glu Gly Val Val Val Ala Val Pro Asp Thr Gly Val Asp Pro 144 40 cac ccc gac ctt cag cgc aat cta atc aaa ggg att gac atc att ccc 192 His Pro Asp Leu Gln Arg Asn Leu Ile Lys Gly Ile Asp Ile Ile Pro ggg ggc aat gga gat ggc cag aaa gat cgc aac agt cac ggc act agc 240 Gly Gly Asn Gly Asp Gly Gln Lys Asp Arg Asn Ser His Gly Thr Ser 65 70 atg gct gga cta atc gca gcc cac gga cag ggc cag agc ggc gcc tta 288 Met Ala Gly Leu Ile Ala Ala His Gly Gln Gly Gln Ser Gly Ala Leu 85 ggc ata gca ccc aga gcc aag atc atg cca atc ctg tct tcc gcg tcg 336 Gly Ile Ala Pro Arg Ala Lys Ile Met Pro Ile Leu Ser Ser Ala Ser 100 105 110 aac aac ctc ggt gat gca gac ggc ttg gct gcg ggt ata gaa ttt gca 384 Asn Asn Leu Gly Asp Ala Asp Gly Leu Ala Ala Gly Ile Glu Phe Ala 115 120 atc tcg cat ggg gcg gat gtc atc aat gtc tcc agc gga ggc gcc 432 Ile Ser His Gly Ala Asp Val Ile Asn Val Ser Ser Gly Gly Ala 130 135 age gtt ega etc atc aag gea atc aga gag geg gte gee gea gae att 480 Ser Val Arg Leu Ile Lys Ala Ile Arg Glu Ala Val Ala Ala Asp Ile 150 155

gta gtt gtc gca gcc gga aac agt ccc gaa gac atg aca att ggc

Val Val Val Ala Ala Gly Asn Ser Pro Glu Asp Met Thr Ile Gly

170

165

											ggc Gly					576
_				_		_		_	_		ccg Pro	_	_	_		624
											tac Tyr 220					672
											ata Ile					720
											ccc Pro					768
											Gly 999					816
											gtt Val					864
											acg Thr 300					912
											gag Glu					960
											acg Thr					1008
gtg Val	gct Ala	gct Ala	gcg Ala 340	ggc Gly	gct Ala	tgg Trp	gcg Ala	ctg Leu 345	gtc Val	gct Ala	cga Arg	cgg Arg	cgt Arg 350	agg Arg	ttg Leu	1056
					ccg Pro											1086
<210> 81 <211> 362 <212> PRT <213> Micromonospora carbonacea																
<220 <223)> 3> e1	/sB														
<400> 81																

Val Arg Ala Ser Pro Glu Thr Asp Gly Ala Leu Arg Ile Arg Ala Asp

Gln Trp His Leu Asn Tyr Leu Lys Ala Ala Glu Ala Gln Lys Leu Ser 20 25 30

Leu Gly Glu Gly Val Val Val Ala Val Pro Asp Thr Gly Val Asp Pro His Pro Asp Leu Gln Arg Asn Leu Ile Lys Gly Ile Asp Ile Ile Pro Gly Gly Asn Gly Asp Gly Gln Lys Asp Arg Asn Ser His Gly Thr Ser Met Ala Gly Leu Ile Ala Ala His Gly Gln Gly Gln Ser Gly Ala Leu Gly Ile Ala Pro Arg Ala Lys Ile Met Pro Ile Leu Ser Ser Ala Ser Asn Asn Leu Gly Asp Ala Asp Gly Leu Ala Ala Gly Ile Glu Phe Ala Ile Ser His Gly Ala Asp Val Ile Asn Val Ser Ser Gly Gly Ala Ser Val Arg Leu Ile Lys Ala Ile Arg Glu Ala Val Ala Ala Asp Ile 155 Val Val Ala Ala Ala Gly Asn Ser Pro Glu Asp Met Thr Ile Gly Tyr Pro Ala Ser Glu Glu Gly Val Val Ala Val Gly Gly Ile Asp Arg 185 Gln Gly Glu His Ala Ser Val Ser Val Gly Pro Glu Val Asp Leu 195 200 Val Ala Pro Ala Val Asp Ile Tyr Ser Thr Ser Tyr Asp Gly Lys Tyr Ser Lys Gly Thr Gly Thr Ser Ser Ala Thr Ala Ile Val Ala Gly Ala Ala Ala Leu Val Arg Ser Lys Phe Pro Asp Leu Pro Ala Ser Glu Val 245 250 Val His Arg Leu Thr Ala Thr Ala Ile Asp Lys Gly Pro Pro Gly His 265 Asp Asp Gln Tyr Gly Tyr Gly Val Ile Asp Leu Val Ala Ala Leu Thr Ala Asp Val Pro Pro Val Gly Phe Glu Ser Ala Thr Ala Asp Val Pro 295 300 Asp Val Pro Gly Ser Thr Thr Ala Val Ala Glu Pro Ala Gly Glu 315 Gly Asp Asp Gly Ala Thr Ala Arg Gly Leu Ala Thr Leu Gly Val Ile Val Ala Ala Ala Gly Ala Trp Ala Leu Val Ala Arg Arg Arg Leu 345 Ser Asp Asp Pro Pro Pro Arg Ile Ser Arg

360

```
<210> 82
<211> 666
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(666)
<220>
<223> evsC
gtg ccg aac tcg att tca ctc cga ctc gtg ctc gcg tcg gcg agc cct
                                                                      48
Val Pro Asn Ser Ile Ser Leu Arg Leu Val Leu Ala Ser Ala Ser Pro
                                       10
gee egt ege aag ete ete eae gee gee gge ate gaa eee gae gtg etg
                                                                      96
Ala Arg Arg Lys Leu Leu His Ala Ala Gly Ile Glu Pro Asp Val Leu
             20
gtc agt ggg gtc gac gag tcc cag gtg acc agc gag cga gcc gag gat
Val Ser Gly Val Asp Glu Ser Gln Val Thr Ser Glu Arg Ala Glu Asp
                                                                      144
         35
ctg tgc ctg gag ctg gcc cgc ctg aag gcg cag gcg gtc gtc ggc cgg
                                                                      192
Leu Cys Leu Glu Leu Ala Arg Leu Lys Ala Gln Ala Val Val Gly Arg
ctg cgc ccg tcg gcc gac gag cgg acg ctg gtg ctc ggc tgc gac tcg
                                                                     240
Leu Arg Pro Ser Ala Asp Glu Arg Thr Leu Val Leu Gly Cys Asp Ser
 65
                      70
gtg ctc gcc ttc gac cgc gag att ctc ggc aag ccg gcc gac gag gcg
                                                                      288
Val Leu Ala Phe Asp Arg Glu Ile Leu Gly Lys Pro Ala Asp Glu Ala
gac get acc egg egt tgg gag egg atg egg ggg ege age ggg gtg eta
                                                                     336
Asp Ala Thr Arg Arg Trp Glu Arg Met Arg Gly Arg Ser Gly Val Leu
            100
                                  105
cac acc ggg cac tgc ctg atc gac gtc atc cac gag acg cgc gcc gag
                                                                     384
His Thr Gly His Cys Leu Ile Asp Val Ile His Glu Thr Arg Ala Glu
                             120
gcg gtc gcc tcg acc acc gtg cgt ttc gct gac atc agc gac gag gag
                                                                      432
Ala Val Ala Ser Thr Thr Val Arg Phe Ala Asp Ile Ser Asp Glu Glu
    130
                         135
att gcc gcg tac gtc gcg acg ggc gaa ccg ctc gcg gtc gcc ggc gcg
                                                                      480
Ile Ala Ala Tyr Val Ala Thr Gly Glu Pro Leu Ala Val Ala Gly Ala
tte ace ate gae gga atg gge ggg geg tte etg gag ggt gte gae gge
                                                                     528
Phe Thr Ile Asp Gly Met Gly Gly Ala Phe Leu Glu Gly Val Asp Gly
                 165
gac ccg ggc acg gtc ggc ctc tcc cta ccg ttg ctg cgc cgg ctt
                                                                      576
Asp Pro Gly Thr Val Val Gly Leu Ser Leu Pro Leu Leu Arg Arg Leu
            180
ctc ggc gag ctg gac ctg cgg atc atc gac ctg tgg acg aag gtc gcg
                                                                     624
Leu Gly Glu Leu Asp Leu Arg Ile Ile Asp Leu Trp Thr Lys Val Ala
        195
                             200
```

666

ccg ggc ggc cag gcg gtc gag gcg gtg ggt acg gtc cag cca Pro Gly Gly Gln Ala Val Glu Ala Val Gly Thr Val Gln Pro <210> 83 <211> 222 <212> PRT <213> Micromonospora carbonacea <220> <223> evsC <400> 83 Val Pro Asn Ser Ile Ser Leu Arg Leu Val Leu Ala Ser Ala Ser Pro Ala Arg Arg Lys Leu Leu His Ala Ala Gly Ile Glu Pro Asp Val Leu Val Ser Gly Val Asp Glu Ser Gln Val Thr Ser Glu Arg Ala Glu Asp Leu Cys Leu Glu Leu Ala Arg Leu Lys Ala Gln Ala Val Val Gly Arg Leu Arg Pro Ser Ala Asp Glu Arg Thr Leu Val Leu Gly Cys Asp Ser Val Leu Ala Phe Asp Arg Glu Ile Leu Gly Lys Pro Ala Asp Glu Ala Asp Ala Thr Arg Arg Trp Glu Arg Met Arg Gly Arg Ser Gly Val Leu 105 His Thr Gly His Cys Leu Ile Asp Val Ile His Glu Thr Arg Ala Glu Ala Val Ala Ser Thr Thr Val Arg Phe Ala Asp Ile Ser Asp Glu Glu 135 Ile Ala Ala Tyr Val Ala Thr Gly Glu Pro Leu Ala Val Ala Gly Ala Phe Thr Ile Asp Gly Met Gly Gly Ala Phe Leu Glu Gly Val Asp Gly 170 Asp Pro Gly Thr Val Val Gly Leu Ser Leu Pro Leu Leu Arg Arg Leu 180 185 Leu Gly Glu Leu Asp Leu Arg Ile Ile Asp Leu Trp Thr Lys Val Ala Pro Gly Gly Gln Ala Val Glu Ala Val Gly Thr Val Gln Pro 215

<210> 84

<211> 651

<212> DNA

<213> Micromonospora carbonacea

<220>

<221> CDS

<222> (1)..(651)

<220>

<223> evbA

<400> 84

atg acg acg aag tcc ctg ccg ctg acc ccg gaa ctg cat gcg tac gtg

Met Thr Thr Lys Ser Leu Pro Leu Thr Pro Glu Leu His Ala Tyr Val

1 5 10 15

gtg gcc cac gga tcg gac ccg gac gag gtg atg cgg gat ctg atc gag 96 Val Ala His Gly Ser Asp Pro Asp Glu Val Met Arg Asp Leu Ile Glu

gag acc ctc gcc gcg ctg ccc gcc gag gcg agg atg cag gtg gcc ccg 144 Glu Thr Leu Ala Ala Leu Pro Ala Glu Ala Arg Met Gln Val Ala Pro

gag caa gcc gcg ttc ctg acg ttc ctc acc cgg ttg atc ggg gcg cgg 192 Glu Gln Ala Ala Phe Leu Thr Phe Leu Thr Arg Leu Ile Gly Ala Arg

cgg gcg gtg gag gtg ggc acc ttc acc ggc ctg tcc tcc ctg gcg atc 240 Arg Ala Val Glu Val Gly Thr Phe Thr Gly Leu Ser Ser Leu Ala Ile 65 70 75 80

gcg cgc ggg ctg gcc gag ggc ggg cgg ttg acc tgc ttc gac atc tcg 288
Ala Arg Gly Leu Ala Glu Gly Gly Arg Leu Thr Cys Phe Asp Ile Ser
85 90 95

gag gag tac acg ggc gtc gcg cgg cgg tac tgg gcg cgg gcc ggg gtg 336 Glu Glu Tyr Thr Gly Val Ala Arg Arg Tyr Trp Ala Arg Ala Gly Val 100 105 110

gcc gac cag atc gac ctg cgg atc ggg ccg gcc ggg gac acg ctg cgc 384
Ala Asp Gln Ile Asp Leu Arg Ile Gly Pro Ala Gly Asp Thr Leu Arg

ggg ttg ccg tac gaa cgg cac ctg gac ttc gcg ttc atc gac gcg gac 432 Gly Leu Pro Tyr Glu Arg His Leu Asp Phe Ala Phe Ile Asp Ala Asp 130 135

aag gtc ggc tac ccg gtc tac tgg gcg gag ttg gtg ccc cgc atg ctc 480 Lys Val Gly Tyr Pro Val Tyr Trp Ala Glu Leu Val Pro Arg Met Leu 145 150 160

ccg ggc ggg gtc atc gcg gtg gac aac acg ttg cgc ggg ggc cgg gtg 528
Pro Gly Gly Val Ile Ala Val Asp Asn Thr Leu Arg Gly Gly Arg Val
165 170 175

ctc gcc ccg cgt gac gcc gac ggc cgg gcc atc gcc gcg ttc aac gac 576 Leu Ala Pro Arg Asp Ala Asp Asp Arg Ala Ile Ala Ala Phe Asn Asp

gag gtg atg gcc gac gtc cgg gtg gag ccg gtg ctg ctg ccg atc gcc 624
Glu Val Met Ala Asp Val Arg Val Glu Pro Val Leu Leu Pro Ile Ala
195 200 205

gac ggg ctg acc ctg gcc cgg gtg cgc Asp Gly Leu Thr Leu Ala Arg Val Arg 210 215

```
<212> PRT
<213> Micromonospora carbonacea
<223> evbA
<400> 85
Met Thr Thr Lys Ser Leu Pro Leu Thr Pro Glu Leu His Ala Tyr Val
Val Ala His Gly Ser Asp Pro Asp Glu Val Met Arg Asp Leu Ile Glu
Glu Thr Leu Ala Ala Leu Pro Ala Glu Ala Arg Met Gln Val Ala Pro
                             40
Glu Gln Ala Ala Phe Leu Thr Phe Leu Thr Arg Leu Ile Gly Ala Arg
Arg Ala Val Glu Val Gly Thr Phe Thr Gly Leu Ser Ser Leu Ala Ile
Ala Arg Gly Leu Ala Glu Gly Gly Arg Leu Thr Cys Phe Asp Ile Ser
Glu Glu Tyr Thr Gly Val Ala Arg Arg Tyr Trp Ala Arg Ala Gly Val
                                105
Ala Asp Gln Ile Asp Leu Arg Ile Gly Pro Ala Gly Asp Thr Leu Arg
Gly Leu Pro Tyr Glu Arg His Leu Asp Phe Ala Phe Ile Asp Ala Asp
                        135
Lys Val Gly Tyr Pro Val Tyr Trp Ala Glu Leu Val Pro Arg Met Leu
Pro Gly Gly Val Ile Ala Val Asp Asn Thr Leu Arg Gly Gly Arg Val
                165
Leu Ala Pro Arg Asp Ala Asp Asp Arg Ala Ile Ala Ala Phe Asn Asp
                                185
Glu Val Met Ala Asp Val Arg Val Glu Pro Val Leu Leu Pro Ile Ala
       195
                            200
Asp Gly Leu Thr Leu Ala Arg Val Arg
   210
                        215
<210> 86
<211> 753
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(753)
<220>
```

<400> 86
atg aag ttc gcc cgc gac acc tgg ctc gtc gcc cag cgc cag atg caa

<223> evbB

Met 1	Lys	Phe	Ala	Arg 5	Asp	Thr	Trp	Leu	Val 10	Ala	Gln	Arg	Gln	Met 15	Gln	
				aat Asn												96
				ctc Leu												144
				gcc Ala												192
				atc Ile												240
				gcc Ala 85												288
				ctg Leu												336
ctg	ctc	gcc	cag	gcc	gtc	atc	atc	acc	ctg	ctc	gcg	ctc	ctg	ttc	gag	384
Leu	Leu	Ala 115	Gln	Ala	Val	Ile	Ile 120	Thr	Leu	Leu	Ala	Leu 125	Leu	Phe	Glu	
				atc Ile												432
ctg Leu 145	atc Ile	gcg Ala	ctg Leu	atg Met	acc Thr 150	tcg Ser	gcc Ala	gtc Val	tcg Ser	tac Tyr 155	ggc Gly	gtc Val	gcg Ala	ctc Leu	aag Lys 160	480
				gac Asp 165												528
				ctc Leu												576
ggc Gly	tgg Trp	ctc Leu 195	cag Gln	cgc Arg	atc Ile	gcc Ala	gag Glu 200	tgg Trp	aac Asn	ccg Pro	ttc Phe	tcc Ser 205	tgg Trp	gcc Ala	gtg Val	624
				gcc Ala												672
				acc Thr												720
				cag Gln 245												753

```
<210> 87
```

<211> 251

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> evbB

<400> 87

Met Lys Phe Ala Arg Asp Thr Trp Leu Val Ala Gln Arg Gln Met Gln 1 5 10 15

Leu Leu Arg Asn Pro Val Trp Val Phe Val Gly Val Phe Gln Pro
20 25 30

Val Met Tyr Leu Leu Leu Phe Ala Pro Leu Leu Lys Pro Ala Leu Asn 35 40 45

Ala Pro Thr Gln Ala Glu Ala Tyr Lys Ile Phe Val Pro Gly Leu Leu 50 55 60

Val Leu Leu Ala Ile Phe Gly Gly Leu Phe Gln Gly Phe Gly Leu Ile 65 70 75 80

Ala Glu Leu Arg Ala Gly Val Ile Glu Arg Ser Arg Val Thr Pro Val 85 90 95

Ser Arg Leu Ala Leu Leu Leu Gly Arg Ala Leu Arg Asp Val Val Ser 100 105 110

Leu Leu Ala Gln Ala Val Ile Ile Thr Leu Leu Ala Leu Leu Phe Glu
115 120 125

Leu Arg Val Phe Ile Gly Asp Leu Leu Leu Ala Tyr Leu Met Leu Ala 130 135 140

Leu Ile Ala Leu Met Thr Ser Ala Val Ser Tyr Gly Val Ala Leu Lys
145 150 155 160

Val Lys Ser Glu Asp Ala Leu Ala Pro Val Met Asn Thr Val Ala Gln 165 170 175

Pro Val Leu Leu Ser Gly Ile Leu Leu Pro Leu Thr Phe Ala Pro 180 185 190

Gly Trp Leu Gln Arg Ile Ala Glu Trp Asn Pro Phe Ser Trp Ala Val 195 200 205

Asp Gly Thr Arg Ala Leu Phe Ala Gly Asp Leu Gly Asn Asp Lys Val 210 215 220

Trp Gln Gly Leu Thr Ile Ile Ala Val Leu Ala Ala Val Gly Val Ala 225 230 235 240

Trp Ala Ala Arg Gln Phe Ala Arg Ser Val Arg 245 250

<210> 88

<211> 957

<212> DNA

<213> Micromonospora carbonacea

<221> CDS <222> (1)..(957) <220> <223> evbC <400> 88 atg atc cag acc aga ggg ctg cgg aag tcg ttt cgc tcc cgc gcc ggt 48 Met Ile Gln Thr Arg Gly Leu Arg Lys Ser Phe Arg Ser Arg Ala Gly cga cag cac aag acg gtc gac gcc gtg cgc gtc gac ctg gac gtc 96 Arg Gln His Lys Thr Val Asp Ala Val Arg Gly Val Asp Leu Asp Val 20 gcc gag ggg gag atc ttc ggg ttc ctc ggc ccc aac ggc gcc ggg aag 144 Ala Glu Gly Glu Ile Phe Gly Phe Leu Gly Pro Asn Gly Ala Gly Lys ace ace etg egg atg etg gee ace etc ate ace eee gae gge gge 192 Thr Thr Leu Arg Met Leu Ala Thr Leu Ile Thr Pro Asp Gly Gly 55 60 cag gcc acc atc gcc ggg gcc gac ctg ctg cgg aac ccg gcc gag gtg 240 Gln Ala Thr Ile Ala Gly Ala Asp Leu Leu Arg Asn Pro Ala Glu Val 70 75 cgt cgc cgg atc ggc tat gtc gcc cag ggc ggc agc acc tgg gac gac 288 Arg Arg Ile Gly Tyr Val Ala Gln Gly Gly Ser Thr Trp Asp Asp 85 90 tee ace gee ege gag gaa etg gte etg cac gee egg atg tac gge ate 336 Ser Thr Ala Arg Glu Glu Leu Val Leu His Ala Arg Met Tyr Gly Ile 105 ggc aag gcc gac gcc ctc cgc cgc gcc gag cgc gca ctg gcc gcc ttc 384 Gly Lys Ala Asp Ala Leu Arg Arg Ala Glu Arg Ala Leu Ala Ala Phe 115 cag etc ace gag tac gec gac egt aag tge aag ace tac tee gge gge 432 Gln Leu Thr Glu Tyr Ala Asp Arg Lys Cys Lys Thr Tyr Ser Gly Gly cag ege ege ege gte gag ate get ete gge ate ate eae gae eee ege 480 Gln Arg Arg Arg Val Glu Ile Ala Leu Gly Ile Ile His Asp Pro Arg 145 150 att gtc ttc ctg gac gag ccg acc agc ggc ctc gac ccg cag agt cgc 528 Ile Val Phe Leu Asp Glu Pro Thr Ser Gly Leu Asp Pro Gln Ser Arg 165 gcc cac atg tgg gac gag atc cgt cgg ctg cgc gcc gag ggg atg acc 576 Ala His Met Trp Asp Glu Ile Arg Arg Leu Arg Ala Glu Gly Met Thr gtc ttc atc acc acg cac tac ctg gac gag gcc gac gcg ctc tgc gac 624 Val Phe Ile Thr Thr His Tyr Leu Asp Glu Ala Asp Ala Leu Cys Asp 200 egg ate geg ate atg gae cae gge gag gtg gte gee gag ggt aeg eeg 672 Arg Ile Ala Ile Met Asp His Gly Glu Val Val Ala Glu Gly Thr Pro 215 ggc ggg ctg aag cgg gag atc tcc ggc gag gtg ctg ctc gtc ggg ctg 720

225	Lys Arg	Glu 230	Ile	Ser	Gly	Glu	Val 235	Leu	Leu	Val	Gly	Leu 240	
gac gcc gcc Asp Ala Ala													768
tac gtc acc Tyr Val Thr	aag ctg Lys Leu 260	gaa Glu	acc Thr	gtc Val	gac Asp 265	ggc Gly	ggc Gly	ggc Gly	ctg Leu	cgc Arg 270	ctg Leu	acc Thr	816
gtc gac gag Val Asp Glu 275													864
cag tcc ggc Gln Ser Gly 290		Leu											912
gac gac gtc Asp Asp Val 305													957
<210> 89 <211> 319 <212> PRT <213> Micro	monospor	a car	bona	ıcea									
<220> <223> evbC													
<400> 89 Met Ile Gln 1	Thr Arg	Gly :	Leu	Arg	Lys	Ser 10	Phe	Arg	Ser	Arg	Ala 15	Gly	
Met Ile Gln	5	_		_	_	10					15	-	
Met Ile Gln 1	Lys Thr	Val .	Asp	Ala	Val 25	10 Arg	Gly	Val	Asp	Leu 30	15 Asp	Val	
Met Ile Gln 1 Arg Gln His Ala Glu Gly	Lys Thr 20 Glu Ile	Val .	Asp Gly	Ala Phe 40	Val 25 Leu	10 Arg Gly	Gly Pro	Val Asn	Asp Gly 45	Leu 30 Ala	15 Asp Gly	Val Lys	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr	Lys Thr 20 Glu Ile Leu Arg	Val .	Asp Gly Leu 55	Ala Phe 40 Ala	Val 25 Leu Thr	10 Arg Gly Leu	Gly Pro	Val Asn Thr	Asp Gly 45 Pro	Leu 30 Ala Asp	15 Asp Gly Gly	Val Lys Gly	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr 50 Gln Ala Thr	Lys Thr 20 Glu Ile Leu Arg Ile Ala	Val A	Asp Gly Leu 55 Ala	Ala Phe 40 Ala Asp	Val 25 Leu Thr	10 Arg Gly Leu Leu	Cly Pro Ile Arg 75	Val Asn Thr 60 Asn	Asp Gly 45 Pro	Leu 30 Ala Asp	15 Asp Gly Gly	Val Lys Gly Val	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr 50 Gln Ala Thr 65	Lys Thr 20 Glu Ile Leu Arg Ile Ala Ile Gly 85	Val A	Asp Gly Leu 55 Ala Val	Ala Phe 40 Ala Asp	Val 25 Leu Thr Leu Gln	10 Arg Gly Leu Leu Gly 90	Cly Pro Ile Arg 75	Val Asn Thr 60 Asn	Asp Gly 45 Pro Pro	Leu 30 Ala Asp Ala Trp	15 Asp Gly Gly Glu Asp 95	Val Lys Gly Val 80 Asp	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr 50 Gln Ala Thr 65 Arg Arg Arg	Lys Thr 20 Glu Ile Leu Arg Ile Ala Ile Gly 85 Arg Glu 100	Val American Phe Gly 70 Tyr Glu	Asp Gly Leu 55 Ala Val Leu	Ala Phe 40 Ala Asp Ala Val	Val 25 Leu Thr Leu Gln Leu 105	10 Arg Gly Leu Leu Gly 90 His	Gly Pro Ile Arg 75 Gly Ala	Val Asn Thr 60 Asn Ser	Asp Gly 45 Pro Pro Thr	Leu 30 Ala Asp Ala Trp Tyr 110	Asp Gly Glu Asp 95	Val Lys Gly Val 80 Asp	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr 50 Gln Ala Thr 65 Arg Arg Arg Ser Thr Ala Gly Lys Ala	Lys Thr 20 Glu Ile Leu Arg Ile Ala Ile Gly 85 Arg Glu 100 Asp Ala	Val Ala	Asp Gly Leu 55 Ala Val Leu	Ala Phe 40 Ala Asp Ala Val Arg	Val 25 Leu Thr Leu Gln Leu 105 Ala	10 Arg Gly Leu Leu Gly 90 His	Gly Pro Ile Arg 75 Gly Ala Arg	Val Asn Thr 60 Asn Ser Arg	Asp Gly 45 Pro Pro Thr Met Leu 125	Leu 30 Ala Asp Ala Trp Tyr 110 Ala	Asp Gly Glu Asp 95 Gly Ala	Val Lys Gly Val 80 Asp Ile	
Met Ile Gln 1 Arg Gln His Ala Glu Gly 35 Thr Thr Thr 50 Gln Ala Thr 65 Arg Arg Arg Ser Thr Ala Gly Lys Ala 115 Gln Leu Thr	Lys Thr 20 Glu Ile Leu Arg Ile Ala Ile Gly 85 Arg Glu 100 Asp Ala Glu Tyr	Phe Met : Gly 70 Tyr Glu : Leu Ala	Asp Gly Leu 55 Ala Val Leu Arg Asp	Ala Phe 40 Ala Asp Ala Val Arg 120 Arg	Val 25 Leu Thr Leu Gln Leu 105 Ala	10 Arg Gly Leu Leu Gly 90 His Glu Cys	Gly Pro Ile Arg 75 Gly Ala Arg	Val Asn Thr 60 Asn Ser Arg Ala Thr 140	Asp Gly 45 Pro Pro Thr Met Leu 125 Tyr	Leu 30 Ala Asp Ala Trp Tyr 110 Ala Ser	Asp Gly Glu Asp 95 Gly Ala	Val Lys Gly Val 80 Asp Ile Phe Gly	

Ala His Met Trp Asp Glu Ile Arg Arg Leu Arg Ala Glu Gly Met Thr

```
Val Phe Ile Thr Thr His Tyr Leu Asp Glu Ala Asp Ala Leu Cys Asp
                            200
Arg Ile Ala Ile Met Asp His Gly Glu Val Val Ala Glu Gly Thr Pro
Gly Gly Leu Lys Arg Glu Ile Ser Gly Glu Val Leu Leu Val Gly Leu
                    230
                                        235
Asp Ala Ala Ala Thr Pro Gln Ala Ala Gln Leu Leu Asp Thr Glu Pro
                245
                                    250
Tyr Val Thr Lys Leu Glu Thr Val Asp Gly Gly Leu Arg Leu Thr
Val Asp Glu Gly Ala Thr Ala Ile Pro Gln Val Leu Arg Arg Leu Asp
Gln Ser Gly Leu Arg Leu Ser Ser Ile Glu Leu His Arg Pro Ser Leu
    290
                        295
                                            300
Asp Asp Val Phe Leu Thr Lys Thr Gly Arg Ser Leu Arg Glu Ser
305
                    310
                                        315
<210> 90
<211> 594
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(594)
<220>
<223> evbC2
atg atg att ctc ggc ctg gtc aag tgg atg cag ccg gtg cac ggc tac
                                                                   48
Met Met Ile Leu Gly Leu Val Lys Trp Met Gln Pro Val His Gly Tyr
gac gtc cgc cgc gag ctg ctc agt tgg ggt gcc gac aag tgg gcc aac
Asp Val Arg Arg Glu Leu Leu Ser Trp Gly Ala Asp Lys Trp Ala Asn
            20
gtg cag ccc ggc tcg atc tac cac gcg ctg cgc aag ctc ggc gag gag
                                                                   144
Val Gln Pro Gly Ser Ile Tyr His Ala Leu Arg Lys Leu Gly Glu Glu
ggg ctg ctc cgc gag gtc gcc acc gag cag gtc ggc gcc cgg cgg gcg
                                                                   192
Gly Leu Leu Arg Glu Val Ala Thr Glu Gln Val Gly Ala Arg Arg Ala
     50
                         55
                                             60
cgg acg acg tac gag atc acc ccg aag ggg gtc gac gag ttc gag acg
                                                                   240
Arg Thr Thr Tyr Glu Ile Thr Pro Lys Gly Val Asp Glu Phe Glu Thr
65
ctg ctg cgc ggc ctg tgg tgg ggc aat cat cag acg agc gat ccg ttc
Leu Leu Arg Gly Leu Trp Trp Gly Asn His Gln Thr Ser Asp Pro Phe
```

85 90 95 gtg gcg gcg ttc gcg ttc ctg ccg gcg ctg ccc agg ccg gag gcg gtg 336 Val Ala Ala Phe Ala Phe Leu Pro Ala Leu Pro Arg Pro Glu Ala Val 100 105 110 gcc gcg ctg cgc agt cgg ggg cag gtg ctg cgg gcc agt gtc gaa acc 384 Ala Ala Leu Arg Ser Arg Gly Gln Val Leu Arg Ala Ser Val Glu Thr 115 atg cgt gcc tcg atg gag tcc tcc tgg atc cgc gac tcc aag ccg gtc 432 Met Arg Ala Ser Met Glu Ser Ser Trp Ile Arg Asp Ser Lys Pro Val 130 135 ggc gtg agc tgg atg tac gag ctg tgg att gcc cgg gga gag gtc gag 480 Gly Val Ser Trp Met Tyr Glu Leu Trp Ile Ala Arg Gly Glu Val Glu gtg gcc tgg tgt gag cgg gtc gcc gac cgg atc gag gcc ggc gtg ccg 528 Val Ala Trp Cys Glu Arg Val Ala Asp Arg Ile Glu Ala Gly Val Pro 165 tat ctg ccc gaa ggg ttg gcc agt cag gac ggc tgg aac gtg ggg gag 576 Tyr Leu Pro Glu Gly Leu Ala Ser Gln Asp Gly Trp Asn Val Gly Glu 185 ggg gcc gac ggt cgc cat 594 Gly Ala Asp Gly Arg His 195 <210> 91 <211> 198 <212> PRT <213> Micromonospora carbonacea <220> <223> evbC2 <400> 91 Met Met Ile Leu Gly Leu Val Lys Trp Met Gln Pro Val His Gly Tyr Asp Val Arg Arg Glu Leu Leu Ser Trp Gly Ala Asp Lys Trp Ala Asn 20 Val Gln Pro Gly Ser Ile Tyr His Ala Leu Arg Lys Leu Gly Glu Glu 40 Gly Leu Leu Arg Glu Val Ala Thr Glu Gln Val Gly Ala Arg Arg Ala Arg Thr Thr Tyr Glu Ile Thr Pro Lys Gly Val Asp Glu Phe Glu Thr Leu Leu Arg Gly Leu Trp Trp Gly Asn His Gln Thr Ser Asp Pro Phe Val Ala Ala Phe Ala Phe Leu Pro Ala Leu Pro Arg Pro Glu Ala Val Ala Ala Leu Arg Ser Arg Gly Gln Val Leu Arg Ala Ser Val Glu Thr 120 Met Arg Ala Ser Met Glu Ser Ser Trp Ile Arg Asp Ser Lys Pro Val

130 135 140 Gly Val Ser Trp Met Tyr Glu Leu Trp Ile Ala Arg Gly Glu Val Glu Val Ala Trp Cys Glu Arg Val Ala Asp Arg Ile Glu Ala Gly Val Pro 165 170 Tyr Leu Pro Glu Gly Leu Ala Ser Gln Asp Gly Trp Asn Val Gly Glu 185 Gly Ala Asp Gly Arg His 195 <210> 92 <211> 1746 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1746) <220> <223> evbD <400> 92 gtg cgc aag gta ctc atc gcc aac cga ggc gag atc gcc gtc cgc gtc 48 Val Arg Lys Val Leu Ile Ala Asn Arg Gly Glu Ile Ala Val Arg Val ate ege gee tge ege gae gee gge etg gge age gte gee gte tae geg 96 Ile Arg Ala Cys Arg Asp Ala Gly Leu Gly Ser Val Ala Val Tyr Ala gac tee gae egg gae gee etg cae geg ace etg gee gae gag geg tae 144 Asp Ser Asp Arg Asp Ala Leu His Ala Thr Leu Ala Asp Glu Ala Tyr 40 gcc ctg ggc ggc gac acc gcc gcc gag acg tac ctg cgg atc gac aag 192 Ala Leu Gly Gly Asp Thr Ala Ala Glu Thr Tyr Leu Arg Ile Asp Lys 55 ctg atc gcc gtc gcg gca cag gcc ggg gcc gac gcc gtc cac ccc ggg 240 Leu Ile Ala Val Ala Ala Gln Ala Gly Ala Asp Ala Val His Pro Gly 70 75 tac ggc ttc ctc gcc gag aac gcc gac ttc gcc cag gcc gtc ctc gac 288 Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Gln Ala Val Leu Asp 85 gcc ggg ctt acc tgg atc ggc ccg acc cca cag gcg atc cgc gac ctg 336 Ala Gly Leu Thr Trp Ile Gly Pro Thr Pro Gln Ala Ile Arg Asp Leu 100 105 ggc gac aag gtc acc gcc cgg cac atc gcc cag cgg gcc ggc gcg ccc 384 Gly Asp Lys Val Thr Ala Arg His Ile Ala Gln Arg Ala Gly Ala Pro 115 ctg gtt ccc ggt acc tcg gac ccg gtc ggc agc ccg gac gag gtg atc 432 Leu Val Pro Gly Thr Ser Asp Pro Val Gly Ser Pro Asp Glu Val Ile

135

gca Ala 145	ttc Phe	gcg Ala	gtc Val	gac Asp	cac His 150	ggc Gly	ctg Leu	ccg Pro	gtc Val	gcc Ala 155	atc Ile	aag Lys	gcc Ala	gcc Ala	ttc Phe 160	480
						ctc Leu										528
ccg Pro	cac His	ctg Leu	ttc Phe 180	gag Glu	tcg Ser	gcc Ala	acc Thr	cgg Arg 185	gag Glu	gcg Ala	gtc Val	gcg Ala	gcg Ala 190	ttc Phe	ggc Gly	576
						gag Glu										624
						gac Asp 215										672
						caa Gln										720
gcc Ala	ccc Pro	gcg Ala	ccg Pro	ttc Phe 245	ctc Leu	acc Thr	gac Asp	gcc Ala	cag Gln 250	cgc Arg	cgg Arg	cag Gln	atc Ile	cac His 255	gac Asp	768
						cgg Arg										816
						acg Thr										864
						gag Glu 295										912
atc Ile 305	gac Asp	ctc Leu	gtc Val	cgc Arg	gag Glu 310	cag Gln	ttc Phe	cgg Arg	atc Ile	gcc Ala 315	gac Asp	ggc Gly	gag Glu	aag Lys	ctg Leu 320	960
						acc Thr										1008
						ggc Gly										1056
gtc Val	acc Thr	gcg Ala 355	ctg Leu	cgg Arg	ctg Leu	ccc Pro	acc Thr 360	ggc Gly	ccc Pro	ggt Gly	gtc Val	cgg Arg 365	gtg Val	gac Asp	acc Thr	1104
ggc Gly	atc Ile 370	tcc Ser	gcc Ala	ggc Gly	gac Asp	gtg Val 375	atc Ile	ggc Gly	ggc Gly	aac Asn	ttc Phe 380	gac Asp	tcc Ser	ctg Leu	ctg Leu	1152
gcc Ala 385	aag Lys	gtg Val	atc Ile	atc Ile	acg Thr 390	ggc Gly	gag Glu	acc Thr	cgc Arg	acc Thr 395	gag Glu	gcc Ala	ctg Leu	gag Glu	cgg Arg 400	1200
gcc	cgg	cgg	gcg	ctg	gac	gag	atg	gtc	gtc	gag	gga	atg	gcc	acg	gcg	1248

Ala Arg Arg A	Ala Leu Asp 405	Glu Met Va	Val Glu Gly 410	Met Ala Thr 415	Ala
ctg ccg ttc c Leu Pro Phe H 4			Asp Pro Ala		
ccg ttc acc g Pro Phe Thr V 435					
gtc ctg ccg t Val Leu Pro P 450	ttc acc gcc Phe Thr Ala	gcc gcc ggc Ala Ala Gly 455	c ccc gcc gag Pro Ala Glu 460	ggc ccg gcc Gly Pro Ala	gag 1392 Glu
cgg gag acc g Arg Glu Thr V 465	gtc gtg gtc Val Val Val 470	Glu Val Gly	ggc aag cgg Gly Lys Arg 475	ctg gag gtg Leu Glu Val	acc 1440 Thr 480
ctc ccc gcc g Leu Pro Ala G					
aag ccg gcc c Lys Pro Ala A 5	egg egg gge Arg Arg Gly 500	ggc ggg gcc Gly Gly Ala 505	Lys Ala Gly	gcg gcg gtc Ala Ala Val 510	ggc 1536 Gly
ggc gac gcc c Gly Asp Ala L 515					
gtc gcg gac g Val Ala Asp G 530					
gag gcg atg a Glu Ala Met L 545					
gtc ggc ggg c Val Gly Gly L	etg tee gee Leu Ser Ala 565	gag gtc ggc Glu Val Gly	gcg gtc ctc Ala Val Leu 570	gcc gcc ggc Ala Ala Gly 575	gcc 1728 Ala
ccc atc tgc a Pro Ile Cys T 5					1746
<210> 93 <211> 582 <212> PRT <213> Micromo	onospora ca	rbonacea			
<220> <223> evbD					
<400> 93 Val Arg Lys V 1	/al Leu Ile 5	Ala Asn Arg	Gly Glu Ile 10	Ala Val Arg 15	Val
Ile Arg Ala C	Cys Arg Asp 20	Ala Gly Let		Ala Val Tyr 30	Ala
Asp Ser Asp A 35	Arg Asp Ala	Leu His Ala 40	Thr Leu Ala	Asp Glu Ala 45	Tyr

Ala Leu Gly Gly Asp Thr Ala Ala Glu Thr Tyr Leu Arg Ile Asp Lys Leu Ile Ala Val Ala Ala Gln Ala Gly Ala Asp Ala Val His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Gln Ala Val Leu Asp Ala Gly Leu Thr Trp Ile Gly Pro Thr Pro Gln Ala Ile Arg Asp Leu 105 Gly Asp Lys Val Thr Ala Arg His Ile Ala Gln Arg Ala Gly Ala Pro 115 120 Leu Val Pro Gly Thr Ser Asp Pro Val Gly Ser Pro Asp Glu Val Ile Ala Phe Ala Val Asp His Gly Leu Pro Val Ala Ile Lys Ala Ala Phe Gly Gly Gly Arg Gly Leu Lys Val Ala Arg Thr Met Glu Glu Ile 170 Pro His Leu Phe Glu Ser Ala Thr Arg Glu Ala Val Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Gln Pro Arg His Val Glu Ala Gln Val Leu Ala Asp Gln His Gly Asn Val Ile Val Val Gly 215 Thr Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Leu Val Glu Glu 230 235 Ala Pro Ala Pro Phe Leu Thr Asp Ala Gln Arg Arg Gln Ile His Asp Ser Ala Lys Ala Ile Cys Arg Glu Ala Gly Tyr His Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Thr Asp Gly Thr Ile Ser Phe Leu Glu Val 280 Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr Ala Gly 295 Ile Asp Leu Val Arg Glu Gln Phe Arg Ile Ala Asp Gly Glu Lys Leu 315 Arg Leu Ala Glu Asp Pro Thr Pro Arg Gly His Ser Ile Glu Phe Arg 330 Ile Asn Gly Glu Asp Pro Gly Arg Asn Phe Leu Pro Ala Pro Gly Thr 345 Val Thr Ala Leu Arg Leu Pro Thr Gly Pro Gly Val Arg Val Asp Thr 360 Gly Ile Ser Ala Gly Asp Val Ile Gly Gly Asn Phe Asp Ser Leu Leu

Ala Lys Val Ile Ile Thr Gly Glu Thr Arg Thr Glu Ala Leu Glu Arg 395 Ala Arg Arg Ala Leu Asp Glu Met Val Val Glu Gly Met Ala Thr Ala 405 Leu Pro Phe His Arg Leu Val Val Arg Asp Pro Ala Phe Thr Ala Ala 425 Pro Phe Thr Val His Thr Arg Trp Ile Glu Thr Glu Phe Asp Asn Thr Val Leu Pro Phe Thr Ala Ala Gly Pro Ala Glu Gly Pro Ala Glu Arg Glu Thr Val Val Glu Val Gly Gly Lys Arg Leu Glu Val Thr 470 Leu Pro Ala Gly Leu Gly Ala Gly Thr Ala Ala Gly Pro Ala Ala Arg Lys Pro Ala Arg Arg Gly Gly Gly Ala Lys Ala Gly Ala Ala Val Gly Gly Asp Ala Leu Thr Ser Pro Met Gln Gly Thr Ile Val Lys Ile Ala Val Ala Asp Gly Asp Thr Val Ala Lys Gly Asp Leu Val Val Leu 535 Glu Ala Met Lys Met Glu Gln Pro Leu His Ala His Lys Ala Gly Thr Val Gly Gly Leu Ser Ala Glu Val Gly Ala Val Leu Ala Ala Gly Ala 570 Pro Ile Cys Thr Ile Thr 580 <210> 94 <211> 1437 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1437) <220> <223> evbE <400> 94 gtg cgg ttc cta cat ggc gcg gtt ccc gcg cac gac ctg acc tac aac Val Arg Phe Leu His Gly Ala Val Pro Ala His Asp Leu Thr Tyr Asn gac gtc ttc atg gcg ccg aac cgc tcc gag gtc ggc tcc cgg ttg gac 96 Asp Val Phe Met Ala Pro Asn Arg Ser Glu Val Gly Ser Arg Leu Asp gtc gac ctg gcc acc tcc gac ggc acg ggc acc acc atc ccg ctg gtg 144 Val Asp Leu Ala Thr Ser Asp Gly Thr Gly Thr Thr Ile Pro Leu Val 40

gtg Val	gcg Ala 50	aac Asn	atg Met	acg Thr	gcg Ala	gtg Val 55	gcc Ala	ggc Gly	cgg Arg	cgg Arg	atg Met 60	gcc Ala	gag Glu	act Thr	gtc Val	192
						gcg Ala										240
						gcc Ala										288
gac Asp	acg Thr	gcg Ala	atc Ile 100	acg Thr	ctc Leu	ggc Gly	ccc Pro	acc Thr 105	gac Asp	acc Thr	gtc Val	ggc Gly	gat Asp 110	gcc Ala	atc Ile	336
						tcg Ser										384
						gtg Val 135										432
						cgc Arg										480
						ccg Pro										528
ggc Gly	cgg Arg	cgg Arg	cgg Arg 180	ctc Leu	gcg Ala	ccg Pro	gtg Val	gtg Val 185	gac Asp	ggc Gly	gac Asp	ggc Gly	cgg Arg 190	ctc Leu	gtc Val	576
						ggc Gly										624
						cgg Arg 215										672
aac Asn 225	ggc Gly	gac Asp	gtc Val	acc Thr	ggc Gly 230	aag Lys	gcc Ala	gcc Ala	gcg Ala	ctg Leu 235	ctg Leu	gag Glu	gcc Ala	gly ggg	gtc Val 240	720
gac Asp	gcc Ala	ctg Leu	gtg Val	gtg Val 245	gac Asp	acc Thr	gcg Ala	cac His	ggc Gly 250	cac His	cag Gln	gcg Ala	cgg Arg	atg Met 255	gtc Val	768
gcc Ala	gcg Ala	ctg Leu	cgg Arg 260	gcg Ala	gtg Val	cgc Arg	aag Lys	ctt Leu 265	cac His	ccg Pro	ggc Gly	gtt Val	ccg Pro 270	gtc Val	gcg Ala	816
gcc Ala	ggc Gly	aac Asn 275	gtg Val	gtc Val	acc Thr	gcc Ala	gat Asp 280	gly aaa	gta Val	cgc Arg	gac Asp	ctc Leu 285	gtc Val	gag Glu	gcc Ala	864
ggc Gly	gcc Ala 290	gac Asp	atc Ile	gtg Val	aag Lys	gtg Val 295	ggc Gly	gtc Val	ggt Gly	ccg Pro	ggc Gly 300	gcg Ala	atg Met	tgc Cys	acc Thr	912

acc cgg atg atg Thr Arg Met Met 305					960
gac tgc gcg gcg Asp Cys Ala Ala					1008
ggc ggg gta cgg Gly Gly Val Arg 340			Leu Ala Leu A		1056
gcg tcg aac gtg Ala Ser Asn Val 355	Met Ile Gly				1104
ccg ggt gac ctg Pro Gly Asp Leu 370					1152
ttc ggg atg gcc Phe Gly Met Ala 385					1200
agc gcg ttc gac Ser Ala Phe Asp					1248
tcg gcc cgg atg Ser Ala Arg Met 420			Pro Gly Val G		1296
atc gac gag atc Ile Asp Glu Ile 435	Ile Ser Gly				1344
gcg cgc agc ctg Ala Arg Ser Leu 450					1392
agc acg gcc ggc Ser Thr Ala Gly 465					1437
<210> 95 <211> 479 <212> PRT <213> Micromonos	spora carbona	cea			
<220> <223> evbE					
<400> 95 Val Arg Phe Leu 1	His Gly Ala 5	Val Pro Ala 10	His Asp Leu T	hr Tyr Asn 15	
Asp Val Phe Met	Ala Pro Asn	Arg Ser Glu 25	Val Gly Ser A	rg Leu Asp 30	
Val Asp Leu Ala 35	Thr Ser Asp	Gly Thr Gly 40	Thr Thr Ile F	ro Leu Val	
Val Ala Asn Met 50	Thr Ala Val 55	Ala Gly Arg	Arg Met Ala G 60	lu Thr Val	

Ala Arg Arg Gly Ala Leu Ala Val Ile Pro Gln Asp Ile Pro Ile Glu Val Val Ala Asn Val Val Ala Trp Val Lys Gln Arg His Leu Val His Asp Thr Ala Ile Thr Leu Gly Pro Thr Asp Thr Val Gly Asp Ala Ile His Leu Leu Pro Lys Arg Ser His Gly Ala Val Val Val Asp Glu Ala Gly Arg Pro Leu Gly Val Val Thr Glu Ala Asp Thr Val Gly Val 135 Asp Arg Phe Ala Gln Leu Arg His Val Met Ser Thr Glu Leu His Thr Val Pro Ala Asp Ala Asp Pro Arg Thr Gly Phe Asp Arg Leu Ser Ala Gly Arg Arg Arg Leu Ala Pro Val Val Asp Gly Asp Gly Arg Leu Val 185 Gly Val Leu Thr Arg Lys Gly Ala Leu Arg Ala Thr Leu Tyr Thr Pro 200 Ala Val Asp Asp Arg Gly Arg Leu Arg Ile Ala Ala Val Gly Ile Asn Gly Asp Val Thr Gly Lys Ala Ala Ala Leu Leu Glu Ala Gly Val 235 Asp Ala Leu Val Val Asp Thr Ala His Gly His Gln Ala Arg Met Val Ala Ala Leu Arg Ala Val Arg Lys Leu His Pro Gly Val Pro Val Ala 265 Ala Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asp Ile Val Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Met Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu 310 315 Asp Cys Ala Ala Ala Arg Asp Leu Gly Arg His Val Trp Ala Asp Gly Gly Val Arg His Pro Arg Asp Val Ala Leu Ala Leu Ala Gly 345 Ala Ser Asn Val Met Ile Gly Ser Trp Phe Ala Gly Thr Tyr Glu Ser 360 Pro Gly Asp Leu Tyr Thr Asp Ala Asp Gly Arg Arg Tyr Lys Glu Ser 370 Phe Gly Met Ala Ser Ser Arg Ala Val Ser Ala Arg Thr Ala Glu Asp 395 Ser Ala Phe Asp Arg Ala Arg Lys Gly Ile Phe Glu Glu Gly Ile Ser

405 410 415 Ser Ala Arg Met Tyr Leu Asp Pro Asp Arg Pro Gly Val Glu Asp Leu 425 Ile Asp Glu Ile Ile Ser Gly Val Arg Ser Ala Cys Thr Tyr Ala Gly Ala Arg Ser Leu Ala Glu Phe Ala Glu Arg Ala Leu Val Gly Val Gln Ser Thr Ala Gly Tyr Thr Glu Gly Met Pro Leu Pro Thr Ser Trp <210> 96 <211> 555 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(555) <220> <223> evbF <400> 96 atg acc gga ccg cgt ggc tac cat cac ggt gac ctg cgt cgc gcc ctg 48 Met Thr Gly Pro Arg Gly Tyr His His Gly Asp Leu Arg Arg Ala Leu 10 ctc gcc gcc gcc gtc gac gcg atc acc gac gcc ggg ccg gcc gcc ctg 96 Leu Ala Ala Ala Val Asp Ala Ile Thr Asp Ala Gly Pro Ala Ala Leu age etg ege gae etg gee ege egg gee ggg gte teg eae gee eee 144 Ser Leu Arg Asp Leu Ala Arg Arg Ala Gly Val Ser His Ala Ala Pro gcg cac cac ttc ggc gac aag gcg ggg ctg ctc acc gcg ctc gcc gtc 192 Ala His His Phe Gly Asp Lys Ala Gly Leu Leu Thr Ala Leu Ala Val gag gga ttc gac ctg ctg gcc ggg gcg ctg tgc gag gcc ggc gac ctg 240 Glu Gly Phe Asp Leu Leu Ala Gly Ala Leu Cys Glu Ala Gly Asp Leu 70 ctc gac gcc ggc gtg gcg tac gtc cgg ttc gcg gtc gac cac cgg gcc 288 Leu Asp Ala Gly Val Ala Tyr Val Arg Phe Ala Val Asp His Arg Ala cac ttc gag gtg atg ttc cgc ccg gag ctc tac cgt cgc gac gac ccc 336 His Phe Glu Val Met Phe Arg Pro Glu Leu Tyr Arg Arg Asp Asp Pro gag gtg aca gcc gcc cgt gat cgg gcc ggc gcg gcg ctg cgg gcc ggg 384 Glu Val Thr Ala Ala Arg Asp Arg Ala Gly Ala Ala Leu Arg Ala Gly 115 432 Val Ala Ala Leu Pro Arg Arg Glu Thr Asp Pro Asp Gln Glu Ala Asp

555

gee etg gee gee tgg teg ate gtg eac gge tte gtg aca etc tgg etg Ala Leu Ala Ala Trp Ser Ile Val His Gly Phe Val Thr Leu Trp Leu gec ggg geg etc eeg eec gge acc gge eeg gac eeg gag gee gec gee Ala Gly Ala Leu Pro Pro Gly Thr Gly Pro Asp Pro Glu Ala Ala Ala 165 cgg acc gtc atc cgt cgc ctc ttc gac Arg Thr Val Ile Arg Arg Leu Phe Asp <210> 97 <211> 185 <212> PRT <213> Micromonospora carbonacea <220> <223> evbF Met Thr Gly Pro Arg Gly Tyr His His Gly Asp Leu Arg Arg Ala Leu Leu Ala Ala Val Asp Ala Ile Thr Asp Ala Gly Pro Ala Ala Leu Ser Leu Arg Asp Leu Ala Arg Arg Ala Gly Val Ser His Ala Ala Pro Ala His His Phe Gly Asp Lys Ala Gly Leu Leu Thr Ala Leu Ala Val Glu Gly Phe Asp Leu Leu Ala Gly Ala Leu Cys Glu Ala Gly Asp Leu Leu Asp Ala Gly Val Ala Tyr Val Arg Phe Ala Val Asp His Arg Ala His Phe Glu Val Met Phe Arg Pro Glu Leu Tyr Arg Arg Asp Asp Pro 105 Glu Val Thr Ala Ala Arg Asp Arg Ala Gly Ala Ala Leu Arg Ala Gly Val Ala Ala Leu Pro Arg Arg Glu Thr Asp Pro Asp Gln Glu Ala Asp Ala Leu Ala Ala Trp Ser Ile Val His Gly Phe Val Thr Leu Trp Leu Ala Gly Ala Leu Pro Pro Gly Thr Gly Pro Asp Pro Glu Ala Ala Ala

Arg Thr Val Ile Arg Arg Leu Phe Asp

<210> 98

<211> 270

<212> DNA

<213> Micromonospora carbonacea

144

192

240

270

```
<220>
<221> CDS
<222> (1)..(270)
<220>
<223> evbF1
<400> 98
atg gtg ccg ccc cga ctg ccc cac ccg ggg ctg ctg gtg acc gtc acc
Met Val Pro Pro Arg Leu Pro His Pro Gly Leu Leu Val Thr Val Thr
                                    10
gge etg etg gag ttg gee gge geg gte geg etg ete gte eee gge aeg
Gly Leu Leu Glu Leu Ala Gly Ala Val Ala Leu Leu Val Pro Gly Thr
            20
                                25
gcg cgg tgg gca gcg gcc ggg ctg ggg ctg ctg ctc gcg atg ttc
Ala Arg Trp Ala Ala Ala Gly Leu Gly Leu Leu Leu Ala Met Phe
ceg gec aac gec teg gec gec egg ege ggg etg acc etg gec gge egg
Pro Ala Asn Ala Ser Ala Ala Arg Arg Gly Leu Thr Leu Ala Gly Arg
                        55
ceg gtg acc ceg etc gtc cec egc geg etg etc eag gtg atc ttc etc
Pro Val Thr Pro Leu Val Pro Arg Ala Leu Leu Gln Val Ile Phe Leu
                    70
acc gcc gcc gcg att tcg ttt ggg ccc
Thr Ala Ala Ala Ile Ser Phe Gly Pro
                85
<210> 99
<211> 90
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evbF1
Met Val Pro Pro Arg Leu Pro His Pro Gly Leu Leu Val Thr Val Thr
Gly Leu Leu Glu Leu Ala Gly Ala Val Ala Leu Leu Val Pro Gly Thr
Ala Arg Trp Ala Ala Ala Gly Leu Gly Leu Leu Leu Ala Met Phe
Pro Ala Asn Ala Ser Ala Ala Arg Arg Gly Leu Thr Leu Ala Gly Arg
Pro Val Thr Pro Leu Val Pro Arg Ala Leu Leu Gln Val Ile Phe Leu
Thr Ala Ala Ala Ile Ser Phe Gly Pro
```

<210> 100 <211> 456 <212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(456)
<220>
<223> evbF2
<400> 100
gtg cca ctc ggc cgg ctg ctg gtg acc gcc ggc cac gtc gtc ggc caa
                                                                   48
Val Pro Leu Gly Arg Leu Leu Val Thr Ala Gly His Val Val Gly Gln
                                     10
egg tgg aac ege tac ete gee gag gag eac gge ete ace eag geg gge
                                                                   96
Arg Trp Asn Arg Tyr Leu Ala Glu Glu His Gly Leu Thr Gln Ala Gly
atg gtc acc ctg atg acc ctg gcc cgg cac ggc gag ctg ccg cac cgg
                                                                   144
Met Val Thr Leu Met Thr Leu Ala Arg His Gly Glu Leu Pro His Arg
gcg gtc gcc gag gcg tgc ttc atc cgc ccg gcc acc cta acc ggc atc
                                                                   192
Ala Val Ala Glu Ala Cys Phe Ile Arg Pro Ala Thr Leu Thr Gly Ile
gtc gac aca ctg gag cgc gac ggc ctc gtc gag cgg caa cgc gac gac
                                                                   240
Val Asp Thr Leu Glu Arg Asp Gly Leu Val Glu Arg Gln Arg Asp Asp
gtc gac egg ege age gtg egg etc gtc etg acc ecc gec ggt egg gaa
                                                                   288
Val Asp Arg Arg Ser Val Arg Leu Val Leu Thr Pro Ala Gly Arg Glu
                                     90
egg gte gee geg ete ace aac gte atg eag tee gga ega eeg atg ace
                                                                   336
Arg Val Ala Ala Leu Thr Asn Val Met Gln Ser Gly Arg Pro Met Thr
tcg gtc gac gcc gac ccg gcg aag gcc gcc gtg atc cgg cag ttc ctg
                                                                   384
Ser Val Asp Ala Asp Pro Ala Lys Ala Ala Val Ile Arg Gln Phe Leu
        115
                            120
                                                 125
ctc gag gtc atc ggc agt gga gag gaa cct cgg gtg acg gcc ctc gac
                                                                   432
Leu Glu Val Ile Gly Ser Gly Glu Glu Pro Arg Val Thr Ala Leu Asp
    130
                        135
gcg agg ccg gag gct ccg gca tgc
                                                                   456
Ala Arg Pro Glu Ala Pro Ala Cys
145
                    150
<210> 101
<211> 152
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evbF2
<400> 101
Val Pro Leu Gly Arg Leu Leu Val Thr Ala Gly His Val Val Gly Gln
Arg Trp Asn Arg Tyr Leu Ala Glu Glu His Gly Leu Thr Gln Ala Gly
```

```
Met Val Thr Leu Met Thr Leu Ala Arg His Gly Glu Leu Pro His Arg
Ala Val Ala Glu Ala Cys Phe Ile Arg Pro Ala Thr Leu Thr Gly Ile
Val Asp Thr Leu Glu Arg Asp Gly Leu Val Glu Arg Gln Arg Asp Asp
Val Asp Arg Arg Ser Val Arg Leu Val Leu Thr Pro Ala Gly Arg Glu
                                     90
Arg Val Ala Ala Leu Thr Asn Val Met Gln Ser Gly Arg Pro Met Thr
            100
                                105
Ser Val Asp Ala Asp Pro Ala Lys Ala Ala Val Ile Arg Gln Phe Leu
Leu Glu Val Ile Gly Ser Gly Glu Glu Pro Arg Val Thr Ala Leu Asp
                        135
Ala Arg Pro Glu Ala Pro Ala Cys
<210> 102
<211> 1671
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1671)
<220>
<223> evbG
atg gcg ttg cag ttc gtc ggc acg atg gcc tcg ctc tac ctg ccg agc
                                                                   48
Met Ala Leu Gln Phe Val Gly Thr Met Ala Ser Leu Tyr Leu Pro Ser
ctc aac gcc gac atc atc gac cag ggt gtg gcc cgg ggc gac acc ggc
                                                                   96
Leu Asn Ala Asp Ile Ile Asp Gln Gly Val Ala Arg Gly Asp Thr Gly
tac atc atg cgt acg ggc ggc tgg atg ctg ctg gtc agc ctg gtg cag
                                                                   144
Tyr Ile Met Arg Thr Gly Gly Trp Met Leu Leu Val Ser Leu Val Gln
ate gee tge tee ace gee geg gte tte etc gge geg ege tee geg atg
                                                                   192
Ile Ala Cys Ser Thr Ala Ala Val Phe Leu Gly Ala Arg Ser Ala Met
ggc ttc ggc cgg gac gta cgc gcc gag gtc ttc gcc cac gtc aac cgg
                                                                   240
Gly Phe Gly Arg Asp Val Arg Ala Glu Val Phe Ala His Val Asn Arg
tto too goo ego gag gtg acc ego tto ggo goa ecc tog etg atc acc
                                                                   288
Phe Ser Ala Arg Glu Val Thr Arg Phe Gly Ala Pro Ser Leu Ile Thr
                                     90
```

ege aac acc aac gac gtg caa cag gtg cag atg etc gte etg atg age

Arg	Asn	Thr	Asn 100	Asp	Val	Gln	Gln	Val 105	Gln	Met	Leu	Val	Leu 110	Met	Ser	
					gcc Ala											384
					gac Asp											432
					atc Ile 150											480
					atg Met											528
					acc Thr											576
					gcg Ala											624
					acc Thr											672
					aac Asn 230											720
					gcc Ala											768
					atg Met											816
					gtc Val											864
gtc Val	gag Glu 290	gtg Val	ctc Leu	gac Asp	acc Thr	gac Asp 295	tcg Ser	acg Thr	gtg Val	atc Ile	ccg Pro 300	ccg Pro	gcc Ala	gcg Ala	ccg Pro	912
_	_				ggc Gly 310			_	_	_	_	_		_		960
					gcg Ala											1008
					cgc Arg											1056
					ctg Leu											1104

355 360 365 gcc ggg gcg gtg ctg gtc gac ggg gtg gac gtg cgt gac ctg gcc ccg 1152 Ala Gly Ala Val Leu Val Asp Gly Val Asp Val Arg Asp Leu Ala Pro 370 375 380 gac gat ttg tgg cgg cgg atc ggg ctg gtg ccg cag cgg ccg tac ctg 1200 Asp Asp Leu Trp Arg Arg Ile Gly Leu Val Pro Gln Arg Pro Tyr Leu 390 ttc agc ggc acg atc gcc agc aac ctg cgg tac ggc aac ccg gac gcc 1248 Phe Ser Gly Thr Ile Ala Ser Asn Leu Arg Tyr Gly Asn Pro Asp Ala 405 acc gac gcg gag ctg tgg gcc gcc ctg gag atc gcc cag gcg cgc gac 1296 Thr Asp Ala Glu Leu Trp Ala Ala Leu Glu Ile Ala Gln Ala Arg Asp 425 ttc gtc gcc gag ttg ccc gaa ggg ctg aac gcc ccg atc acg cag ggc 1344 Phe Val Ala Glu Leu Pro Glu Gly Leu Asn Ala Pro Ile Thr Gln Gly ggc acc aat atc tcc ggc ggg cag cgc cag cgc ctc gcg atc gcc cgg 1392 Gly Thr Asn Ile Ser Gly Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg 455 gcc ctg gtc cgc aag ccg gag atc tac ctg ttc gac gac tcg ttc tcg 1440 Ala Leu Val Arg Lys Pro Glu Ile Tyr Leu Phe Asp Asp Ser Phe Ser 470 475 geg ete gae etg gge ace gae gee egg etg ege geg eta ega eeg 1488 Ala Leu Asp Leu Gly Thr Asp Ala Arg Leu Arg Ala Ala Leu Arg Pro 485 490 gtc acc gcg gac gcg acg gtg ctg atc gtg gcc cag cgg gtc tcc acq 1536 Val Thr Ala Asp Ala Thr Val Leu Ile Val Ala Gln Arg Val Ser Thr 500 505 ate gte gae gee gae cag ate ate gtg ett gag gae ggg gge ate gte 1584 Ile Val Asp Ala Asp Gln Ile Ile Val Leu Glu Asp Gly Gly Ile Val 515 520 525 ggg atg ggc cga cac gcc gaa cta ctg gaa gac tgc ccg acg tac gcg 1632 Gly Met Gly Arg His Ala Glu Leu Leu Glu Asp Cys Pro Thr Tyr Ala 530 535 540 gag atc gtc gcc tcc cag cag acg gcg ggg gtg ccg gca 1671 Glu Ile Val Ala Ser Gln Gln Thr Ala Gly Val Pro Ala 545 550 <210> 103 <211> 557 <212> PRT <213> Micromonospora carbonacea <220> <223> evbG <400> 103 Met Ala Leu Gln Phe Val Gly Thr Met Ala Ser Leu Tyr Leu Pro Ser Leu Asn Ala Asp Ile Ile Asp Gln Gly Val Ala Arg Gly Asp Thr Gly

25

Tyr Ile Met Arg Thr Gly Gly Trp Met Leu Leu Val Ser Leu Val Gln Ile Ala Cys Ser Thr Ala Ala Val Phe Leu Gly Ala Arg Ser Ala Met Gly Phe Gly Arg Asp Val Arg Ala Glu Val Phe Ala His Val Asn Arg Phe Ser Ala Arg Glu Val Thr Arg Phe Gly Ala Pro Ser Leu Ile Thr 90 Arg Asn Thr Asn Asp Val Gln Gln Val Gln Met Leu Val Leu Met Ser 105 Cys Thr Met Leu Val Ala Ala Pro Ile Met Ser Val Gly Gly Val Phe Met Ala Leu Arg Glu Asp Val Gly Leu Ser Trp Leu Met Leu Val Ser 135 Val Pro Ala Leu Ala Ile Ala Leu Met Leu Ile Ile Arg Arg Met Val 145 150 155 Pro Gly Phe Arg Leu Met Gln Thr Arg Ile Asp Ala Val Asn Arg Val Leu Arg Glu Gln Ile Thr Gly Ile Arg Val Val Arg Ala Phe Val Arg Glu Pro Tyr Glu Thr Ala Arg Phe Gly Arg Ala Asn Ala Asp Leu Thr 200 Ala Thr Ala Leu Arg Thr Gly Arg Leu Met Ala Leu Ile Phe Pro Val Val Thr Leu Val Leu Asn Val Ser Ser Val Ala Val Leu Trp Phe Gly 235 Ala Asp Arg Val Asp Ala Gly Gln Ile Gln Val Gly Ala Leu Thr Ala 250 Phe Leu Gln Tyr Leu Met Gln Ile Leu Met Ala Val Met Leu Ala Thr Phe Ile Leu Met Met Val Pro Arg Ala Ala Val Cys Ala Glu Arg Ile Val Glu Val Leu Asp Thr Asp Ser Thr Val Ile Pro Pro Ala Ala Pro 295 Thr Ala Glu Val Thr Gly Arg Gly Glu Leu Glu Leu Arg Gly Val Arg 315 Phe Gln Tyr Pro Gly Ala Ser Ala Pro Val Leu His Asp Ile Ser Phe Arg Ala Thr Pro Gly Arg Thr Thr Ala Ile Ile Gly Ser Thr Gly Ala 345 Gly Lys Thr Thr Leu Leu Thr Leu Ile Pro Arg Leu Ile Asp Ala Thr 360 Ala Gly Ala Val Leu Val Asp Gly Val Asp Val Arg Asp Leu Ala Pro

370 375 380 Asp Asp Leu Trp Arg Arg Ile Gly Leu Val Pro Gln Arg Pro Tyr Leu 395 Phe Ser Gly Thr Ile Ala Ser Asn Leu Arg Tyr Gly Asn Pro Asp Ala 405 410 Thr Asp Ala Glu Leu Trp Ala Ala Leu Glu Ile Ala Gln Ala Arg Asp Phe Val Ala Glu Leu Pro Glu Gly Leu Asn Ala Pro Ile Thr Gln Gly Gly Thr Asn Ile Ser Gly Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg 455 Ala Leu Val Arg Lys Pro Glu Ile Tyr Leu Phe Asp Asp Ser Phe Ser 475 Ala Leu Asp Leu Gly Thr Asp Ala Arg Leu Arg Ala Ala Leu Arg Pro Val Thr Ala Asp Ala Thr Val Leu Ile Val Ala Gln Arg Val Ser Thr 505 Ile Val Asp Ala Asp Gln Ile Ile Val Leu Glu Asp Gly Gly Ile Val 515 Gly Met Gly Arg His Ala Glu Leu Leu Glu Asp Cys Pro Thr Tyr Ala 535 Glu Ile Val Ala Ser Gln Gln Thr Ala Gly Val Pro Ala 550 <210> 104 <211> 1935 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1935) <220> <223> evbH <400> 104 atg age gee gge atg eeg gee gag aag teg atg aac tte ggg eeg tee 48 Met Ser Ala Gly Met Pro Ala Glu Lys Ser Met Asn Phe Gly Pro Ser 96 acc ege egg etg etg ege egg etg ega eeg eac ege ete eag etg gee Thr Arg Arg Leu Leu Arg Arg Leu Arg Pro His Arg Leu Gln Leu Ala gcc atc gtc ctg ctc tcg ctg gtc agc gtc ggt tgc aac gtg tac ggg 144 Ala Ile Val Leu Leu Ser Leu Val Ser Val Gly Cys Asn Val Tyr Gly ccg aag gtg ctc ggc cac gcc acc gac ctg atc ttc agc ggg gtg atc 192 Pro Lys Val Leu Gly His Ala Thr Asp Leu Ile Phe Ser Gly Val Ile

55

60

	cag Gln								240
	gcg Ala							Met	288
	gtg Val								336
	ttc Phe 115								384
	ggc Gly								432
	gcc Ala								480
	cgg Arg								528
	aac Asn								576
	ctg Leu 195								624
	ctg Leu								672
	acc Thr								720
	acg Thr								768
	cac His								816
	ttc Phe 275								864
	ttc Phe								912
	agc Ser								960

					atc Ile											1008
					ccg Pro											1056
					gcc Ala											1104
					ccg Pro											1152
					gaa Glu 390											1200
					acc Thr											1248
					Gly 999											1296
aac Asn	ctg Leu	gtg Val 435	atg Met	cgc Arg	ttc Phe	tac Tyr	gag Glu 440	ctg Leu	gac Asp	gcc Ala	ggc Gly	cgg Arg 445	atc Ile	acc Thr	ctc Leu	1344
					acc Thr											1392
					cag Gln 470											1440
_					ggc Gly		_	_		_					_	1488
gcc Ala	gcc Ala	gcc Ala	cgg Arg 500	gcg Ala	acg Thr	ttc Phe	gtg Val	gac Asp 505	cgg Arg	ttc Phe	gtg Val	cgt Arg	agc Ser 510	ctc Leu	ccc Pro	1536
					gtc Val											1584
					atc Ile											1632
					gac Asp 550											1680
					cgg Arg											1728
agc	ttc	gtc	atc	gcc	cac	cgt	ttg	tcc	acc	atc	cgc	gac	gcg	gac	ctg	1776

Ser	Phe	Val	Ile 580	Ala	His	Arg	Leu	Ser 585	Thr	Ile	Arg	Asp	Ala 590	Asp	Leu	
											cag Gln					1824
											ctt Leu 620					1872
											ccc Pro					1920
_	tcg Ser	_														1935
<21 <21	0> 10 1> 64 2> PI 3> M:	45 RT	monos	spora	a cai	rbona	acea									
<22 <22	0> 3> ev	vbH														
	0> 10 Ser		Gly	Met 5	Pro	Ala	Glu	Lys	Ser 10	Met	Asn	Phe	Gly	Pro 15	Ser	
Thr	Arg	Arg	Leu 20	Leu	Arg	Arg	Leu	Arg 25	Pro	His	Arg	Leu	Gln 30	Leu	Ala	
Ala	Ile	Val 35	Leu	Leu	Ser	Leu	Val 40	Ser	Val	Gly	Cys	Asn 45	Val	Tyr	Gly	
Pro	Lys 50	Val	Leu	Gly	His	Ala 55	Thr	Asp	Leu	Ile	Phe 60	Ser	Gly	Val	Ile	
Gly 65	Arg	Gln	Leu	Pro	Ala 70	Gly	Thr	Thr	Ala	Glu 75	Gln	Ala	Val	Ala	Ala 80	
Ala	Arg	Ala	Ala	Gly 85	Asn	Asp	Ser	Phe	Ala 90	Asp	Met	Leu	Ala	Arg 95	Met	
Asp	Val	Val	Pro 100	Gly	Val	Gly	Ile	Asp 105	Phe	Thr	Ala	Leu	Gly 110	Arg	Val	
Leu	Leu	Phe 115	Val	Leu	Ala	Leu	Tyr 120	Leu	Ala	Ala	Ser	Val 125	Leu	Leu	Trp	
Trp	Gln 130	Gly	Trp	Leu	Leu	Asn 135	Gly	Val	Val	Gln	Arg 140	Thr	Val	Leu	Arg	
Leu 145	Arg	Ala	Asp	Val	Glu 150	Asp	Lys	Leu	Asn	Arg 155	Leu	Pro	Leu	Pro	Tyr 160	
Phe	Asp	Arg	Gln	Pro 165	Arg	Gly	Glu	Leu	Leu 170	Ser	Arg	Val	Thr	Asn 175	Asp	
Ile	Asp	Asn	Ile 180	Ser	Gln	Ser	Leu	Gln 185	Gln	Thr	Leu	Ser	Gln 190	Leu	Leu	

Thr	Ser	Leu 195	Leu	Thr	Val	Val	Gly 200	Val	Leu	Ala	Met	Met 205	Phe	Trp	Ile
Ser	Pro 210	Leu	Leu	Ala	Leu	Val 215	Ser	Leu	Val	Ala	Val 220	Pro	Met	Ser	Val
Val 225	Val	Thr	Ser	Leu	Val 230	Ala	Lys	Arg	Ser	Gln 235	Gln	Arg	Phe	Ile	Ala 240
Gln	Trp	Thr	His	Thr 245	Gly	Glu	Leu	Asn	Gly 250	Gln	Ile	Glu	Glu	Ala 255	Phe
Thr	Gly	His	Glu 260	Leu	Val	Lys	Val	Phe 265	Gly	Arg	Gln	Arg	Glu 270	Val	Glu
Ala	Ala	Phe 275	Thr	Ala	Lys	Asn	Glu 280	Glu	Leu	Phe	Arg	Ala 285	Ser	Phe	Gly
Ala	Gln 290	Phe	Ile	Ser	Gly	Ile 295	Ile	Met	Pro	Ala	Met 300	Met	Phe	Ile	Gly
Asn 305	Leu	Ser	Tyr	Val	Ala 310	Ile	Ala	Val	Val	Gly 315	Gly	Leu	Arg	Val	Ala 320
Ser	Gly	Ser	Met	Ser 325	Ile	Gly	Asp	Val	Gln 330	Ala	Phe	Ile	Gln	Tyr 335	Ser
Leu	Gln	Phe	Thr 340	Gln	Pro	Leu	Thr	Arg 345	Val	Ala	Ser	Met	Ala 350	Asn	Leu
Leu	Gln	Ser 355	Gly	Val	Ala	Ser	Ala 360	Glu	Arg	Val	Phe	Ala 365	Val	Leu	Asp
Ala	Glu 370	Glu	Gln	Ser	Pro	Asp 375	Pro	Ala	Val	Pro	Ala 380	Arg	Val	Ala	Asp
Gln 385	Arg	Gly	Arg	Val	Glu 390	Phe	Asp	His	Val	Ser 395	Phe	Arg	Tyr	Glu	Pro 400
Asp	Lys	Pro	Leu	Ile 405	Thr	Asp	Leu	Ser	Leu 410	Val	Ala	Glu	Pro	Gly 415	His
Thr	Val	Ala	Ile 420	Val	Gly	Pro	Thr	Gly 425	Ala	Gly	Lys	Thr	Thr 430	Leu	Val
Asn	Leu	Val 435	Met	Arg	Phe	Tyr	Glu 440	Leu	Asp	Ala	Gly	Arg 445	Ile	Thr	Leu
Asp	Gly 450	Val	Asp	Ile	Thr	Thr 455	Leu	Ser	Arg	Asp	Asp 460	Leu	Arg	Gly	Arg
Ile 465	Gly	Met	Val	Leu	Gln 470	Asp	Thr	Trp	Leu	Phe 475	Gly	Gly	Thr	Ile	Arg 480
Asp	Asn	Ile	Ala	Tyr 485	Gly	Arg	Pro	Asp	Ala 490	Ser	Glu	Glu	Glu	Ile 495	Val
Ala	Ala	Ala	Arg 500	Ala	Thr	Phe	Val	Asp 505	Arg	Phe	Val	Arg	Ser 510	Leu	Pro
Asp	Gly	Tyr 515	Asp	Thr	Val	Ile	Asp 520	Ser	Glu	Gly	Ser	Asn 525	Val	Ser	Ala
Gly	Glu 530	Lys	Gln	Leu	Ile	Thr 535	Ile	Ala	Arg	Ala	Phe 540	Leu	Ala	Glu	Pro

Ser Leu Leu Ile Leu Asp Glu Ala Thr Ser Ser Val Asp Thr Arg Thr Glu Val Leu Leu Gln Arg Ala Met Ala Ala Leu Arg Ser Asp Arg Thr Ser Phe Val Ile Ala His Arg Leu Ser Thr Ile Arg Asp Ala Asp Leu Ile Leu Met Met Glu His Gly Arg Ile Val Glu Gln Gly Thr His Glu Gln Leu Leu Ala Ala Arg Gly Ala Tyr His Arg Leu Tyr Gln Ala Gln 615 Phe Thr Gln Pro Asp Pro Ala Ala Val Gly Asp Pro Glu Pro Gln Pro 635 Ala Ser Val Arg Gly <210> 106 <211> 1401 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1401) <220> <223> evbI <400> 106 gtg agc cag atc gtg atc atc ggc ggg ggg ccg gcc ggg tac gag gcg 48 Val Ser Gln Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu Ala gcc ctg gtc gcc gcc cag ttg gac gct gat gtc acc gtg gtg gag gcc 96 Ala Leu Val Ala Ala Gln Leu Asp Ala Asp Val Thr Val Val Glu Ala 25 gag ggg gcc ggc ggt gcc tgc gtg ctg tcc gac tgc gta ccg tcg aaa 144 Glu Gly Ala Gly Gly Ala Cys Val Leu Ser Asp Cys Val Pro Ser Lys 40 acg ttc atc gcc agc tcg gag gtg gtc acc ggg tac cgg gac acc gag 192 Thr Phe Ile Ala Ser Ser Glu Val Val Thr Gly Tyr Arg Asp Thr Glu gag ttc ggg gtg cac tcc gac ggg ctg gag gcg gtc acc gtc gac gcc 240 Glu Phe Gly Val His Ser Asp Gly Leu Glu Ala Val Thr Val Asp Ala egg gee gtg cae gag egg gte aag egg ete gee etg gee eag tee gee 288 Arg Ala Val His Glu Arg Val Lys Arg Leu Ala Leu Ala Gln Ser Ala gac atc cac gcg aag ctg gtg aaa gcc ggc gtc acc ttc gtg gcc ggc 336 Asp Ile His Ala Lys Leu Val Lys Ala Gly Val Thr Phe Val Ala Gly

	acg Thr	gcc Ala	cgg Arg 115	ctc Leu	ggc Gly	gag Glu	gac Asp	atg Met 120	ctg Leu	ggc Gly	cac His	acc Thr	cac His 125	cgc Arg	gtc Val	gtc Val	384
						ggc Gly											432
						ggc Gly 150											480
						atc Ile											528
						ctg Leu											576
						tac Tyr											624
						gtg Val											672
						ttc Phe 230											720
	tcc Ser	cgc Arg	gcc Ala	gag Glu	agg Arg 245	gtc Val	cag Gln	cgc Arg	atc Ile	gcc Ala 250	gac Asp	Gly ggg	gtg Val	gag Glu	gtc Val 255	gaa Glu	768
	ctg Leu	gcc Ala	gac Asp	ggc Gly 260	cgg Arg	ctg Leu	gtg Val	cac His	ggc Gly 265	tcg Ser	cac His	gcg Ala	ctc Leu	atc Ile 270	gcg Ala	gtc Val	816
						acc Thr											864
						ggc Gly											912
	aac Asn 305	gtc Val	ccc Pro	Gly aaa	atc Ile	tac Tyr 310	gct Ala	gcc Ala	ggc Gly	gac Asp	tgc Cys 315	acc Thr	gly ggg	gtg Val	ttg Leu	ccg Pro 320	960
						gcc Ala											1008
	ctc Leu	ggc Gly	gag Glu	gcg Ala 340	gtc Val	cgg Arg	ccg Pro	ctg Leu	cgg Arg 345	ctg Leu	cgt Arg	acg Thr	gtg Val	gcc Ala 350	gcg Ala	aac Asn	1056
						gag Glu											1104
,	gtg	gac	gcc	ggc	aag	acc	ccg	gcc	cgc	cag	gtg	atg	ctg	ccg	ctg	tcg	1152

Val Asp Ala 370	Gly Lys	Thr	Pro 375	Ala	Arg	Gln	Val	Met 380	Leu	Pro	Leu	Ser	
ggc aac gcc Gly Asn Ala 385	cgg gcg Arg Ala	aag Lys 390	atg Met	gac Asp	gac Asp	ctc Leu	gcc Ala 395	gac Asp	ggc Gly	ttc Phe	gtg Val	aag Lys 400	1200
ctg ttc tgc Leu Phe Cys		Ala											1248
gca ccg aag Ala Pro Lys			_		_	_			_				1296
aac aac ctc Asn Asn Leu 435													1344
agc ctg tcg Ser Leu Ser 450	ggc tcg Gly Ser	Ile	acc Thr 455	gag Glu	gcc Ala	gcc Ala	cgc Arg	cag Gln 460	ctc Leu	atg Met	ctc Leu	cac His	1392
gag ctg gag Glu Leu Glu 465													1401
<210> 107 <211> 467 <212> PRT <213> Micro	monospor	a car	bona	ıcea									
<220> <223> evbI													
	Ile Val	Ile	Ile	Gly	Gly	Gly 10	Pro	Ala	Gly	Tyr	Glu 15	Ala	
<223> evbI <400> 107 Val Ser Gln	5					10					15		
<223> evbI <400> 107 Val Ser Gln 1	5 Ala Ala 20	Gln	Leu	Asp	Ala 25	10 Asp	Val	Thr	Val	Val 30	15 Glu	Ala	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala	Ala Ala 20 Gly Gly	Gln Ala	Leu Cys	Asp Val 40	Ala 25 Leu	10 Asp Ser	Val Asp	Thr Cys	Val Val 45	Val 30 Pro	15 Glu Ser	Ala Lys	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala 35 Thr Phe Ile	Ala Ala 20 Gly Gly Ala Ser	Gln Ala Ser	Leu Cys Glu 55	Asp Val 40 Val	Ala 25 Leu Val	10 Asp Ser Thr	Val Asp Gly	Thr Cys Tyr 60	Val Val 45 Arg	Val 30 Pro	15 Glu Ser Thr	Ala Lys Glu	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala 35 Thr Phe Ile 50 Glu Phe Gly	Ala Ala 20 Gly Gly Ala Ser Val His	Gln Ala Ser Ser 70 Arg	Leu Cys Glu 55 Asp	Asp Val 40 Val Gly	Ala 25 Leu Val Leu	10 Asp Ser Thr	Val Asp Gly Ala 75	Thr Cys Tyr 60 Val	Val Val 45 Arg	Val 30 Pro Asp	15 Glu Ser Thr	Ala Lys Glu Ala 80	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala 35 Thr Phe Ile 50 Glu Phe Gly 65	Ala Ala 20 Gly Gly Ala Ser Val His His Glu	Gln Ala Ser Ser 70 Arg	Leu Cys Glu 55 Asp Val	Asp Val 40 Val Gly Lys	Ala 25 Leu Val Leu Arg	10 Asp Ser Thr Glu Leu 90	Val Asp Gly Ala 75 Ala	Thr Cys Tyr 60 Val Leu	Val Val 45 Arg Thr	Val 30 Pro Asp Val Gln	15 Glu Ser Thr Asp Ser 95	Ala Lys Glu Ala 80 Ala	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala 35 Thr Phe Ile 50 Glu Phe Gly 65 Arg Ala Val	Ala Ala 20 Gly Gly Ala Ser Val His His Glu 85 Ala Lys 100	Gln Ala Ser Ser 70 Arg Leu	Leu Cys Glu 55 Asp Val	Asp Val 40 Val Gly Lys	Ala 25 Leu Val Leu Arg Ala 105	Asp Ser Thr Glu Leu 90 Gly	Val Asp Gly Ala 75 Ala Val	Thr Cys Tyr 60 Val Leu Thr	Val Val 45 Arg Thr Ala Phe	Val 30 Pro Asp Val Gln Val 110	15 Glu Ser Thr Asp Ser 95 Ala	Ala Lys Glu Ala 80 Ala Gly	
<223> evbI <400> 107 Val Ser Gln 1 Ala Leu Val Glu Gly Ala 35 Thr Phe Ile 50 Glu Phe Gly 65 Arg Ala Val Asp Ile His Thr Ala Arg	Ala Ala 20 Gly Gly Ala Ser Val His His Glu 85 Ala Lys 100 Leu Gly	Gln Ala Ser Ser 70 Arg Leu Glu Gly	Leu Cys Glu 55 Asp Val Val	Asp Val 40 Val Gly Lys Lys Met 120	Ala 25 Leu Val Leu Arg Ala 105 Leu	Asp Ser Thr Glu Leu 90 Gly	Val Asp Gly Ala 75 Ala Val	Thr Cys Tyr 60 Val Leu Thr	Val Val 45 Arg Thr Ala Phe His	Val 30 Pro Asp Val Gln Val 110 Arg	15 Glu Ser Thr Asp Ser 95 Ala	Ala Lys Glu Ala 80 Ala Gly Val	

145					150					15 5					160
Pro	Asp	Gly	Glu	Arg 165	Ile	Leu	Thr	Trp	Arg 170	Gln	Val	Tyr	Asp	Leu 175	Pro
His	Leu	Pro	Glu 180	His	Leu	Ile	Val	Val 185	Gly	Ser	Gly	Val	Thr 190	Gly	Ala
Glu	Phe	Ala 195	Ser	Ala	Tyr	Leu	Ala 200	Met	Gly	Val	Pro	Val 205	Thr	Leu	Val
Ser	Ser 210	Arg	Asp	Arg	Val	Met 215	Pro	His	Glu	Asp	Ala 220	Asp	Ala	Ala	Met
Ala 225	Ile	Glu	Arg	Val	Phe 230	Arg	Ser	Arg	Gly	Met 235	Thr	Ile	Leu	Asn	Asn 240
Ser	Arg	Ala	Glu	Arg 245	Val	Gln	Arg	Ile	Ala 250	Asp	Gly	Val	Glu	Val 255	Glu
			260		Leu			265					270		
Gly	Ser	Ile 275	Pro	Asn	Thr	Ala	Asn 280	Leu	Gly	Leu	Ala	Glu 285	Tyr	Gly	Val
Glu	Leu 290	Ala	Arg	Gly	Gly	Tyr 295	Val	Thr	Val	Asp	Arg 300	Val	Ser	Arg	Thr
Asn 305	Val	Pro	Gly	Ile	Tyr 310	Ala	Ala	Gly	Asp	Cys 315	Thr	Gly	Val	Leu	Pro 320
				325	Ala			_	330					335	
			340		Arg			345					350		
Val	Phe	Thr 355	Asp	Pro	Glu	Leu	Ala 360	Thr	Val	Gly	Val	Ser 365	Gln	Asp	Glu
Val	Asp 370	Ala	Gly	Lys	Thr	Pro 375	Ala	Arg	Gln	Val	Met 380	Leu	Pro	Leu	Ser
Gly 385	Asn	Ala	Arg	Ala	Lys 390	Met	Asp	Asp	Leu	Ala 395	Asp	Gly	Phe	Val	Lys 400
Leu	Phe	Cys	Arg	Pro 405	Ala	Ser	Gly	Gln	Val 410	Ile	Gly	Gly	Val	Val 415	Val
Ala	Pro	Lys	Ala 420	Ser	Glu	Leu	Ile	Leu 425	Pro	Ile	Thr	Met	Ala 430	Val	Glu
Asn	Asn	Leu 435	Thr	Val	Asn	Glu	Leu 440	Ala	Gln	Thr	Ile	Thr 445	Ile	Tyr	Pro
Ser	Leu 450	Ser	Gly	Ser	Ile	Thr 455	Glu	Ala	Ala	Arg	Gln 460	Leu	Met	Leu	His
Glu 465	Leu	Glu													

```
<211> 453
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(453)
<220>
<223> evbJ
<400> 108
gtg cgt cac tac gcc gcc tac ggc tca aac ctg gac ccc gcc cgg atg
                                                                   48
Val Arg His Tyr Ala Ala Tyr Gly Ser Asn Leu Asp Pro Ala Arg Met
                                     10
ege gee tae tge eeg cae tee eeg atg gte gge gte gge tgg etg gag
                                                                   96
Arg Ala Tyr Cys Pro His Ser Pro Met Val Gly Val Gly Trp Leu Glu
ggc tgg cgg ctc acc ttc gcg ggt gag ggc gcg atc ggc tgg gag ggc
                                                                   144
Gly Trp Arg Leu Thr Phe Ala Gly Glu Gly Ala Ile Gly Trp Glu Gly
                             40
gcg gtc agc acc atc gtc gag tcc ccc ggt gat cgg gtg ttc gtg gcg
                                                                   192
Ala Val Ser Thr Ile Val Glu Ser Pro Gly Asp Arg Val Phe Val Ala
                         55
ctc tac gac atc cac ccg tac gac gcc gtc cag ctc gac gag atc gag
                                                                   240
Leu Tyr Asp Ile His Pro Tyr Asp Ala Val Gln Leu Asp Glu Ile Glu
                     70
ggg gtg gcc tcc ggg acg tac cgc aag ctg cac gtc cgc gtc tcc acc
                                                                   288
Gly Val Ala Ser Gly Thr Tyr Arg Lys Leu His Val Arg Val Ser Thr
ctc gac ggc gac gtg acc gcg tgg gtc tac gtc ttc gac ggg tac gag
                                                                   336
Leu Asp Gly Asp Val Thr Ala Trp Val Tyr Val Phe Asp Gly Tyr Glu
            100
ggc ggc ctg ccg acg gcg tgg tat ctg tcg gag atc gcc aac gcc gcc
                                                                   384
Gly Gly Leu Pro Thr Ala Trp Tyr Leu Ser Glu Ile Ala Asn Ala Ala
        115
gag aag gcg gcc gcc gac gac tac gtc agc gag ctg cgg tcc cgc
                                                                   432
Glu Lys Ala Gly Ala Pro Asp Asp Tyr Val Ser Glu Leu Arg Ser Arg
ccc acc ggc acg gcg tcg gcg
                                                                   453
Pro Thr Gly Thr Ala Ser Ala
<210> 109
<211> 151
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evbJ
<400> 109
Val Arg His Tyr Ala Ala Tyr Gly Ser Asn Leu Asp Pro Ala Arg Met
                  5
```

Arg Ala Tyr Cys Pro His Ser Pro Met Val Gly Val Gly Trp Leu Glu Gly Trp Arg Leu Thr Phe Ala Gly Glu Gly Ala Ile Gly Trp Glu Gly Ala Val Ser Thr Ile Val Glu Ser Pro Gly Asp Arg Val Phe Val Ala Leu Tyr Asp Ile His Pro Tyr Asp Ala Val Gln Leu Asp Glu Ile Glu Gly Val Ala Ser Gly Thr Tyr Arg Lys Leu His Val Arg Val Ser Thr Leu Asp Gly Asp Val Thr Ala Trp Val Tyr Val Phe Asp Gly Tyr Glu 105 Gly Gly Leu Pro Thr Ala Trp Tyr Leu Ser Glu Ile Ala Asn Ala Ala Glu Lys Ala Gly Ala Pro Asp Asp Tyr Val Ser Glu Leu Arg Ser Arg 135 Pro Thr Gly Thr Ala Ser Ala <210> 110 <211> 963 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(963) <220> <223> evbK <400> 110 gtg act ctt ccc gct gac tgg gcg gcg cgc ccc acc ctc gac gac Val Thr Leu Pro Ala Asp Trp Ala Ala Arg Arg Pro Thr Leu Asp Asp gtc cct ggg atc ctc gcc gtc gtg cac gcc gca gac acc ttc gcg atc 96 Val Pro Gly Ile Leu Ala Val Val His Ala Ala Asp Thr Phe Ala Ile 20 25 gge cae eeg gae tte gae gee gaa gae gte aag gee gee etg aeg gee 144 Gly His Pro Asp Phe Asp Ala Glu Asp Val Lys Ala Ala Leu Thr Ala ccc ttc ttc gac ccg gcg cgc gac tcc tgg ctg gtc agc gac ccg cag 192 Pro Phe Phe Asp Pro Ala Arg Asp Ser Trp Leu Val Ser Asp Pro Gln ggc cgg ctc gtc gcc tgg tcg gtg gtg gac aac ccg acc ggg gtg ggc 240 Gly Arg Leu Val Ala Trp Ser Val Val Asp Asn Pro Thr Gly Val Gly 70 cgg gag ttc gtc gac gtc ctc gtc gac ccg gag cgc gcc gag gcg gta 288 Arg Glu Phe Val Asp Val Leu Val Asp Pro Glu Arg Ala Glu Ala Val

90

cgc Arg	gcc Ala	ccg Pro	ctg Leu 100	ctc Leu	gct Ala	ctg Leu	atg Met	ctg Leu 105	gac Asp	cgg Arg	gtc Val	gcc Ala	gag Glu 110	cgg Arg	gcc Ala	336
										cgc Arg						384
										gag Glu						432
										ctg Leu 155						480
										cgg Arg						528
										atc Ile						576
										tac Tyr						624
										gag Glu						672
										tcg Ser 235						720
										tcg Ser						768
										tgg Trp						816
										ctc Leu						864
										tcg Ser						912
atg Met 305	cgc Arg	tgg Trp	acc Thr	gac Asp	atg Met 310	tac Tyr	gag Glu	cgc Arg	acc Thr	gtc Val 315	ccc Pro	gcc Ala	gcc Ala	acg Thr	gcg Ala 320	960
gtg Val																963

<210> 111 <211> 321 <212> PRT <213> Micromonospora carbonacea

<220> <223> evbK

<400> 111

Val Thr Leu Pro Ala Asp Trp Ala Ala Arg Arg Pro Thr Leu Asp Asp 1 5 10 15

Val Pro Gly Ile Leu Ala Val Val His Ala Ala Asp Thr Phe Ala Ile 20 25 30

Gly His Pro Asp Phe Asp Ala Glu Asp Val Lys Ala Ala Leu Thr Ala 35 40 45

Pro Phe Phe Asp Pro Ala Arg Asp Ser Trp Leu Val Ser Asp Pro Gln 50 55 60

Gly Arg Leu Val Ala Trp Ser Val Val Asp Asn Pro Thr Gly Val Gly
65 70 75 80

Arg Glu Phe Val Asp Val Leu Val Asp Pro Glu Arg Ala Glu Ala Val 85 90 95

Arg Ala Pro Leu Leu Ala Leu Met Leu Asp Arg Val Ala Glu Arg Ala 100 105 110

Ala Glu Arg Ser Leu Pro Ala Leu Thr Val Arg Ala Ser Ala Tyr Pro 115 120 125

Pro Glu Thr Arg Trp Val Thr Glu Leu Thr Glu Ala Gly Phe Ser Arg 130 135 140

Val Lys Arg Tyr Val Arg Met Ser Arg Asp Leu Ala Gly Leu Pro Ala 145 150 155 160

Glu Pro Pro Pro Pro Gly Val Thr Val Arg Pro Leu Arg Ala Gly
165 170 175

Asp Glu Asp Asp Leu Arg Leu Phe His Arg Ile Tyr Asp Thr Ala Phe 180 185 190

Arg Asp Thr Pro Asp Tyr Glu Pro Ala Gly Tyr Asp His Trp Arg Glu 195 200 205

Arg Leu Pro Ala Tyr Asp Arg Thr Trp Asp Glu Trp Phe Val Ala Glu 210 215 220

Val Asp Gly Glu Pro Ala Gly Ala Leu Gln Ser Ser Asp Gln Ala Leu 225 230 235 240

Glu Gln Asp Ser Gly Trp Val Arg Thr Leu Ser Val Leu Pro Lys Tyr 245 250 255

Arg Arg His Gly Val Gly Ala Ala Leu Leu Trp Arg Ala Phe Thr Val 260 265 270

Tyr Ala Ala Lys Gly Arg Arg His Ala Gly Leu Gly Val Asp Leu Thr 275 280 285

Asn Pro Thr Ser Pro Ala Thr Leu Tyr Arg Ser Val Gly Leu Arg Glu

Met Arg Trp Thr Asp Met Tyr Glu Arg Thr Val Pro Ala Ala Thr Ala 305 310 315 320 Val

```
<210> 112
<211> 747
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(747)
<220>
<223> evbL
<400> 112
atg acg ccg gag cag gtc gcc gcc gcg agc aag ccg ttg gtg ctg gag
                                                                48
Met Thr Pro Glu Gln Val Ala Ala Ala Ser Lys Pro Leu Val Leu Glu
ctc ggg gag atg ttc gcc cgc tgc ccg gcc acc ctg cac cgg gcc cgt
                                                                96
Leu Gly Glu Met Phe Ala Arg Cys Pro Ala Thr Leu His Arg Ala Arg
ctg ctg ggc atc tcc ggc tgg gcc ttc cac atc gcc ggc cgg gcc ggg
                                                                144
Leu Leu Gly Ile Ser Gly Trp Ala Phe His Ile Ala Gly Arg Ala Gly
                            40
                                                                192
gtg etc ggc gac gtc ggg gcc gcc acg gtg agc gcg gcc ctc ggc ttc
Val Leu Gly Asp Val Gly Ala Ala Thr Val Ser Ala Ala Leu Gly Phe
                        55
gte gee eee gae geg gte gee gae ggg tgg gae gee gee ege gtg
                                                                240
Val Ala Pro Asp Ala Val Ala Asp Gly Trp Asp Ala Ala Ala Arg Val
                                                                288
cac get eeg etg gag gtg gee aeg geg aac etg gee gag tge tge egg
His Ala Pro Leu Glu Val Ala Thr Ala Asn Leu Ala Glu Cys Cys Arg
                85
                                    90
tgg ggc agc gag cac ctg acc gcc gtg ccc ggc gtg atc cgt ctg gcg
                                                                336
Trp Gly Ser Glu His Leu Thr Ala Val Pro Gly Val Ile Arg Leu Ala
           100
acg ctg ctg cac cgg gtg gtc gac gcc gcg gac gcc agc ggg atg cca
                                                                384
Thr Leu Leu His Arg Val Val Asp Ala Asp Ala Ser Gly Met Pro
       115
                           120
432
Leu Phe Ala Ala Trp Arg Ala Val Pro Pro Pro Asp Asp Thr Pro Gly
gcc cgt gcc gcc ggg ctg ctg ctg ctt cgg gag cac ttc gcc ggg
                                                                480
Ala Arg Ala Ala Ala Gly Leu Leu Leu Arg Glu His Phe Ala Gly
                                       155
gcg tac ctg ctg gcg gtg cgg gcc ggc ggg atg acg ccg ctg gag gcg
                                                                528
Ala Tyr Leu Leu Ala Val Arg Ala Gly Gly Met Thr Pro Leu Glu Ala
                                   170
                                                                576
gtg ctg gcc ggg ccg gag ggg gag gcc ggg gcg ctg gcc tgc ggc tgg
Val Leu Ala Gly Pro Glu Gly Glu Ala Gly Ala Leu Ala Cys Gly Trp
                               185
                                                  190
           180
```

ccg Pro	ccg Pro	ccg Pro 195	tac Tyr	ccc Pro	cgg Arg	gtc Val	999 Gly 200	ccg Pro	ctg Leu	gtg Val	cgc Arg	cgc Arg 205	cgg Arg	ctg Leu	tgg Trp
tcg Ser	gag Glu 210	gcg Ala	gtg Val	acc Thr	gac Asp	cgg Arg 215	ctg Leu	gtg Val	tcg Ser	acc Thr	gga Gly 220	ttc Phe	cgg Arg	gcg Ala	ctc Leu
			gag Glu												
gcc Ala	gtg Val	gtg Val	caa Gln	gga Gly 245	agg Arg	gcc Ala	cct Pro	tac Tyr							
<213	<210> 113 <211> 249 <212> PRT <213> Micromonospora carbonacea														
	<220> <223> evbL														
)> 11 Thr		Glu	Gln 5	Val	Ala	Ala	Ala	Ser 10	Lys	Pro	Leu	Val	Leu 15	Glu
Leu	Gly	Glu	Met 20	Phe	Ala	Arg	Cys	Pro 25	Ala	Thr	Leu	His	Arg 30	Ala	Arg
Leu	Leu	Gly 35	Ile	Ser	Gly	Trp	Ala 40	Phe	His	Ile	Ala	Gly 45	Arg	Ala	Gly
Val	Leu 50	Gly	Asp	Val	Gly	Ala 55	Ala	Thr	Val	Ser	Ala 60	Ala	Leu	Gly	Phe
Val 65	Ala	Pro	Asp	Ala	Val 70	Ala	Asp	Gly	Trp	Asp 75	Ala	Ala	Ala	Arg	Val 80
His	Ala	Pro	Leu	Glu 85	Val	Ala	Thr	Ala	Asn 90	Leu	Ala	Glu	Сув	Сув 95	Arg
Trp	Gly	Ser	Glu 100	His	Leu	Thr	Ala	Val 105	Pro	Gly	Val	Ile	Arg 110	Leu	Ala
Thr	Leu	Leu 115	His	Arg	Val	Val	Asp 120	Ala	Ala	Asp	Ala	Ser 125	Gly	Met	Pro
Leu	Phe 130	Ala	Ala	Trp	Arg	Ala 135	Val	Pro	Pro	Pro	Asp 140	Asp	Thr	Pro	Gly
Ala 145	Arg	Ala	Ala	Ala	Gly 150	Leu	Leu	Leu	Leu	Arg 155	Glu	His	Phe	Ala	Gly 160
Ala	Tyr	Leu	Leu	Ala 165	Val	Arg	Ala	Gly	Gly 170	Met	Thr	Pro	Leu	Glu 175	Ala
Val	Leu	Ala	Gly 180	Pro	Glu	Gly	Glu	Ala 185	Gly	Ala	Leu	Ala	Cys 190	Gly	Trp
Pro	Pro	Pro 195	Tyr	Pro	Arg	Val	Gly 200	Pro	Leu	Val	Arg	Arg 205	Arg	Leu	Trp

Ser Glu Ala Val Thr Asp Arg Leu Val Ser Thr Gly Phe Arg Ala Leu 215 Thr Pro Ala Glu Gly Thr Ala Leu Leu Asp Leu Leu Thr Thr Ala Arg 235 Ala Val Val Gln Gly Arg Ala Pro Tyr 245 <210> 114 <211> 918 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(918) <220> <223> evbM <400> 114 gtg ccg ccc ccg cag agc ctc ctc cgg cgg ctc tac acc gag ccg ccg Val Pro Pro Pro Gln Ser Leu Leu Arg Arg Leu Tyr Thr Glu Pro Pro 10 gag aag ttc gtc gcc acc cgc gac gcc gtc gcc gag gcc cgg cgc 96 Glu Lys Phe Val Ala Thr Arg Asp Ala Ala Val Ala Glu Ala Arg Arg 20 25 tee gge gae eeg gee aeg gee ege gag ate gee egg etg ege eeg 144 Ser Gly Asp Pro Ala Thr Ala Arg Glu Ile Ala Arg Leu Arg Arg Pro acc gtg gcc gcg tgg ctg gtc aac ctg ctc gcc ctg cgc cgc ccc gag 192 Thr Val Ala Ala Trp Leu Val Asn Leu Leu Ala Leu Arg Arg Pro Glu ctg gtc gcc gac ctg acc caa ctc gcc gag gcg ctg cgc cgc gcc cag 240 Leu Val Ala Asp Leu Thr Gln Leu Ala Glu Ala Leu Arg Arg Ala Gln cgc gac ctg cgc ggc ccc cgg ctg cgg gaa ctc tcc gcc cag cgg cgg 288 Arg Asp Leu Arg Gly Pro Arg Leu Arg Glu Leu Ser Ala Gln Arg Arg 85 90 gcg gcg gtc gcc gcg ctg gtc gcc gag gcg cgc cgg ctg gcc gcc gac 336 Ala Ala Val Ala Ala Leu Val Ala Glu Ala Arg Arg Leu Ala Ala Asp 105 gcc gag ggc ggc ccg ccg gcc ggg aag ctg ccg ctg ggc gag gtg gag 384 Ala Glu Gly Gly Pro Pro Ala Gly Lys Leu Pro Leu Gly Glu Val Glu 115 120 gcg acg ctc gac gcc gcg ctc tcc gac acg gag gtg gcc ggg cag gtg 432 Ala Thr Leu Asp Ala Ala Leu Ser Asp Thr Glu Val Ala Gly Gln Val 130 ege tee gge egg etg etg egg gee gee age tae gee gge tte gge gag 480

Arg Ser Gly Arg Leu Leu Arg Ala Ala Ser Tyr Ala Gly Phe Gly Glu

		cgc Arg														528
		acc Thr														576
		gcc Ala 195														624
		ctg Leu														672
		ggc Gly														720
		gag Glu		_	_	_		_		_	_	_	_		_	768
		gaa Glu														816
		acc Thr 275														864
		gtc Val								Thr						912
	gac Asp															⁻ 918
<21:	0 > 1: 1 > 3: 2 > PI 3 > M:	06	monos	spora	a cai	rbona	acea									
<22 <22	0> 3> er	vbM														
_	0> 1: Pro	l5 Pro	Pro	Gln 5	Ser	Leu	Leu	Arg	Arg 10	Leu	Tyr	Thr	Glu	Pro 15	Pro	
Glu	Lys	Phe	Val 20	Ala	Thr	Arg	Asp	Ala 25	Ala	Val	Ala	Glu	Ala 30	Arg	Arg	
Ser	Gly	Asp 35	Pro	Ala	Thr	Ala	Arg 40	Glu	Ile	Ala	Arg	Leu 45	Arg	Arg	Pro	
Thr	Val 50	Ala	Ala	Trp	Leu	Val 55	Asn	Leu	Leu	Ala	Leu 60	Arg	Arg	Pro	Glu	
Leu 65	Val	Ala	Asp	Leu	Thr 70	Gln	Leu	Ala	Glu	Ala 75	Leu	Arg	Arg	Ala	Gln 80	

```
Arg Asp Leu Arg Gly Pro Arg Leu Arg Glu Leu Ser Ala Gln Arg Arg
Ala Ala Val Ala Ala Leu Val Ala Glu Ala Arg Arg Leu Ala Ala Asp
            100
                                105
Ala Glu Gly Gly Pro Pro Ala Gly Lys Leu Pro Leu Gly Glu Val Glu
Ala Thr Leu Asp Ala Ala Leu Ser Asp Thr Glu Val Ala Gly Gln Val
    130
                        135
Arg Ser Gly Arg Leu Leu Arg Ala Ala Ser Tyr Ala Gly Phe Gly Glu
Val Pro Arg Pro Gln Leu Arg Leu Val Thr Gly Gly Glu Gln Pro
Pro Pro Thr His Pro Pro Pro Arg Ala Lys Arg Ala Ala Arg Glu Ala
                                185
Glu Arg Ala Ala Arg Ala Glu Arg Ala Arg Gln Arg Arg Met Leu Glu
                            200
Arg Glu Leu Ala Arg Ala Arg Thr Asp Gln Glu Arg Ala Glu Ala Glu
Leu Ala Gly Ala Val Glu Ala Glu His Asp Gly Ala Glu Glu Leu Thr
                    230
                                        235
Gly Ile Glu Arg Ser Leu Ala Glu Leu Glu Arg Ser Arg Ala Glu Ala
                245
                                    250
Glu Gln Glu Leu Ser Arg Arg Lys Leu Ala Arg Arg Ala Ala Glu Arg
Ala Val Thr Ala Ala Gln Arg Arg Thr Gly Glu Ile Glu Gly Ala Ile
Glu Ala Val Asp Ala Glu Asp Gly Ala Val Thr Glu Gly Pro Gly Gly
                        295
Ala Asp
305
<210> 116
<211> 627
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(627)
<220>
<223> evbN
<400> 116
atg cag ctc acc aaa ttc gcc cac tcc tgc ctc cgc gtc gag cac gac
Met Gln Leu Thr Lys Phe Ala His Ser Cys Leu Arg Val Glu His Asp
ggc ggt gtg ctg gtc gtc gac ccg ggc gtc ttc agc gac ccg acc gcg
                                                                   96
```

Gly G	Gly	Val	Leu 20	Val	Val	Asp	Pro	Gly 25	Val	Phe	Ser	Asp	Pro 30	Thr	Ala	
ctg c Leu A																144
gtg g Val A																192
atc t Ile T 65																240
gcc c Ala I																288
gcg g Ala V																336
ccg g Pro V	-		_					_	_		_	_	_			384
ccc c Pro 0	_	_	_	_		_			_	_			_			432
ttc g Phe A 145																480
ttc a		_		_	_	_	_	_	_		-	_		_		528
ctg c Leu I																576
ctg t Leu S																624
gtc Val																627
<210 > <211 > <212 > <213 > <	> 20 > PF) 9 RT	nonos	spora	a cai	cbona	acea									
<220> <223>		/bN														
<400> Met 0			Thr	Lys 5	Phe	Ala	His	Ser	Cys 10	Leu	Arg	Val	Glu	His 15	Asp	
Gly G	3ly	Val	Leu 20	Val	Val	Asp	Pro	Gly 25	Val	Phe	Ser	Asp	Pro 30	Thr	Ala	

Leu Asp Gly Ala Asp Ala Val Leu Ile Thr His Glu His Pro Asp His

```
Val Asp Val Ala Ala Leu Thr Arg Gln Leu Asp Arg Trp Pro Phe Arg
Ile Tyr Gly Pro Ala Ser Leu Ala Gly Ala Leu Gly Asp Val Ala Glu
Ala Leu Glu Pro Ile Ser Pro Gly Gln Ala Phe Thr Ala Ala Gly Val
Ala Val Arg Ala Tyr Gly Gly Arg His Ala Val Ile His Pro Asp Ile
                                105
Pro Val Val Asp Asn Leu Gly Tyr Leu Leu Asn Asp Val Val Tyr His
Pro Gly Asp Ala Leu Val Ala Pro Glu Asp Ala Pro Val Asp Thr Leu
                        135
Phe Ala Pro Ile His Ala Pro Trp Ser Lys Phe Ser Glu Val Leu Asp
145
                    150
                                        155
Phe Ile Arg Ala Val Ala Pro Arg Arg Ala Phe Ala Leu His Asp Gly
Leu Leu Asn Asp Asn Gly Leu Ala Val Leu Asn Arg Gln Tyr Ala Ala
                                185
Leu Ser Gly Thr Asp Tyr Gln Arg Leu Glu Pro Gly Ser Arg Leu Asp
        195
                            200
Val
<210> 118
<211> 690
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(690)
<220>
<223> evb0
<400> 118
atg egg gtg egg gtg gae gat gtg gae gee gee egg tee gee ate
Met Arg Val Arg Val Asp Asp Val Asp Ala Ala Arg Ser Ala Ile
acg gcg gtc acc ggc gtc ggc ggc ttc gtc ggc ggc gac gag cgc agc
Thr Ala Val Thr Gly Val Gly Gly Phe Val Gly Gly Asp Glu Arg Ser
age gge gga ace gee gae gee egg geg gag ttg caa etg egg gtg eeg
Ser Gly Gly Thr Ala Asp Ala Arg Ala Glu Leu Gln Leu Arg Val Pro
```

geg gag egg tte acg gee gte etg gag gag ttg geg agg ete gge egg

Ala(Glu 50	Arg	Phe	Thr	Ala	Val 55	Leu	Glu	Glu	Leu	Ala 60	Arg	Leu	Gly	Arg	
cag (Gln (240
gat o Asp 1																288
cgc a																336
gag a Glu s																384
aag a Lys I																432
acc o Thr I 145																480
ggc t Gly I																528
ctg g Leu (576
gcc (Ala I																624
cgg o Arg A																672
gca g Ala A 225																690
<210: <211: <212: <213:	> 23 > PR	0 RT	nonos	spora	a cai	rbona	acea									
<220: <223:		rb0														
<4002 Met <i>A</i>		_	Arg	Val 5	Asp	Asp	Val	Asp	Ala 10	Ala	Ala	Arg	Ser	Ala 15	Ile	
Thr A	Ala	Val	Thr 20	Gly	Val	Gly	Gly	Phe 25	Val	Gly	Gly	Asp	Glu 30	Arg	Ser	
Ser (Gly	Gly 35	Thr	Ala	Asp	Ala	Arg 40	Ala	Glu	Leu	Gln	Leu 45	Arg	Val	Pro	

```
Ala Glu Arg Phe Thr Ala Val Leu Glu Glu Leu Ala Arg Leu Gly Arg
Gln Glu Gln Arg Ala Ile Arg Thr Glu Asp Val Thr Glu Glu Thr Val
Asp Leu Asp Ala Arg Ile Ala Thr Gln Arg Ala Arg Val Glu Ser Gly
Arg Lys Leu Leu Ala Arg Ala Thr Ser Ile Gly Asp Leu Val Thr Leu
Glu Ser Glu Val Ala Arg Arg Glu Ala Asp Leu Ala Ser Leu Glu Ala
Lys Lys Arg Arg Leu Ala Asp Leu Thr Ser Leu Ser Thr Ile Thr Leu
Thr Leu Val Gly Pro Glu Ala Glu Ala Arg Asp Thr Glu Pro Asp Thr
                                        155
Gly Phe Val Val Gly Leu Arg Gly Gly Trp Thr Ala Phe Val Ala Ser
                165
                                    170
Leu Gly Val Leu Leu Thr Val Leu Gly Ala Leu Leu Pro Phe Ala Val
Ala Leu Gly Val Pro Val Ala Val Leu Leu Ala Val Leu Arg Arg Arg
        195
Arg Arg Pro Pro Ala Pro Ala Val Asn Ala Pro Pro Pro Val Pro
    210
                        215
                                           - 220
Ala Ala Arg Ser Ala Pro
<210> 120
<211> 1260
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1260)
<220>
<223> evbP
<400> 120
gtg acg agt gcg ttg acg ctg ccg aac ggc agc cac ctg gcg tcg tcg
Val Thr Ser Ala Leu Thr Leu Pro Asn Gly Ser His Leu Ala Ser Ser
gcc tgg ccg gag tcg ccg tcc ggg tcg cag cct ttg ccc ttc gag ctc
Ala Trp Pro Glu Ser Pro Ser Gly Ser Gln Pro Leu Pro Phe Glu Leu
gac cat ctg ctc qcc ctc cqg atq ccc qqc ctt atc qcc acc cqc cqq
Asp His Leu Leu Ala Leu Arg Met Pro Gly Leu Ile Ala Thr Arg Arg
```

cac atc cac tcc cac ccg gag ctc tcc ggc gag gag ttc gag acg gcg

His	Ile 50	His	Ser	His	Pro	Glu 55	Leu	Ser	Gly	Glu	Glu 60	Phe	Glu	Thr	Ala	
							tcg Ser									240
_		_				_	atc Ile	_	_		_		_		_	288
	_		_			_	gcc Ala	_		_	~ ~	_	_	_		336
							cgg Arg 120									384
_	_			_			acc Thr			_			_			432
ctg Leu 145	ctg Leu	gcc Ala	caa Gln	ctc Leu	gcc Ala 150	aac Asn	ctc Leu	ggc Gly	gaa Glu	ttg Leu 155	gac Asp	ggc Gly	cgg Arg	gtc Val	cgg Arg 160	480
							gag Glu									528
							gac Asp									576
							gtc Val 200									624
							aac Asn									672
ggc Gly 225	Gly 399	cac His	acc Thr	gct Ala	cgc Arg 230	ccg Pro	cac His	ctg Leu	acc Thr	gtc Val 235	gac Asp	ctg Leu	gtc Val	gac Asp	gcg Ala 240	720
							gtg Val									768
							ctc Leu									816
							tcc Ser 280									864
							tgg Trp									912
							gcc Ala									960

305	310	315	320
Glu Tyr Leu Arg (gtg acc aac gac gcc cg Val Thr Asn Asp Ala Ar 330	
		gcc gcg ctc ggc ccg ga Ala Ala Leu Gly Pro Gl 345 35	u Gly Val
		ggc gag gac ttc tcc tg Gly Glu Asp Phe Ser Tr 365	
gag tac gtc ccc g Glu Tyr Val Pro G 370	ggc gcg ctg gcc Sly Ala Leu Ala 375	cgc ctc ggc gtc ggc cg Arg Leu Gly Val Gly Ar 380	g tcc ggc 1152 g Ser Gly
		tcg ttc gac gtc gac ga Ser Phe Asp Val Asp Gl 395	
Ile Ala Val Gly	atc cgg gtc atg [le Arg Val Met 105	gtg cag acc gcg ctg cg Val Gln Thr Ala Leu Arc 410	g gca ctg 1248 g Ala Leu 415
gcg gcg gcg cgt Ala Ala Ala Arg 420			1260
<210> 121 <211> 420 <212> PRT <213> Micromonosp	pora carbonacea		
<211> 420 <212> PRT	pora carbonacea		
<211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121		Asn Gly Ser His Leu Al	a Ser Ser 15
<211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala II	Leu Thr Leu Pro 5	_	15 e Glu Leu
<211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala II Ala Trp Pro Glu S 20	Leu Thr Leu Pro 5 Ser Pro Ser Gly	10 Ser Gln Pro Leu Pro Ph	15 e Glu Leu O
<pre><211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala I 1 Ala Trp Pro Glu S 20 Asp His Leu Leu A 35</pre>	Ser Pro Ser Gly Ala Leu Arg Met	Ser Gln Pro Leu Pro Ph 25 3 Pro Gly Leu Ile Ala Th	15 e Glu Leu 0 r Arg Arg
<pre><211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala I 1 Ala Trp Pro Glu S 20 Asp His Leu Leu A 35 His Ile His Ser H 50</pre>	Ser Pro Ser Gly Ala Leu Arg Met 40 His Pro Glu Leu 55	Ser Gln Pro Leu Pro Ph 25 3 Pro Gly Leu Ile Ala Th 45	15 e Glu Leu 0 r Arg Arg u Thr Ala
<pre><211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala I Ala Trp Pro Glu S</pre>	Leu Thr Leu Pro 5 Ser Pro Ser Gly Ala Leu Arg Met 40 His Pro Glu Leu 55 Arg Glu Leu Ser	Ser Gln Pro Leu Pro Pho 25 3 Pro Gly Leu Ile Ala Tho 45 Ser Gly Glu Glu Phe Gl 60 Leu Ala Gly Leu Arg Pro	15 e Glu Leu 0 r Arg Arg u Thr Ala o Arg Leu 80
<pre><211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala I 1 Ala Trp Pro Glu S 20 Asp His Leu Leu A 35 His Ile His Ser H 50 Ala Leu Ile Ala A 65</pre> Leu Pro Lys Gly A	Ger Pro Ser Gly Ala Leu Arg Met 40 His Pro Glu Leu 55 Arg Glu Leu Ser 70 Asn Gly Val Ile	Ser Gln Pro Leu Pro Pho 25 3 Pro Gly Leu Ile Ala Tho 45 Ser Gly Glu Glu Phe Gl 60 Leu Ala Gly Leu Arg Pro 75 Cys Asp Ile Asp Gly Arg	15 e Glu Leu 0 r Arg Arg u Thr Ala o Arg Leu 80 g Pro Asp 95 o Leu Thr
<pre><211> 420 <212> PRT <213> Micromonosp <220> <223> evbP <400> 121 Val Thr Ser Ala I Ala Trp Pro Glu S 20 Asp His Leu Leu A 35 His Ile His Ser B 50 Ala Leu Ile Ala A 65 Leu Pro Lys Gly A Gly Pro Val Val A 100</pre>	Leu Thr Leu Pro 5 Ser Pro Ser Gly Ala Leu Arg Met 40 His Pro Glu Leu 55 Arg Glu Leu Ser 70 Asn Gly Val Ile 85 Ala Leu Arg Ala	Ser Gln Pro Leu Pro Pho 25 3 Pro Gly Leu Ile Ala Tho 45 Ser Gly Glu Glu Phe Glo 60 Leu Ala Gly Leu Arg Pro 75 Cys Asp Ile Asp Gly Arg 90 Asp Ile Asp Ala Leu Pro 100 100 100 100 100 100 100 100 100 10	15 e Glu Leu 0 r Arg Arg u Thr Ala o Arg Leu 80 g Pro Asp 95 o Leu Thr

		130					135					140				
	Leu 145	Leu	Ala	Gln	Leu	Ala 150	Asn	Leu	Gly	Glu	Leu 155	Asp	Gly	Arg	Val	Arg 160
	Leu	Ile	Phe	Gln	Pro 165	Ala	Glu	Glu	Ile	Leu 170	Pro	Cys	Gly	Ser	Leu 175	Glu
•	Val	Ile	Glu	Ala 180	Gly	Gly	Leu	Asp	Asp 185	Val	Val	Gln	Ile	Phe 190	Ala	Leu
1	His	Сув	Asp 195	Pro	Asn	Gln	Pro	Val 200	Gly	Lys	Val	Gly	Leu 205	Arg	Val	Gly
	Pro	Ile 210	Thr	Ala	Ala	Ala	Asp 215	Asn	Val	Thr	Val	Arg 220	Leu	Thr	Gly	Pro
	Gly 225	Gly	His	Thr	Ala	Arg 230	Pro	His	Leu	Thr	Val 235	Asp	Leu	Val	Asp	Ala 240
	Leu	Gly	Arg	Leu	Val 245	Thr	Glu	Val	Pro	Ala 250	Leu	Val	Ser	Arg	Arg 255	Val
	Pro	Ala	Asn	Ser 260	Gly	Leu	Leu	Leu	Val 265	Phe	Gly	His	Ala	Ser 270	Ala	Gly
•	Thr	Arg	Tyr 275	Asn	Val	Ile	Pro	Ser 280	Glu	Ala	Ser	Ala	Ser 285	Gly	Thr	Leu
1	Arg	Val 290	Met	Asp	Arg	Asp	Thr 295	Trp	Asp	Gln	Ala	Pro 300	Lys	Ile	Val	Ala
	Gln 305	Val	Val	Arg	Asp	Val 310	Ile	Ala	Pro	Thr	Gly 315	Ala	Thr	Val	Asp	Leu 320
•	Glu	Tyr	Leu	Arg	Gly 325	Arg	Pro	Pro	Val	Thr 330	Asn	Asp	Ala	Arg	Ala 335	Ile
•	Gln	Val	Leu	Thr 340	Ala	Ala	Thr	His	Ala 345	Ala	Leu	Gly	Pro	Glu 350	Gly	Val
1	Ala	Glu	Thr 355	Pro	Gln	Ser	Met	Gly 360	Gly	Glu	Asp	Phe	Ser 365	Trp	Tyr	Leu
•	Glu	Tyr 370	Val	Pro	Gly	Ala	Leu 375	Ala	Arg	Leu	Gly	Val 380	Gly	Arg	Ser	Gly
	Pro 385	Asn	Val	Asp	Leu	His 390	Arg	Ala	Ser	Phe	Asp 395	Val	Asp	Glu	Gly	Ala 400
	Ile	Ala	Val	Gly	Ile 405	Arg	Val	Met	Val	Gln 410	Thr	Ala	Leu	Arg	Ala 415	Leu
ì	Ala	Ala	Ala	Arg												

<210> 122

<211> 1581

<212> DNA

<213> Micromonospora carbonacea

420

<220>

<221> CDS

<222> (1)..(1581) <220> <223> evbQ <400> 122 atg agt gaa ccg cgg tcg agc gag tcc ggc ttc ccg atc aag ggt gtc Met Ser Glu Pro Arg Ser Ser Glu Ser Gly Phe Pro Ile Lys Gly Val tac acc cag agg gac ctg ccg gag ggt ctg ccc gag cgg ctg ggc gag 96 Tyr Thr Gln Arg Asp Leu Pro Glu Gly Leu Pro Glu Arg Leu Gly Glu ccg ggg gag ttc ccg tac acc cgt ggg gtc tac tcc acc atg tac acc 144 Pro Gly Glu Phe Pro Tyr Thr Arg Gly Val Tyr Ser Thr Met Tyr Thr 35 teg egg eeg tgg aeg atg ege eag tae gee gge tte gge aee geq aeq 192 Ser Arg Pro Trp Thr Met Arg Gln Tyr Ala Gly Phe Gly Thr Ala Thr gag age aac geg ege tac cac cag etc etg ege gee gge acc atg gge 240 Glu Ser Asn Ala Arg Tyr His Gln Leu Leu Arg Ala Gly Thr Met Gly 70 ctc tcc gtc gct ttt gat ctg ccc acc cag atg ggg tac gac tcg gac 288 Leu Ser Val Ala Phe Asp Leu Pro Thr Gln Met Gly Tyr Asp Ser Asp 90 gac ccg atc gcc cac ggc gag gtc ggc aag gtc ggc gtc gcc atc gac 336 Asp Pro Ile Ala His Gly Glu Val Gly Lys Val Gly Val Ala Ile Asp 100 105 tcg atc gag gac atg cgg ctg ctg ttc cac ggc atc ccg ttg gac aag 384 Ser Ile Glu Asp Met Arg Leu Leu Phe His Gly Ile Pro Leu Asp Lys 115 gtt tcc acc tcg atg acg atc aac gcc ccg ggg tcg gtg ctg ctg ctg 432 Val Ser Thr Ser Met Thr Ile Asn Ala Pro Gly Ser Val Leu Leu Leu 130 135 ctc tac cag ctc gtc gcc gag gag gcg gtg ccg ggc gcg gcg ctc 480 Leu Tyr Gln Leu Val Ala Glu Glu Ala Gly Val Pro Gly Ala Ala Leu 145 aac ggc acc atc cag aac gac atc ctc aag gag tac atc gcc cgg ggc 528 Asn Gly Thr Ile Gln Asn Asp Ile Leu Lys Glu Tyr Ile Ala Arg Gly 165 acg tac atc ttc ccg ccg aag ccc tcg ctg cgg ctg gtc gcc gac acg 576 Thr Tyr Ile Phe Pro Pro Lys Pro Ser Leu Arg Leu Val Ala Asp Thr ttc gcc tac tgc cgg gcg gag gtg ccg aag tgg aac acc atc tcc atc 624 Phe Ala Tyr Cys Arg Ala Glu Val Pro Lys Trp Asn Thr Ile Ser Ile tcc ggc tac cac atg gcc gag gcc ggc gcg tcg ccc gcg cag gag atc 672 Ser Gly Tyr His Met Ala Glu Ala Gly Ala Ser Pro Ala Gln Glu Ile geg tte acg etg gee aac gge gte gag tac gte egg gee geg ete gee 720

Ala Phe Thr Leu Ala Asn Gly Val Glu Tyr Val Arg Ala Ala Leu Ala

235

gcc Ala	ggg Gly	ctg Leu	gcg Ala	gtg Val 245	gac Asp	gac Asp	ttc Phe	gcg Ala	ccc Pro 250	cgg Arg	ctg Leu	tcg Ser	ttc Phe	ttc Phe 255	ttc Phe	768
gtc Val	gcc Ala	cgg Arg	acc Thr 260	acc Thr	ctg Leu	ctg Leu	gag Glu	gag Glu 265	gtc Val	gcg Ala	aag Lys	ttc Phe	cgt Arg 270	gcc Ala	gcc Ala	816
cgg Arg	cgg Arg	atc Ile 275	tgg Trp	gcc Ala	cgg Arg	ctg Leu	atg Met 280	cgc Arg	gac Asp	gag Glu	ttc Phe	ggc Gly 285	gcg Ala	aag Lys	aac Asn	864
					ctg Leu											912
ctc Leu 305	acc Thr	gcc Ala	cag Gln	cag Gln	ccc Pro 310	gag Glu	gtg Val	aac Asn	ctg Leu	gtc Val 315	cgg Arg	gtg Val	gcg Ala	atc Ile	cag Gln 320	960
					ctc Leu											1008
ttc Phe	gac Asp	gag Glu	gcc Ala 340	atc Ile	gcg Ala	ctg Leu	ccc Pro	acc Thr 345	gag Glu	aag Lys	gcc Ala	gcc Ala	cgg Arg 350	ctg Leu	gcg Ala	1056
ctg Leu	cgc Arg	acc Thr 355	cag Gln	cag Gln	gtg Val	ctc Leu	gcg Ala 360	tac Tyr	gag Glu	acg Thr	gac Asp	ctg Leu 365	acc Thr	gcc Ala	acc Thr	1104
					Gly 333											1152
					gtg Val 390											1200
tcg Ser	gtg Val	gtc Val	gac Asp	gcc Ala 405	atc Ile	gag Glu	gcg Ala	ggc Gly	ttc Phe 410	cag Gln	aag Lys	cgg Arg	gag Glu	atc Ile 415	gag Glu	1248
cag Gln	tcc Ser	gcg Ala	tac Tyr 420	cgg Arg	atc Ile	gcc Ala	cag Gln	gag Glu 425	atc Ile	gac Asp	tcg Ser	ggc Gly	gag Glu 430	cgg Arg	gtg Val	1296
gtg Val	gtc Val	ggc Gly 435	ctc Leu	aac Asn	cgg Arg	ttc Phe	acg Thr 440	gtc Val	gac Asp	gcc Ala	gac Asp	gag Glu 445	ccg Pro	tac Tyr	gag Glu	1344
					ccg Pro											1392
gcc Ala 465	aag Lys	ctg Leu	cga Arg	gtg Val	gag Glu 470	cgc Arg	gac Asp	agc Ser	gac Asp	gcc Ala 475	gtc Val	gag Glu	cgc Arg	gcg Ala	ctg Leu 480	1440
					gcc Ala											1488

atg aag gag gcg ctg cgg gcc cgg gcc acg gtg ggc gag gtc tgt ggc Met Lys Glu Ala Leu Arg Ala Arg Ala Thr Val Gly Glu Val Cys Gly 500 505 510	1536
acc ctg cgc cag gtg tgg ggg acg tac cgc ccc agc gac cgg ttc Thr Leu Arg Gln Val Trp Gly Thr Tyr Arg Pro Ser Asp Arg Phe 515 520 525	1581
<210> 123 <211> 527 <212> PRT <213> Micromonospora carbonacea	
<220> <223> evbQ	
<400> 123 Met Ser Glu Pro Arg Ser Ser Glu Ser Gly Phe Pro Ile Lys Gly Val 1 5 10 15	
Tyr Thr Gln Arg Asp Leu Pro Glu Gly Leu Pro Glu Arg Leu Gly Glu 20 25 30	
Pro Gly Glu Phe Pro Tyr Thr Arg Gly Val Tyr Ser Thr Met Tyr Thr 35 40 45	
Ser Arg Pro Trp Thr Met Arg Gln Tyr Ala Gly Phe Gly Thr Ala Thr 50 55 60	
Glu Ser Asn Ala Arg Tyr His Gln Leu Leu Arg Ala Gly Thr Met Gly 65 70 75 80	
Leu Ser Val Ala Phe Asp Leu Pro Thr Gln Met Gly Tyr Asp Ser Asp 85 90 95	
Asp Pro Ile Ala His Gly Glu Val Gly Lys Val Gly Val Ala Ile Asp 100 105 110	
Ser Ile Glu Asp Met Arg Leu Leu Phe His Gly Ile Pro Leu Asp Lys 115 120 125	
Val Ser Thr Ser Met Thr Ile Asn Ala Pro Gly Ser Val Leu Leu 130 135 140	
Leu Tyr Gln Leu Val Ala Glu Glu Ala Gly Val Pro Gly Ala Ala Leu 145 150 155 160	
Asn Gly Thr Ile Gln Asn Asp Ile Leu Lys Glu Tyr Ile Ala Arg Gly 165 170 175	
Thr Tyr Ile Phe Pro Pro Lys Pro Ser Leu Arg Leu Val Ala Asp Thr 180 185 190	
Phe Ala Tyr Cys Arg Ala Glu Val Pro Lys Trp Asn Thr Ile Ser Ile 195 200 205	
Ser Gly Tyr His Met Ala Glu Ala Gly Ala Ser Pro Ala Gln Glu Ile 210 215 220	
Ala Phe Thr Leu Ala Asn Gly Val Glu Tyr Val Arg Ala Ala Leu Ala 225 230 235 240	
Ala Gly Leu Ala Val Asp Asp Phe Ala Pro Arg Leu Ser Phe Phe Phe 245 250 255	

Val Ala Arg Thr Thr Leu Leu Glu Glu Val Ala Lys Phe Arg Ala Ala Arg Arg Ile Trp Ala Arg Leu Met Arg Asp Glu Phe Gly Ala Lys Asn 280 Pro Lys Ser Met Met Leu Arg Phe His Thr Gln Thr Ala Gly Val Gln 295 Leu Thr Ala Gln Gln Pro Glu Val Asn Leu Val Arg Val Ala Ile Gln 310 315 Gly Leu Gly Ala Val Leu Gly Gly Thr Gln Ser Leu His Thr Asn Ser 325 330 Phe Asp Glu Ala Ile Ala Leu Pro Thr Glu Lys Ala Ala Arg Leu Ala Leu Arg Thr Gln Gln Val Leu Ala Tyr Glu Thr Asp Leu Thr Ala Thr Val Asp Pro Phe Ala Gly Ser Tyr Val Val Glu Ala Met Thr Ala Glu 370 375 Ile Glu Ala Ala Val Val Glu Leu Met Glu Arg Val Ala Asp His Gly 390 395 Ser Val Val Asp Ala Ile Glu Ala Gly Phe Gln Lys Arg Glu Ile Glu Gln Ser Ala Tyr Arg Ile Ala Gln Glu Ile Asp Ser Gly Glu Arg Val 425 Val Val Gly Leu Asn Arg Phe Thr Val Asp Ala Asp Glu Pro Tyr Glu Pro Leu Arg Val Asp Pro Thr Ile Glu Ala Ala Gln Ala Glu Arg Leu Ala Lys Leu Arg Val Glu Arg Asp Ser Asp Ala Val Glu Arg Ala Leu 475 Gly Glu Leu Arg Ala Ala Ala Glu Gly Thr Ala Asn Val Leu His Pro 485 Met Lys Glu Ala Leu Arg Ala Arg Ala Thr Val Gly Glu Val Cys Gly 505 Thr Leu Arg Gln Val Trp Gly Thr Tyr Arg Pro Ser Asp Arg Phe 520

```
<210> 124

<211> 2088

<212> DNA

<213> Micromonospora carbonacea

<220>

<221> CDS

<222> (1)..(2088)

<220>
```

<223> evbR

<400> 124							
atg ggc acg Met Gly Thr 1							
gcg gtg aag Ala Val Lys		_		_			
gac gcc ato Asp Ala Met 35	Tyr Glu A		Arg Glu				
atc cag cac Ile Gln His 50							
ggt cgc ccc Gly Arg Pro 65	Trp Ile V						a
gac atg gtg Asp Met Val							
atc ggc atc Ile Gly Ile							
gtg ctg cac Val Leu His 115	s Arg Asp V		Ala Asn				
ggc cgg tgc Gly Arg Cys 130							
gtg cag ctc Val Gln Leu 145	ı Thr Thr P						е
tcc ccc gag Ser Pro Glu				Gly Pro			
ttc tcc ctc Phe Ser Leu	ggc gtc a Gly Val T 180	eg ete tae nr Leu Tyr	acg gcg Thr Ala 185	gtg gag Val Glu	ggc cgg Gly Arg 190	ccc ccc Pro Pro	g 576 o
ttc gac agg Phe Asp Arg 195	Gly Asp P		Thr Met				
ccg ccg gcc Pro Pro Ala 210							
ggg ctg ctg Gly Leu Leu 225	ı Glu Lys A						a
cgc gcg atg Arg Ala Met							

				tcg Ser												816
				gtc Val												864
_		_		ggc Gly				_		_				_	_	912
				gcg Ala												960
				gcc Ala 325												1008
				cac His												1056
				tac Tyr												1104
				ccg Pro												1152
				cag Gln												1200
				ccc Pro 405												1248
				cgc Arg												1296
agc Ser	cag Gln	ccc Pro 435	ggc Gly	gcg Ala	acg Thr	cag Gln	ccg Pro 440	gtc Val	ccc Pro	ggc Gly	ttc Phe	ggc Gly 445	gcg Ala	tcg Ser	ccg Pro	1344
				cgg Arg												1392
				ggc Gly												1440
				ggc Gly 485												1488
				cgc Arg												1536

gtg Val	ctg Leu	ctg Leu 515	ctg Leu	atc Ile	ggc Gly	gtg Val	ttc Phe 520	gcc Ala	ctc Leu	ttc Phe	ggc Gly	ggc Gly 525	gac Asp	gac Asp	ccg Pro	1584
					ccg Pro											1632
					atg Met 550											1680
					tgg Trp											1728
gtc Val	_			_	ccg Pro		_		_	_	_		_			1776
					ggc Gly											1824
					cgg Arg											1872
					cag Gln 630											1920
					gac Asp											1968
					ggc Gly											2016
gac Asp																2064
					G1 999											2088
<210 <211 <212 <213	.> 69 !> PF	96 RT	nonos	spora	a cai	cbona	acea									
<220 <223		/bR														
<400 Met 1	_	_	Val	Trp 5	Arg	Ala	Thr	Asp	Thr 10	Leu	Leu	Arg	Arg	Asp 15	Val	
Ala	Val	Lys	Glu 20	Val	Val	Leu	Pro	Pro 25	Gly	Leu	Ala	Pro	Ser 30	Asp	Arg	

Asp Ala Met Tyr Glu Arg Thr Leu Arg Glu Ala Arg Ala Ala Ala

45

40

35

Ile Gln His Pro Ala Val Val Gln Val Tyr Asp Val Val Thr Glu Gly 55 Gly Arg Pro Trp Ile Val Met Glu Leu Leu Asp Ala Arg Ser Leu Ala Asp Met Val Ile Glu Asp Gly Pro Val Ala Pro Arg Ala Val Ala Lys Ile Gly Ile Ala Leu Leu Gly Ala Leu Glu Val Ala His Ala Ile Gly Val Leu His Arg Asp Val Lys Pro Ala Asn Val Leu Ile Cys Thr Asp Gly Arg Cys Val Leu Thr Asp Phe Gly Val Ala Lys Leu Pro Thr Asp 135 Val Gln Leu Thr Thr Pro Gly Met Val Leu Gly Ser Pro His Phe Ile 150 155 Ser Pro Glu Arg Ala Met Gly Gln Glu Phe Gly Pro Pro Ser Asp Leu Phe Ser Leu Gly Val Thr Leu Tyr Thr Ala Val Glu Gly Arg Pro Pro Phe Asp Arg Gly Asp Pro Ile Glu Thr Met His Ala Val Val Glu Asp 200 Pro Pro Ala Thr Pro Gln Arg Ser Gly Pro Leu Thr Arg Val Leu Met Gly Leu Leu Glu Lys Asp Pro Ala Arg Arg Leu Asp Val His Thr Ala 235 Arg Ala Met Leu Arg Glu Leu Leu Ala Gly Pro Leu Thr Ser Thr Ala 250 Thr Ala Val Asn Ser Val Thr Asp Pro Tyr Ala Val Val Pro Val Lys Gln Arg Pro Ala Val Ala Pro Pro Pro Ser Ala Ala Glu Pro Lys Pro 280 Ser Gly Gln Ile Gly Gly Arg Ala Met Leu Ala Pro Gly Glu Ser Leu Thr Asp Arg Leu Ala Ala Leu Arg Arg Gly Glu Lys Thr Arg Lys Arg Lys Thr Thr Thr Ala Ala Ala Leu Asp Asp Thr Ser Ala Asp Ala Leu Ala Gly Pro Leu His Thr Pro Thr Gly Ala Met Pro Ala Pro Pro Pro 345 Ala Gly Arg Thr Tyr Gly Gly Ser Ser Glu Ala Thr Gln Arg Val Asp 360 Ala Gly Thr Ala Pro Glu Ala Thr Gln Arg Met Thr Tyr Gly Ser Pro 370

Pro Asp Ala Thr Gln Arg Val Ser His Gly Ser Gly Pro Ser Glu Ala Thr Gln Arg Val Pro Tyr Gly Gly Gly Ser Ala Asp Ala Thr Gln Gln 405 Val Pro Phe Gly Arg Arg Pro Asp Ala Thr Gln Arg Val Pro Tyr Gly 425 Ser Gln Pro Gly Ala Thr Gln Pro Val Pro Gly Phe Gly Ala Ser Pro Asp Ala Thr Gln Arg Val Gly Gly Ala Tyr Gly Gly Gln Trp Ser Val Pro Gly Thr Gly Gln Pro Trp Ala Thr Pro Ala Thr Ala Pro Ala 475 Pro Ala Thr Ala Gly Gly Gly Val Gly Arg Leu Val Ala Thr Val Lys Gly Trp Pro Arg Lys Val Gln Leu Ala Ala Ala Gly Gly Val Ala 505 Val Leu Leu Ile Gly Val Phe Ala Leu Phe Gly Gly Asp Asp Pro Glu Gln Pro Thr Thr Pro Gln Gly Gln Pro Ser Ala Gly Ala Pro Ala 535 Gly Pro Gly Val Glu Met Gln Glu Gln Ser Ala Lys Gly Val Thr Val 550 555 Gln Val Pro Lys Gly Trp Glu Arg Arg Ser Ala Asp Gly Gly Val Trp 570 Val Asp Tyr Ile Asp Pro Glu Asp Asn Ser Arg Lys Val Arg Ile Leu 585 Ala Glu Arg Trp Ser Gly Thr Ser Thr Arg Trp Ala Glu Thr Ala Ala 605 Asn Gly Leu Arg Thr Arg Ser Ala Ser Cys Gln Lys Pro Tyr Asn Gln Val Ser Met Thr Glu Glu Leu Asp Gly Lys Ala Ala Ala Glu Phe Glu Tyr Thr Cys Gly Asp Gly Glu Gly Lys Arg His Gly Val Trp Arg 650 Gly Val Val His Glu Gly Lys Val Tyr Ser Phe Tyr Leu Ser Ser Thr Asp Ala Arg Phe Ala Glu Ser Lys Pro Ile Phe Asp Gln Met Val Ala Ser Phe Lys Leu Arg Gly Ser Asp 690 695

<210> 126

<211> 1728

<212> DNA

```
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1728)
<220>
<223> evbS
<400> 126
atg gcg gcg gac acc act gac ctc gac gac acg cgc gat ctg gac gac
Met Ala Ala Asp Thr Thr Asp Leu Asp Asp Thr Arg Asp Leu Asp Asp
ett ege gae egg gee egg egg tgg ete gae gae gae eee gae eeg gee
                                                                 96
Leu Arg Asp Arg Ala Arg Arg Trp Leu Asp Asp Asp Pro Asp Pro Ala
acc cgc gac gag ctg gag gcc gtg ctc gac ggg ctg ccg gcg agc gcg
                                                                 144
Thr Arg Asp Glu Leu Glu Ala Val Leu Asp Gly Leu Pro Ala Ser Ala
gcc gag ctg gcc gac cgg ttc gcc ggg cca ctg acc ttc ggc acc gcc
                                                                 192
Ala Glu Leu Ala Asp Arg Phe Ala Gly Pro Leu Thr Phe Gly Thr Ala
ggg ctg cgc ggc ccg ctg cgc gcc ggc ccc aac ggg atg aac ctc gcc
                                                                 240
Gly Leu Arg Gly Pro Leu Arg Ala Gly Pro Asn Gly Met Asn Leu Ala
288
gac gec acc ggg eeg etg gtc atc ggg tac gac gec egg cac ggc teg
                                                                 336
Asp Ala Thr Gly Pro Leu Val Ile Gly Tyr Asp Ala Arg His Gly Ser
            100
                               105
egg gag tte gee gag ege ace gee eag gtg gee ace gge geg gge ege
                                                                 384
Arg Glu Phe Ala Glu Arg Thr Ala Gln Val Ala Thr Gly Ala Gly Arg
        115
                           120
                                               125
ccg gcg ctg ctg ccc cgc ccg ctg ccc acc ccc gtg ctg gcg tac
                                                                 432
Pro Ala Leu Leu Pro Arg Pro Leu Pro Thr Pro Val Leu Ala Tyr
    130
gcg gtg cgg cag ctc gac gcg gcg gcc ggc gtg atg gtg acc gcc agc
                                                                 480
Ala Val Arg Gln Leu Asp Ala Ala Ala Gly Val Met Val Thr Ala Ser
145
                   150
                                       155
                                                           160
cac aac ccg ccc cag gac aac ggc tac aag gtc tac ctc ggc gcg cag
                                                                 528
His Asn Pro Pro Gln Asp Asn Gly Tyr Lys Val Tyr Leu Gly Ala Gln
etc ggc ggc gag etg ggc gcg ggg gcg cag atc gtg ccg ccg gcc gac
                                                                 576
Leu Gly Gly Glu Leu Gly Ala Gly Ala Gln Ile Val Pro Pro Ala Asp
           180
                               185
                                                   190
acc ggc atc gag gcc gcc atc cgg gcg gtc ggc ccg ctg gcc gac gta
                                                                 624
Thr Gly Ile Glu Ala Ala Ile Arg Ala Val Gly Pro Leu Ala Asp Val
                           200
eeg etg gge eeg gee ggg eag gte gte gge gae gae gtg gte gtg teg
                                                                 672
Pro Leu Gly Pro Ala Gly Gln Val Val Gly Asp Asp Val Val Val Ser
   210
                       215
                                           220
```

					gcc Ala 230											720
ctg Leu	aag Lys	gtg Val	gcc Ala	tac Tyr 245	acg Thr	ccg Pro	ctg Leu	cac His	ggc Gly 250	gtg Val	ggc Gly	gcg Ala	gcc Ala	gtg Val 255	ctg Leu	768
					cgc Arg											816
					gac Asp											864
					gcg Ala											912
			_	_	gcg Ala 310		_		_		_		_	_	_	960
					gac Asp											1008
					atg Met											1056
					cgc Arg											1104
Ala	Asp	His 355 tcg	Leu	Met		Arg	Gly 360 cgg	Val	His atg	Gly tgc	Leu	Tyr 365 gcc	Ala	Thr	Thr ctg	1104
Ala atc Ile	Asp gtg Val 370 tac	His 355 tcg ser gac	tcg Ser	Met tcc Ser	Arg	cta Leu 375	Gly 360 cgg Arg	Val gcc Ala ttc	His atg Met	Gly tgc Cys	gcc Ala 380 atc	Tyr 365 gcc Ala gtc	Ala cgt Arg	Thr ggc Gly gcc	Thr ctg Leu ggc	
Ala atc Ile ccg Pro 385	Asp gtg Val 370 tac Tyr	His 355 tcg Ser gac Asp	tcg Ser gag Glu	Met tcc Ser acg Thr	ctg Leu ctg Leu	cta Leu 375 acc Thr	Gly 360 cgg Arg ggc Gly	Val gcc Ala ttc Phe	His atg Met aag Lys	Gly tgc Cys tgg Trp 395 ccg	gcc Ala 380 atc Ile	Tyr 365 gcc Ala gtc Val	Ala cgt Arg cgg Arg	Thr ggc Gly gcc Ala	Ctg Leu ggc Gly 400 tac	1152
Ala atc Ile ccg Pro 385 ggc Gly	Asp gtg Val 370 tac Tyr gga Gly	His 355 tcg Ser gac Asp ccg Pro	tcg ser gag Glu ctg Leu	Met tcc ser acg Thr ggt Gly 405	ctg Leu ctg Leu 390	cta Leu 375 acc Thr	Gly 360 cgg Arg ggc Gly ggc Gly	yal gcc Ala ttc Phe tcc Ser	His atg Met aag Lys gac Asp 410 ccg	tgc Cys tgg Trp 395 ccg Pro	gcc Ala 380 atc Ile ctg Leu	Tyr 365 gcc Ala gtc Val gtc Val	Ala cgt Arg cgg Arg ttc Phe	ggc Gly 415	Ctg Leu ggc Gly 400 tac Tyr	1152 1200
Ala atc Ile ccg Pro 385 ggc Gly gag Glu gac	Asp gtg Val 370 tac Tyr gga Gly gag Glu	His 355 tcg Ser gac Asp ccg Pro	tcg ser gag Glu ctg Leu ctg Leu 420	Met tcc ser acg Thr ggt Gly 405 ggc Gly	ctg Leu ctg Leu 390 gag Glu	cta Leu 375 acc Thr gcc Ala tgc Cys	Gly 360 cgg Arg ggc Gly ggc Gly gtc Val	yal gcc Ala ttc Phe tcc Ser gcc Ala 425	His atg Met aag Lys gac Asp 410 ccg Pro	tgc Cys tgg Trp 395 ccg Pro	gcc Ala 380 atc Ile ctg Leu cac His ctg	Tyr 365 gcc Ala gtc Val gtc Val gtc	Ala cgt Arg cgg Arg ttc Phe cgc Arg 430 gcc	ggc Gly 415 gac Asp	Ctg Leu ggc Gly 400 tac Tyr aag Lys	1152 1200 1248
Ala atc Ile ccg Pro 385 ggc Gly gag Glu gac Asp	gtg Val 370 tac Tyr gga Gly gag Glu	His 355 tcg Ser gac Asp ccg Pro gcg Ala atc Ile 435	tcg ser gag Glu ctg Leu ctg Leu 420 acc Thr	Met tcc ser acg Thr ggt Gly 405 ggc Gly gcc Ala	ctg Leu ctg Leu 390 gag Glu tac Tyr	cta Leu 375 acc Thr gcc Ala tgc Cys	Gly 360 cgg Arg ggc Gly ggc Gly gtc Val acc Thr 440 acc	yal gcc Ala ttc Phe tcc Ser gcc Ala 425 gtc Val	His atg Met aag Lys gac Asp 410 ccg Pro gcc Ala	tgc Cys tgg Trp 395 ccg Pro gag Glu gag Glu	gcc Ala 380 atc Ile ctg Leu cac His ctg Leu gac	Tyr 365 gcc Ala gtc Val gtc Val gtc Val gtc Val gtc yal	cgt Arg cgg Arg ttc Phe cgc Arg 430 gcc Ala	ggc Gly 415 gac Asp Gly Gly	Thr ctg Leu ggc Gly 400 tac Tyr aag Lys ctg Leu	1152 1200 1248 1296

						gcg Ala									1488
_		_			_	ccg Pro						_	_		1536
						ctg Leu									1584
_	_	_				ccg Pro 535	_		_			-			 1632
						gac Asp									1680
_	_	_		_		cgc Arg	~	_		_	_	_		_	 1728
<210> 127 <211> 576 <212> PRT															

<213> Micromonospora carbonacea

<220>

<223> evbS

<400> 127

Met Ala Ala Asp Thr Thr Asp Leu Asp Asp Thr Arg Asp Leu Asp Asp

Leu Arg Asp Arg Ala Arg Arg Trp Leu Asp Asp Pro Asp Pro Ala

Thr Arg Asp Glu Leu Glu Ala Val Leu Asp Gly Leu Pro Ala Ser Ala

Ala Glu Leu Ala Asp Arg Phe Ala Gly Pro Leu Thr Phe Gly Thr Ala

Gly Leu Arg Gly Pro Leu Arg Ala Gly Pro Asn Gly Met Asn Leu Ala

Val Val Thr Gln Ala Ala Gly Leu Val Ala Trp Leu Ala Ala Gln

Asp Ala Thr Gly Pro Leu Val Ile Gly Tyr Asp Ala Arg His Gly Ser 105

Arg Glu Phe Ala Glu Arg Thr Ala Gln Val Ala Thr Gly Ala Gly Arg 120

Pro Ala Leu Leu Pro Arg Pro Leu Pro Thr Pro Val Leu Ala Tyr

Ala Val Arg Gln Leu Asp Ala Ala Ala Gly Val Met Val Thr Ala Ser 150

His Asn Pro Pro Gln Asp Asn Gly Tyr Lys Val Tyr Leu Gly Ala Gln

165 170 175 Leu Gly Gly Glu Leu Gly Ala Gly Ala Gln Ile Val Pro Pro Ala Asp 185 Thr Gly Ile Glu Ala Ala Ile Arg Ala Val Gly Pro Leu Ala Asp Val Pro Leu Gly Pro Ala Gly Gln Val Val Gly Asp Asp Val Val Ser 215 Tyr Val Asp Arg Ala Ala Ala Val Val Asp Pro Ala Gly Pro Arg Ser Leu Lys Val Ala Tyr Thr Pro Leu His Gly Val Gly Ala Ala Val Leu Thr Ala Ala Phe Ala Arg Ala Gly Phe Gly Ile Pro Gly Val Val Pro Glu Gln Ala Val Pro Asp Pro Asp Phe Arg Thr Val Ser Phe Pro Asn 280 Pro Glu Glu Pro Gly Ala Val Asp Leu Leu Val Ala Leu Ala Glu Arg Thr Gly Ala Asp Leu Ala Ile Ala Asn Asp Pro Asp Ala Asp Arg Cys Ala Val Ala Val Arg Asp Gly Arg Ala Ala Gly Pro Ala Pro Val Ser 325 Gly Gly Ala Trp Arg Met Leu Arg Gly Asp Glu Val Gly Ala Leu Leu Ala Asp His Leu Met Arg Arg Gly Val His Gly Leu Tyr Ala Thr Thr Ile Val Ser Ser Leu Leu Arg Ala Met Cys Ala Ala Arg Gly Leu 375 Pro Tyr Asp Glu Thr Leu Thr Gly Phe Lys Trp Ile Val Arg Ala Gly Gly Gly Pro Leu Gly Glu Ala Gly Ser Asp Pro Leu Val Phe Gly Tyr 410 Glu Glu Ala Leu Gly Tyr Cys Val Ala Pro Glu His Val Arg Asp Lys 420 425 Asp Gly Ile Thr Ala Ala Leu Thr Val Ala Glu Leu Ala Ala Gly Leu Lys Ala Gln Gly Arg Thr Leu Thr Asp Arg Leu Asp Glu Leu Ala Ala Glu Phe Gly Val His His Thr Asp Gln Leu Ser Val Arg Val Asp Asp 475 Leu Arg Ile Ile Ala Asp Ala Met Ala Arg Val Arg Ala Ala Thr Pro 490 Thr Thr Leu Leu Gly Arg Pro Val Thr Glu Ala Arg Asp Leu Leu Pro

505

Glu Ala Asp Val Val Ile Leu Arg Thr Asp Gly Ala Arg Val Val Ile
515 520 525

```
Arg Pro Ser Gly Thr Glu Pro Lys Leu Lys Ala Tyr Leu Glu Val Val
    530
                        535
                                             540
Glu Pro Val Ala Asp Gly Asp Val Pro Ala Ala Arg Thr Arg Ala Ala
Ala Thr Leu Ala Ala Leu Arg Thr Glu Ile Ala Ala Leu Val Gln Gly
                                    570
<210> 128
<211> 858
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(858)
<220>
<223> evbT
<400> 128
gtg ccg cga cgg cag ctc ggc agg ctg ctc acc cag ctc cgc gag agc
                                                                   48
Val Pro Arg Arg Gln Leu Gly Arg Leu Leu Thr Gln Leu Arg Glu Ser
gcc cat atc agc atc gac gcg gcg gcc gac ctg gac tgc tcg cgg
                                                                   96
Ala His Ile Ser Ile Asp Ala Ala Ala Gly Glu Leu Asp Cys Ser Arg
             20
cag aag ctc tgg cgg atc gag cgg ggg ctg acc tcg gcc aag aca ccg
                                                                   144
Gln Lys Leu Trp Arg Ile Glu Arg Gly Leu Thr Ser Ala Lys Thr Pro
gac gtc cgg gtg ctc tgc gag ctg tac cgg gcc acg ccc gac cag gcg
                                                                   192
Asp Val Arg Val Leu Cys Glu Leu Tyr Arg Ala Thr Pro Asp Gln Ala
age gtg ctg ctc ggg ctc gcc gag gtg age cgg gcc gag ggg tgg tgg
                                                                   240
Ser Val Leu Leu Gly Leu Ala Glu Val Ser Arg Ala Glu Gly Trp Trp
cac gcc cac ggc agc tcc gtg ccg gcc tgg ttc tcg ctc tac gtc ggc
                                                                   288
His Ala His Gly Ser Ser Val Pro Ala Trp Phe Ser Leu Tyr Val Gly
                 85
ctg gag aac gtc gcg agc agc att cgg cac tac aac gcg gag ctg gtg
                                                                   336
Leu Glu Asn Val Ala Ser Ser Ile Arg His Tyr Asn Ala Glu Leu Val
ccg ggg ctg ttg cag acc ccc ggc tac gcc acc gcg ctc ttc gag cac
                                                                   384
Pro Gly Leu Leu Gln Thr Pro Gly Tyr Ala Thr Ala Leu Phe Glu His
        115
                            120
aac cgg ccc gag ctg ggc gag gag cga aag aag gcg gtg ggc ttc
                                                                   432
Asn Arg Pro Glu Leu Gly Glu Glu Glu Arg Lys Lys Ala Val Gly Phe
    130
                        135
```

egg act cag egg cag ggg etg etg gee egg egg etg eee eeg gee eee

Arg Thr Gln Arg Gln Gly Leu Leu Ala Arg Arg Leu Pro Pro Ala Pro

145	150	155	160
		g gtg ctg cgc cgc ccg gt a Val Leu Arg Arg Pro Va 170 17	l Pro
ggc cga tcg gtg atg Gly Arg Ser Val Met 180	gcc gac cag ctc Ala Asp Gln Let 18	c cgg cac ctg ctg gcc gt u Arg His Leu Leu Ala Va 5 190	c ggc 576 L Gly
		g ctg ccg ctg gcc gcc gg l Leu Pro Leu Ala Ala Gl 205	
		c gtg ctg ctc gac ttc cc e Val Leu Leu Asp Phe Pro 220	
tcg gcg ctc ggc agc Ser Ala Leu Gly Ser 225	ccg acc gag ccg Pro Thr Glu Pro 230	g ccg acc gtc tac gtc gag o Pro Thr Val Tyr Val Glo 235	g ggg 720 1 Gly 240
ctc acc ggc gcg ctc Leu Thr Gly Ala Leu 245	tac ctc gac cag Tyr Leu Asp Gli	g ccg acg gag atc gcc gc n Pro Thr Glu Ile Ala Ala 250 25	a Tyr
		g ctc gcc ctc ggc gcg cga r Leu Ala Leu Gly Ala Arg 5 270	
tca gcg gag ctg atc Ser Ala Glu Leu Ile		g gga gag tgc tat gag	858
275	280	g Gly Glu Cys Tyr Glu 285	
	280		
275 <210> 129 <211> 286 <212> PRT	280		
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129	280 a carbonacea		
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129 Val Pro Arg Arg Gln 1 5	280 a carbonacea Leu Gly Arg Leu	u Leu Thr Gln Leu Arg Glu 10 19 a Gly Glu Leu Asp Cys Se	5
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129 Val Pro Arg Arg Gln	280 a carbonacea Leu Gly Arg Leu Asp Ala Ala Ala 29	u Leu Thr Gln Leu Arg Glu 10 19 a Gly Glu Leu Asp Cys Se	Arg
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129 Val Pro Arg Arg Gln	280 A carbonacea Leu Gly Arg Leu Asp Ala Ala Ala 2! Ile Glu Arg Gly 40	285 u Leu Thr Gln Leu Arg Glu 10 19 a Gly Glu Leu Asp Cys Sen 5 30 y Leu Thr Ser Ala Lys The	Arg
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129 Val Pro Arg Arg Gln	280 A carbonacea Leu Gly Arg Leu Asp Ala Ala Ala 2! Ile Glu Arg Gly 40 Cys Glu Leu Tyr 55	285 u Leu Thr Gln Leu Arg Glu 10 19 a Gly Glu Leu Asp Cys Sen 30 y Leu Thr Ser Ala Lys The 45 r Arg Ala Thr Pro Asp Glu	Arg Pro
275 <210> 129 <211> 286 <212> PRT <213> Micromonospora <220> <223> evbT <400> 129 Val Pro Arg Arg Gln	Leu Gly Arg Leu Asp Ala Ala Ala 2! Ile Glu Arg Gly 40 Cys Glu Leu Tyr 55 Leu Ala Glu Vai	285 u Leu Thr Gln Leu Arg Glu 10 1! a Gly Glu Leu Asp Cys Sen 30 y Leu Thr Ser Ala Lys Thm 45 r Arg Ala Thr Pro Asp Glu 60 l Ser Arg Ala Glu Gly Tr	Arg Pro Ala Trp 80

```
Pro Gly Leu Leu Gln Thr Pro Gly Tyr Ala Thr Ala Leu Phe Glu His
Asn Arg Pro Glu Leu Gly Glu Glu Glu Arg Lys Lys Ala Val Gly Phe
    130
                        135
Arg Thr Gln Arg Gln Gly Leu Leu Ala Arg Arg Leu Pro Pro Ala Pro
Glu Leu Thr Val Ile Leu Ser Glu Ala Val Leu Arg Arg Pro Val Pro
                165
Gly Arg Ser Val Met Ala Asp Gln Leu Arg His Leu Leu Ala Val Gly
                                185
Glu Arg His Asn Ile Thr Val Arg Val Leu Pro Leu Ala Ala Gly Pro
Pro Leu Ala Ala Glu Ala Gly Thr Phe Val Leu Leu Asp Phe Pro Leu
                        215
Ser Ala Leu Gly Ser Pro Thr Glu Pro Pro Thr Val Tyr Val Glu Gly
                                        235
Leu Thr Gly Ala Leu Tyr Leu Asp Gln Pro Thr Glu Ile Ala Ala Tyr
Glu Arg Val Trp Arg Gly Leu Asp Ser Leu Ala Leu Gly Ala Arg Gln
                                265
Ser Ala Glu Leu Ile Asp Ala Ile Arg Gly Glu Cys Tyr Glu
        275
                            280
<210> 130
<211> 606
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(606)
<220>
<223> evbU
<400> 130
atg ccg cgg atc agc ctc gac ctc ggg atg gcc gcc gcc gtc ctg atc
                                                                   48
Met Pro Arg Ile Ser Leu Asp Leu Gly Met Ala Ala Val Leu Ile
gag ctg gcc ctc gcc ggc cgg gtc gcg tac gtc gat ggg aac ctg gtg
                                                                   96
Glu Leu Ala Leu Ala Gly Arg Val Ala Tyr Val Asp Gly Asn Leu Val
gtc acg gac ccc gcg ccc acc ggc gaa ccg atc ctg gac gag gtc ctg
                                                                   144
Val Thr Asp Pro Ala Pro Thr Gly Glu Pro Ile Leu Asp Glu Val Leu
ggc cgg atg gcc gcc gac acg ccg cac acc ccg tcc tcc tgg gtg cag
                                                                   192
Gly Arg Met Ala Ala Asp Thr Pro His Thr Pro Ser Ser Trp Val Gln
                         55
```

egg etg ege cae gge etg ege gae egg ate ete gge gae etg gte gee

65	Arg	His	Gly	Leu 70	Arg	Asp	Arg	Ile	Leu 75	Gly	Asp	Leu	Val	Ala 80	
cgg ggc Arg Gly															288
gtg cac Val His	cgc Arg	tac Tyr 100	ccg Pro	acg Thr	gcg Ala	gac Asp	gcc Ala 105	acc Thr	gtg Val	gag Glu	gag Glu	gac Asp 110	tcc Ser	cgg Arg	336
cgg cgg Arg Arg															384
acg gcg Thr Ala 130	gcg Ala	ctg Leu	gcc Ala	acc Thr	ctg Leu 135	gtc Val	gcg Ala	gtg Val	ctc Leu	cgg Arg 140	atg Met	gag Glu	ccg Pro	gcg Ala	432
ctc ggc Leu Gly 145	ctg Leu	acc Thr	ggc Gly	gac Asp 150	gcc Ala	gcc Ala	gtc Val	gac Asp	gcc Ala 155	cgg Arg	cgt Arg	cgg Arg	ctg Leu	gag Glu 160	480
gag atc Glu Ile															528
tcg gtg Ser Val	gtc Val	cgc Arg 180	ccc Pro	tcg Ser	gtg Val	gcc Ala	ctg Leu 185	gtc Val	gtc Val	acc Thr	gcc Ala	ctg Leu 190	ggc Gly	aag Lys	576
gcg gtc Ala Val															606
<210> 131 <211> 202 <212> PRT <213> Micromonospora carbonacea															
<212> P		onos	pora	ı car	bona	ıcea									
<212> P	crom	onos	spora	ı car	rbona	ıcea									
<212> PI <213> Mi <220>	crom bu						Gly	Met 10	Ala	Ala	Ala	Val	Leu 15	Ile	
<212> PI <213> MS <220> <223> ev <400> 13 Met Pro	crom bU 31 Arg	Ile	Ser 5	Leu	Asp	Leu	_	10					15		
<212> PI <213> MS <220> <223> es <400> 13 Met Pro 1	crom bU 31 Arg Ala	Ile Leu 20	Ser 5 Ala	Leu Gly	Asp Arg	Leu Val	Ala 25	10 Tyr	Val	Asp	Gly	Asn 30	15 Leu	Val	
<212> PI <213> MS <220> <223> ex <400> 13 Met Pro 1 Glu Leu	rbU 31 Arg Ala Asp 35	Ile Leu 20 Pro	Ser 5 Ala Ala	Leu Gly Pro	Asp Arg Thr	Leu Val Gly 40	Ala 25 Glu	10 Tyr Pro	Val Ile	Asp Leu	Gly Asp 45	Asn 30 Glu	15 Leu Val	Val Leu	
<pre><212> PI <213> M: <220> <223> ex <400> 1: Met Pro</pre>	rbU 31 Arg Ala Asp 35	Ile Leu 20 Pro	Ser 5 Ala Ala Ala	Leu Gly Pro Asp	Asp Arg Thr Thr 55	Leu Val Gly 40 Pro	Ala 25 Glu His	10 Tyr Pro Thr	Val Ile Pro	Asp Leu Ser 60	Gly Asp 45 Ser	Asn 30 Glu Trp	15 Leu Val Val	Val Leu Gln	
<pre><212> PI <213> M: <220> <223> ex <400> 1: Met Pro</pre>	rbU 31 Arg Ala Asp 35 Met	Ile Leu 20 Pro Ala His	Ser 5 Ala Ala Ala Gly	Leu Gly Pro Asp Leu 70	Asp Arg Thr Thr 55 Arg	Leu Val Gly 40 Pro	Ala 25 Glu His	10 Tyr Pro Thr	Val Ile Pro Leu 75	Asp Leu Ser 60 Gly	Gly Asp 45 Ser Asp	Asn 30 Glu Trp Leu	15 Leu Val Val	Val Leu Gln Ala 80	

Arg Arg Leu Ala Glu Ala Leu Ala Gly Gly Gln Ile Pro Asp Glu Ala 115 Thr Ala Ala Leu Ala Thr Leu Val Ala Val Leu Arg Met Glu Pro Ala 135 Leu Gly Leu Thr Gly Asp Ala Ala Val Asp Ala Arg Arg Leu Glu Glu Ile Ala Gly Gly Ala Gly Phe Ser Gly Thr Val Ser Leu Asp Asp Ser Val Val Arg Pro Ser Val Ala Leu Val Val Thr Ala Leu Gly Lys 185 Ala Val Asp Ala Ala Leu Gly Lys Arg Ala <210> 132 <211> 579 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(579) <220> <223> evbV atg egg gae geg ege ace gae tee tee aac tte egg gee geg etg eac Met Arg Asp Ala Arg Thr Asp Ser Ser Asn Phe Arg Ala Ala Leu His gag etc acc acc atg etc gtg tac gag gec gec ege tec tte eec gte Glu Leu Thr Thr Met Leu Val Tyr Glu Ala Ala Arg Ser Phe Pro Val 20 gag aag tac ccg gtg cag acc ccc gtc acc gac gcc gag ggc acc cgg Glu Lys Tyr Pro Val Gln Thr Pro Val Thr Asp Ala Glu Gly Thr Arg 35 ctg gcc aac ccg ccg ctg ctg gta ccc gtg ctg cgg gcc ggt ctc ggc 192 Leu Ala Asn Pro Pro Leu Leu Val Pro Val Leu Arg Ala Gly Leu Gly 50 55 atg gcc gac gcc gcg ctc gcc ctg ctc ccc gag tcg tcc atg ggc ttc 240 Met Ala Asp Ala Ala Leu Ala Leu Leu Pro Glu Ser Ser Met Gly Phe gtc ggc ctc gcc cgc gac gag gag acg tac gag ccg cgc gcg tac atg 288 Val Gly Leu Ala Arg Asp Glu Glu Thr Tyr Glu Pro Arg Ala Tyr Met 90 gag teg etg eeg ege gae ete gee gge etg eee gtg etg gte ete gae 336 Glu Ser Leu Pro Arg Asp Leu Ala Gly Leu Pro Val Leu Val Leu Asp 100 105 ccg atg ctg gcc acc ggc ggc tcc ctg gag cac tgc tgc cgg ctg ctg 384

Pro Met Leu Ala Thr Gly Gly Ser Leu Glu His Cys Cys Arg Leu Leu

125

120

gcc gag cgg g Ala Glu Arg G 130														
ccc gtc ggc a Pro Val Gly I 145														
gtc acc gcc g Val Thr Ala A														
ccg ggc ctc g Pro Gly Leu G														
ttc Phe					579									
<210> 133 <211> 193 <212> PRT <213> Micromonospora carbonacea														
<2213> Micromonospora carbonacea <220> <223> evbV														
<400> 133 Met Arg Asp A	Ala Arg Thr 5	Asp Ser Ser	Asn Phe Arg	Ala Ala Leu 15	His									
Glu Leu Thr T	Thr Met Leu 20	Val Tyr Glu 25	Ala Ala Arg	Ser Phe Pro 30	Val									
Glu Lys Tyr F	Pro Val Gln	Thr Pro Val	Thr Ásp Ala	Glu Gly Thr 45	Arg									
Leu Ala Asn F 50	Pro Pro Leu	Leu Val Pro 55	Val Leu Arg 60	Ala Gly Leu	Gly									
Met Ala Asp A 65	Ala Ala Leu 70	Ala Leu Leu	Pro Glu Ser 75	Ser Met Gly	Phe 80									
Val Gly Leu A	Ala Arg Asp 85	Glu Glu Thr	Tyr Glu Pro 90	Arg Ala Tyr 95	Met									
Glu Ser Leu F	Pro Arg Asp 100	Leu Ala Gly 105	Leu Pro Val	Leu Val Leu 110	Asp									
Pro Met Leu A	Ala Thr Gly	Gly Ser Leu 120	Glu His Cys	Cys Arg Leu 125	Leu									
Ala Glu Arg G 130	Gly Cys Thr	Asp Ile Thr	Val Leu Cys 140	Val Leu Ala	Ala									
Pro Val Gly I 145	Ile Ala Arg 150	Leu Glu Gln	Ser Gly Leu 155	Pro Leu Arg	Leu 160									
Val Thr Ala A	Ala Ile Asp 165	Glu Ser Leu	Asn Asp Arg 170	Met Phe Ile 175	Val									
Pro Gly Leu G	Gly Asp Ala 180	Gly Asp Arg 185	Gln Phe Gly	Gly Met Pro 190	Arg									

Phe

```
<210> 134
<211> 1014
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1014)
<220>
<223> evbW
<400> 134
atg acg gcg aca gcg acg tcg gcc cgg tcg gac ctc tcc gag ctg gga
                                                                   48
Met Thr Ala Thr Ala Thr Ser Ala Arg Ser Asp Leu Ser Glu Leu Gly
ega tee gag ace get ttg egg aac tte etg cae gge etg eeg gge gtg
Arg Ser Glu Thr Ala Leu Arg Asn Phe Leu His Gly Leu Pro Gly Val
gac cag gtc ggc gcg gag cag cgg gcc cag ctc ggc acc cgc tcg
                                                                   144
Asp Gln Val Gly Ala Glu Gln Arg Ala Ala Gln Leu Gly Thr Arg Ser
atc aag acc acg gcc aag gcc cgg gcg atc gac ctg gcg atc cgg atg
                                                                   192
Ile Lys Thr Thr Ala Lys Ala Arg Ala Ile Asp Leu Ala Ile Arg Met
gte gae etg ace ace etg gag ggg gee gae ace eee gge aag gtg egg
                                                                   240
Val Asp Leu Thr Thr Leu Glu Gly Ala Asp Thr Pro Gly Lys Val Arg
gcg ctc gcg gcc aaa gca ctg cgc ccc gac ccg gcc gac ccg tcc tgc
                                                                   288
Ala Leu Ala Ala Lys Ala Leu Arg Pro Asp Pro Ala Asp Pro Ser Cys
                 85
                                      90
                                                          95
ccg cac gtc ggc gca gtc tgc gtc tac ccg gcg atg gtc ccg tac gtg
                                                                   336
Pro His Val Gly Ala Val Cys Val Tyr Pro Ala Met Val Pro Tyr Val
            100
gcc gag gtg ctg cgc gga tcc gcc ggg tcc ggg cgg ccg tcc ggc gga
                                                                   384
Ala Glu Val Leu Arg Gly Ser Ala Gly Ser Gly Arg Pro Ser Gly Gly
        115
                            120
ccg gac ggc aac gcg ccg gcc gga ccc ggc gtg gtg cac ctg gcc agc
                                                                   432
Pro Asp Gly Asn Ala Pro Ala Gly Pro Gly Val Val His Leu Ala Ser
gtg gcc acc gcg ttt ccg tcc ggg cag gca ccc ctg gag gtc aag ctc
                                                                   480
Val Ala Thr Ala Phe Pro Ser Gly Gln Ala Pro Leu Glu Val Lys Leu
145
                    150
                                         155
gcc gac acc cgg gcc gca gtg gcg gct ggc gcg gac gag atc gac atg
                                                                   528
Ala Asp Thr Arg Ala Ala Val Ala Ala Gly Ala Asp Glu Ile Asp Met
                165
                                    170
gtg atc aac egg gge geg tte etg gee gge ege tae ege gag gte tae
                                                                   576
Val Ile Asn Arg Gly Ala Phe Leu Ala Gly Arg Tyr Arg Glu Val Tyr
            180
                                185
                                                     190
```

gac gag atc gtg Asp Glu Ile Val 195	g gcc acc aaa . Ala Thr Lys	cag gcg tgc Gln Ala Cys 200	ggg gac gcc cac Gly Asp Ala His 205	ctc aag 624 Leu Lys
gtg atc ctg gaa Val Ile Leu Glu 210	acc ggc gag Thr Gly Glu 215	Leu Ala Thr	tac gac aac gtg Tyr Asp Asn Val 220	cgc cgg 672 Arg Arg
			gac ttc atc aag Asp Phe Ile Lys 235	
			ccg gtg acg ctg Pro Val Thr Leu	
	. Arg Asp Phe		acc ggg cgg cag Thr Gly Arg Gln 270	
			aag gac gcg atc Lys Asp Ala Ile 285	
		Val Gly Pro	gac tgg ctg gac Asp Trp Leu Asp 300	
		Ser Leu Leu	aac gac ctg ctc Asn Asp Leu Leu 315	
			ggt ccc gac tac Gly Pro Asp Tyr	
ctg gac Leu Asp				1014
<210> 135 <211> 338 <212> PRT <213> Micromono	espora carbon	acea		
<220> <223> evbW				
<400> 135 Met Thr Ala Thr 1	Ala Thr Ser	Ala Arg Ser	Asp Leu Ser Glu	Leu Gly 15
Arg Ser Glu Thr	_	Asn Phe Leu 25	His Gly Leu Pro	Gly Val
Asp Gln Val Gly	Ala Glu Gln	Arg Ala Ala 40	Gln Leu Gly Thr 45	Arg Ser
Ile Lys Thr Thr	Ala Lys Ala 55	_	Asp Leu Ala Ile 60	Arg Met
Val Asp Leu Thr 65	Thr Leu Glu 70	Gly Ala Asp	Thr Pro Gly Lys 75	Val Arg 80

```
Ala Leu Ala Ala Lys Ala Leu Arg Pro Asp Pro Ala Asp Pro Ser Cys
Pro His Val Gly Ala Val Cys Val Tyr Pro Ala Met Val Pro Tyr Val
Ala Glu Val Leu Arg Gly Ser Ala Gly Ser Gly Arg Pro Ser Gly Gly
Pro Asp Gly Asn Ala Pro Ala Gly Pro Gly Val Val His Leu Ala Ser
Val Ala Thr Ala Phe Pro Ser Gly Gln Ala Pro Leu Glu Val Lys Leu
Ala Asp Thr Arg Ala Ala Val Ala Ala Gly Ala Asp Glu Ile Asp Met
Val Ile Asn Arg Gly Ala Phe Leu Ala Gly Arg Tyr Arg Glu Val Tyr
Asp Glu Ile Val Ala Thr Lys Gln Ala Cys Gly Asp Ala His Leu Lys
                            200
Val Ile Leu Glu Thr Gly Glu Leu Ala Thr Tyr Asp Asn Val Arg Arg
Ala Ser Trp Leu Ala Met Leu Ala Gly Gly Asp Phe Ile Lys Thr Ser
                    230
Thr Gly Lys Val Pro Val Ala Ala Thr Leu Pro Val Thr Leu Val Met
                245
Leu Glu Ala Val Arg Asp Phe Arg Ala Ala Thr Gly Arg Gln Val Gly
                                265
Val Lys Pro Ala Gly Gly Ile Lys Asn Thr Lys Asp Ala Ile Lys Tyr
Leu Val Met Val Asn Glu Thr Val Gly Pro Asp Trp Leu Asp Pro Asp
                        295
                                            300
Trp Phe Arg Phe Gly Ala Ser Ser Leu Leu Asn Asp Leu Leu Met Gln
Arg Thr Lys Leu Thr Thr Gly Val Tyr Ser Gly Pro Asp Tyr Phe Thr
Leu Asp
```

```
<210> 136
<211> 1431
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1431)
```

<223> evbX

<400> 136								
gtg atc tt Val Ile Ph 1	_	Ala Pro	_		_			
ctc aag co Leu Lys Pr				Asp Gl				
gcc gac gg Ala Asp Gl 3								
ctc gcc ga Leu Ala Gl 50								
cgc gcc gc Arg Ala Al 65				Val Tr			Pro Gl	
cgg gac cg Arg Asp Ar		_		_				_
cgc tcc cg Arg Ser Ar				Ser Le				
atc cgg ga Ile Arg Gl 11	u Ser Arg		_	_	u Val A			
ttc tac ta Phe Tyr Ty 130								
ccg aac cc Pro Asn Pr 145					n Val :			n
ttc ccg ct Phe Pro Le								
ggc aac ac Gly Asn Th	g gtg gtg r Val Val 180	ctc aag Leu Lys	ccg gcg Pro Ala 185	Glu Th	c acc our Thr I	ccg ctg Pro Leu 190	acc go Thr Al	g 576 .a
ctg ctg tt Leu Leu Ph 19	e Ala Glu				u Leu l			
gtc aac at Val Asn Il 210								
cac ccg gg His Pro Gl 225					y Ser :			y
aag gcc at Lys Ala Il								

gag ct Glu Le												816
gac ca Asp Gl												864
cac gt His Va 29	ıl Cys											912
gag ca Glu Gl 305		_	 _	_	_	_	_	_	 _	_	 _	960
ggc ga Gly As												1008
gcc ca Ala Gl												1056
ggg go		_	 _	_	_	_		_		_		1104
tgg tt Trp Ph	e Ala											1152
gcc cg Ala Ar 385												1200
acc cc Thr Pr												1248
tcg go Ser Al												1296
gac co Asp Ar												1344
gac co Asp Pr 45	o Thr											1392
gag gg Glu Gl 465												1431

<210> 137

<211> 477

<212> PRT

<213> Micromonospora carbonacea

<220> <223> evbX

<400> 137 Val Ile Phe Glu Tyr Ala Pro Ala Pro Glu Ser Arg Ser Val Val Asp Leu Lys Pro Ser Tyr Gly Leu Phe Val Asp Gly Glu Phe Val Asp Pro Ala Asp Gly Gly Phe Lys Ser Val Asn Pro Ala Ser Glu Glu Val Leu Ala Glu Ile Ala Glu Ala Gly Ser Ala Asp Val Asp Arg Ala Val Arg Ala Arg Thr Ala Tyr Glu Lys Val Trp Gly Pro Met Pro Gly Arg Asp Arg Ala Lys Tyr Leu Phe Arg Ile Ala Arg Ile Ile Gln Glu Arg Ser Arg Glu Leu Ala Val Leu Glu Ser Leu Asp Asn Gly Lys Pro 105 Ile Arg Glu Ser Arg Asp Val Asp Leu Pro Leu Val Ala Ala His Phe 115 120 Phe Tyr Tyr Ala Gly Trp Ala Asp Lys Leu Pro Tyr Ala Gly Phe Gly Pro Asn Pro Arg Pro Leu Gly Val Ala Ala Gln Val Ile Pro Trp Asn Phe Pro Leu Leu Met Leu Ala Trp Lys Ile Ala Pro Ala Leu Ala Ala 165 170 Gly Asn Thr Val Val Leu Lys Pro Ala Glu Thr Thr Pro Leu Thr Ala Leu Leu Phe Ala Glu Ile Cys Gln Gln Ala Glu Leu Pro Ala Gly Val Val Asn Ile Val Thr Gly Ala Gly Asp Thr Gly Arg Ala Leu Val Glu 215 His Pro Gly Val Asp Lys Val Ala Phe Thr Gly Ser Thr Glu Val Gly Lys Ala Ile Ala Arg Ser Val Ala Gly Thr Gly Lys Lys Val Thr Leu Glu Leu Gly Gly Lys Ala Ala Asn Ile Val Phe Asp Asp Ala Pro Val 265 Asp Gln Ala Val Glu Gly Ile Val Asn Gly Ile Phe Phe Asn Gln Gly His Val Cys Cys Ala Gly Ser Arg Leu Leu Val Gln Glu Ser Val Ala 295 Glu Gln Val Leu Glu Ser Leu Lys Arg Arg Met Ala Leu Leu Arg Val Gly Asp Pro Leu Asp Lys Asn Thr Asp Ile Gly Ala Ile Asn Ser Ala 330 Ala Gln Leu Ala Arg Ile Arg Glu Leu Ser Ala Ala Gly Glu Ala Glu

			340					345					350			
Gly	Ala	Glu 355	Arg	Trp	Ser	Pro	Pro 360	Cys	Glu	Leu	Pro	Glu 365	Arg	Gly	Phe	
Trp	Phe 370	Ala	Pro	Thr	Ile	Phe 375	Thr	Gly	Val	Thr	Gln 380	Ala	His	Arg	Ile	
Ala 385	Arg	Glu	Glu	Ile	Phe 390	Gly	Pro	Val	Leu	Ser 395	Val	Leu	Thr	Phe	Arg 400	
Thr	Pro	Ala	Glu	Ala 405	Val	Glu	Lys	Ala	Asn 410	Asn	Thr	Pro	Tyr	Gly 415	Leu	
Ser	Ala	Gly	Ile 420	Trp	Thr	Asp	Lys	Gly 425	Ser	Arg	Ile	Leu	Trp 430	Met	Ala	
Asp	Arg	Leu 435	Arg	Ala	Gly	Val	Val 440	Trp	Ala	Asn	Thr	Phe 445	Asn	Lys	Phe	
Asp	Pro 450	Thr	Ser	Pro	Phe	Gly 455	Gly	Tyr	Lys	Glu	Ser 460	Gly	Tyr	Gly	Arg	
Glu 465	Gly	Gly	Arg	His	Gly 470	Leu	Glu	Gly	Tyr	Leu 475	Gly	Val				
<212 <213 <220 <223 <223	<210> 138 <211> 735 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)(735) <220>															
	3> e															
gtg	0> 13 caa Gln	tcc	gcg Ala	aac Asn 5	gtg Val	tcg Ser	ctg Leu	gcc Ala	tcc Ser 10	cgc Arg	aag Lys	gac Asp	gcg Ala	cgg Arg 15	gac Asp	48
gcc Ala	gtg Val	gtc Val	gcc Ala 20	gcc Ala	cgc Arg	gcc Ala	gcc Ala	gtg Val 25	aag Lys	ggc Gly	tgg Trp	gcc Ala	30 gly ggg	gcg Ala	acc Thr	96
gcg Ala	tac Tyr	aac Asn 35	cgg Arg	ggt Gly	cag Gln	atc Ile	ctc Leu 40	tac Tyr	cgg Arg	gtc Val	gcc Ala	gag Glu 45	atg Met	ctg Leu	gag Glu	144
						gtc Val 55										192
gac Asp 65	gcg Ala	gcg Ala	atc Ile	gac Asp	cgc Arg 70	tgg Trp	gtc Val	tgg Trp	tac Tyr	gcg Ala 75	ggc Gly	tgg Trp	tcc Ser	gac Asp	aag Lys 80	240
ctc Leu	ccc Pro	cag Gln	gtg Val	tac Tyr 85	ggc Gly	ggt Gly	gcg Ala	aac Asn	cct Pro 90	gtc Val	gcc Ala	gly ggg	ccg Pro	tac Tyr 95	ttc Phe	288

														gcc Ala		336
	_			_			_	_	_			_	_	gcg Ala		384
														ccc Pro		432
														ccc Pro		480
														ccg Pro 175		528
														gtg Val		576
														aac Asn		624
														gcc Ala		672
														gtc Val		720
		aag Lys		_					٦							735
<213 <213	0> 13 1> 24 2> PI 3> Ma	15 RT	mono:	spora	a cai	rbona	acea									
<220 <220	0> 3> e1	ybY														
_	0> 13 Gln		Ala	Asn 5	Val	Ser	Leu	Ala	Ser 10	Arg	Lys	Asp	Ala	Arg 15	Asp	
Ala	Val	Val	Ala 20	Ala	Arg	Ala	Ala	Val 25	Lys	Gly	Trp	Ala	Gly 30	Ala	Thr	
Ala	Tyr	Asn 35	Arg	Gly	Gln	Ile	Leu 40	Tyr	Arg	Val	Ala	Glu 45	Met	Leu	Glu	
Gly	Arg 50	Arg	Glu	Gln	Phe	Val 55	Ala	Leu	Gly	Val	Pro 60	Ala	Asp	Glu	Val	
Asp 65	Ala	Ala	Ile	Asp	Arg 70	Trp	Val	Trp	Tyr	Ala 75	Gly	Trp	Ser	Asp	Lys 80	

```
Leu Pro Gln Val Tyr Gly Gly Ala Asn Pro Val Ala Gly Pro Tyr Phe
Asn Leu Ser Ala Pro Glu Pro Thr Gly Val Val Ala Val Ala Pro
            100
                                  105
Glu Ala Pro Ala Leu Leu Gly Leu Val Ser Val Ile Ala Pro Ala Ile
Val Thr Gly Asn Thr Val Val Val Ala Ala Ser Pro Thr Gln Pro Leu
Ala Ser Val Thr Leu Ala Glu Val Leu Ala Thr Ser Asp Leu Pro Gly
Gly Val Val Asn Val Leu Thr Gly Ala Ile Thr Glu Thr Val Pro Thr
                 165
Leu Ala Ala His Leu Asp Val Asn Ala Ile Asp Leu Thr Gly Val Gly
Asp Ala Ser Leu Ala Thr Glu Leu Glu Val Arg Ala Ala Glu Asn Leu
                              200
Lys Arg Val Ile Arg Pro Ala Pro Ala Asp His Asp Trp Tyr Ala Asp
Pro Gly Leu Thr Arg Met Thr Thr Leu Leu Glu Thr Lys Thr Val Trp
                     230
                                          235
His Pro Lys Gly Val
                 245
<210> 140
<211> 411
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1) ... (411)
<220>
<223> evbZ
<400> 140
atg gac gtg ctg tgg gac acc gtc ccg ggc acg tcg gac ggg gtg acg
                                                                      48
Met Asp Val Leu Trp Asp Thr Val Pro Gly Thr Ser Asp Gly Val Thr
gtg cgc gag gtc gcc gag gcc ctc gac ggc cgc gag ctg gcg tac acg
                                                                      96
Val Arg Glu Val Ala Glu Ala Leu Asp Gly Arg Glu Leu Ala Tyr Thr
acg gtg atg acc gtg ctg gac cgg ctc gcc ggc aag ggc atg gtg cgg
Thr Val Met Thr Val Leu Asp Arg Leu Ala Gly Lys Gly Met Val Arg
                                                                      144
ege cag egg gag ggg egg gee tgg ege tae cag gee geg gee age ege
                                                                      192
Arg Gln Arg Glu Gly Arg Ala Trp Arg Tyr Gln Ala Ala Ala Ser Arg
```

gag gcg cac atc gcc cag ctc atg ctc gac gcg ctg gac ctc ggc ggc

Glu Ala His Ile Ala Gln Leu Met Leu Asp Ala Leu Asp Leu Gly Gly age egg gae gee geg etg gtg ege tte gee egg teg gtg ace gge ace 288 Ser Arg Asp Ala Ala Leu Val Arg Phe Ala Arg Ser Val Thr Gly Thr 85 90 gag gcc gag gtg ctg cgc gcc gcc ctc ggc gcc gag gcg ggc ggc ccg 336 Glu Ala Glu Val Leu Arg Ala Ala Leu Gly Ala Glu Ala Gly Gly Pro ctg acc gac cgc gtc gac gcg ccg cgc gcc gac cgg gcc ggg cag ccg 384 Leu Thr Asp Arg Val Asp Ala Pro Arg Ala Asp Arg Ala Gly Gln Pro 120 gcc ctg gcc gac gag gcg acg gac cgg 411 Ala Leu Ala Asp Glu Ala Thr Asp Arg <210> 141 <211> 137 <212> PRT <213> Micromonospora carbonacea <220> <223> evbZ <400> 141 Met Asp Val Leu Trp Asp Thr Val Pro Gly Thr Ser Asp Gly Val Thr Val Arg Glu Val Ala Glu Ala Leu Asp Gly Arg Glu Leu Ala Tyr Thr Thr Val Met Thr Val Leu Asp Arg Leu Ala Gly Lys Gly Met Val Arg Arg Gln Arg Glu Gly Arg Ala Trp Arg Tyr Gln Ala Ala Ala Ser Arg Glu Ala His Ile Ala Gln Leu Met Leu Asp Ala Leu Asp Leu Gly Gly Ser Arg Asp Ala Ala Leu Val Arg Phe Ala Arg Ser Val Thr Gly Thr Glu Ala Glu Val Leu Arg Ala Ala Leu Gly Ala Glu Ala Gly Gly Pro 100 105 Leu Thr Asp Arg Val Asp Ala Pro Arg Ala Asp Arg Ala Gly Gln Pro Ala Leu Ala Asp Glu Ala Thr Asp Arg 130 135 <210> 142 <211> 903 <212> DNA <213> Micromonospora carbonacea

<220> <221> CDS <222> (1)..(903) <220> <223> evcA <400> 142 ate geg ate gte tge tgg cag geg gte ggg ete geg ete ggg ete tee Ile Ala Ile Val Cys Trp Gln Ala Val Gly Leu Ala Leu Gly Leu Ser

atg gcg tac gcc gtg cac ttc gcc gcg acg gtc ctg gcc tgc tac ctg 48 Met Ala Tyr Ala Val His Phe Ala Ala Thr Val Leu Ala Cys Tyr Leu ace get cag gte etg geg geg tee ace tgg acg tgg egg gee eee egg 96 Thr Ala Gln Val Leu Ala Ala Ser Thr Trp Thr Trp Arg Ala Pro Arg 144

40 gcg atg ggc ctg ccg atg gcg ctc ggc gtg gcc gcg tac gac cgg ccg 192 Ala Met Gly Leu Pro Met Ala Leu Gly Val Ala Ala Tyr Asp Arg Pro

ace gge age geg ttg etc gee etg gee ace gae etg ace eae gge ace 240 Thr Gly Ser Ala Leu Leu Ala Leu Ala Thr Asp Leu Thr His Gly Thr

ctg ccg gcc ggg ctc ggc gcg gtc cac ctc ggt ctg gtc ggg gtc ggg 288 Leu Pro Ala Gly Leu Gly Ala Val His Leu Gly Leu Val Gly Val Gly 90

ttc ggc atc ggg gcg gcg ctc ctc gcc acg acg gta cgc agc gtg cag 336 Phe Gly Ile Gly Ala Ala Leu Leu Ala Thr Thr Val Arg Ser Val Gln 100 105

gcg acc gtc cgg gcc cag cgg cag cac cgg gac ctg ctc gcc ctg gtg 384 Ala Thr Val Arg Ala Gln Arg Gln His Arg Asp Leu Leu Ala Leu Val 115 120

gcc cgg cgg gac ccg gag gtg ccg ggg gcg ctg gtg ctg gac cat ccg 432 Ala Arg Arg Asp Pro Glu Val Pro Gly Ala Leu Val Leu Asp His Pro 130 135

480 Ser Ala Ala Tyr Cys Leu Pro Gly Val Arg Pro Arg Val Val Val 145 150

age gee ggg geg ete age atg ete gae egg gee gag etg geg geg gtg 528 Ser Ala Gly Ala Leu Ser Met Leu Asp Arg Ala Glu Leu Ala Ala Val 165 170

ctg acc cac gag cgg gcg cac gcc cag gag cgc cac gac ctt gtg ctg 576 Leu Thr His Glu Arg Ala His Ala Gln Glu Arg His Asp Leu Val Leu

ctg ccg ttc acc gcg ctg tgc cgt gcg ctg ccc tgg ttc cgt tgg gta 624 Leu Pro Phe Thr Ala Leu Cys Arg Ala Leu Pro Trp Phe Arg Trp Val 195

ege gac geg cac gag egg gte gee etg etg gte gag atg ege gee gae 672 Arg Asp Ala His Glu Arg Val Ala Leu Leu Val Glu Met Arg Ala Asp 215

gac aag gcc cgg gag ctg cac gcc gag gct ccc ctc gcg ggg gcg ttg 720 Asp Lys Ala Arg Glu Leu His Ala Glu Ala Pro Leu Ala Gly Ala Leu 225 230 235

cgc cgg ttc gcc gcg gcc ggc cac cgg atc gcg ccg gcc ggc acc ctc Arg Arg Phe Ala Ala Ala Gly His Arg Ile Ala Pro Ala Gly Thr Leu 245 250 255
ggc ctg ggc gac cgg gac ctg gac gtc cgg gtc cag cgg ctg ctg gtc Gly Leu Gly Asp Arg Asp Leu Asp Val Arg Val Gln Arg Leu Leu Val 260 265 270
gcc gac cgg ccg ccc cgg ctg atc ggg gcc gcc gcg ctg gcg gtg gcg Ala Asp Arg Pro Pro Arg Leu Ile Gly Ala Ala Ala Leu Ala Val Ala 275 280 285
gtc acc ctg gtc gcg ctg ccg gtc tcc ctc ttc ctg agc Val Thr Leu Val Ala Leu Pro Val Ser Leu Phe Leu Ser 290 295 300
<210> 143 <211> 301 <212> PRT <213> Micromonospora carbonacea
<220> <223> evcA
<400> 143 Met Ala Tyr Ala Val His Phe Ala Ala Thr Val Leu Ala Cys Tyr Leu 1 5 10 15
Thr Ala Gln Val Leu Ala Ala Ser Thr Trp Thr Trp Arg Ala Pro Arg 20 25 30
Ile Ala Ile Val Cys Trp Gln Ala Val Gly Leu Ala Leu Gly Leu Ser 35 40 45
Ala Met Gly Leu Pro Met Ala Leu Gly Val Ala Ala Tyr Asp Arg Pro 50 55 60
Thr Gly Ser Ala Leu Leu Ala Leu Ala Thr Asp Leu Thr His Gly Thr 65 70 75 80
Leu Pro Ala Gly Leu Gly Ala Val His Leu Gly Leu Val Gly Val Gly 85 90 95
Phe Gly Ile Gly Ala Ala Leu Leu Ala Thr Thr Val Arg Ser Val Gln 100 105 110
Ala Thr Val Arg Ala Gln Arg Gln His Arg Asp Leu Leu Ala Leu Val 115 120 125
Ala Arg Arg Asp Pro Glu Val Pro Gly Ala Leu Val Leu Asp His Pro 130 135 140
Ser Ala Ala Ala Tyr Cys Leu Pro Gly Val Arg Pro Arg Val Val 145 150 150 160
Ser Ala Gly Ala Leu Ser Met Leu Asp Arg Ala Glu Leu Ala Ala Val 165 170 175
Leu Thr His Glu Arg Ala His Ala Gln Glu Arg His Asp Leu Val Leu 180 185 190
Leu Pro Phe Thr Ala Leu Cys Arg Ala Leu Pro Trp Phe Arg Trp Val 195 200 205

210 215 220	
Asp Lys Ala Arg Glu Leu His Ala Glu Ala Pro Leu Ala Gly Ala Leu 225 230 235 240	
Arg Arg Phe Ala Ala Ala Gly His Arg Ile Ala Pro Ala Gly Thr Leu 245 250 255	
Gly Leu Gly Asp Arg Asp Leu Asp Val Arg Val Gln Arg Leu Leu Val 260 265 270	
Ala Asp Arg Pro Pro Arg Leu Ile Gly Ala Ala Ala Leu Ala Val Ala 275 280 285	
Val Thr Leu Val Ala Leu Pro Val Ser Leu Phe Leu Ser 290 295 300	•
<210> 144 <211> 1248 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)(1248)	
<220> <223> evcB	
<pre><400> 144 atg gat caa ctg ctc ctc gcc cgt ctc cag ttc gcc acg acc acc tcg Met Asp Gln Leu Leu Leu Ala Arg Leu Gln Phe Ala Thr Thr Thr Ser 1 5 10 15</pre>	48
ctg cac ttc ctc ttc gtc gtc gtc acg ctc ggt ctg gtc acc ctg ctc Leu His Phe Leu Phe Val Val Val Thr Leu Gly Leu Val Thr Leu Leu 20 25 30	96
gtc ggg ctc cag acg gcc tgg acg atc acc ggc aat ccc gtc cac gag Val Gly Leu Gln Thr Ala Trp Thr Ile Thr Gly Asn Pro Val His Glu	144
35 40 45	
	192
35 40 45 cgg ctg acc cgg ttc tgg ggt cag ctc tac gtg atc aac tac gtg ctc Arg Leu Thr Arg Phe Trp Gly Gln Leu Tyr Val Ile Asn Tyr Val Leu	192 240
cgg ctg acc cgg ttc tgg ggt cag ctc tac gtg atc aac tac gtg ctc Arg Leu Thr Arg Phe Trp Gly Gln Leu Tyr Val Ile Asn Tyr Val Leu 50 55 60 ggc atc gcc acc ggc ctg ctc atg gag ttc cag ttc ggg ctg aac tgg Gly Ile Ala Thr Gly Leu Leu Met Glu Phe Gln Phe Gly Leu Asn Trp	
cgg ctg acc cgg ttc tgg ggt cag ctc tac gtg atc aac tac gtg ctc Arg Leu Thr Arg Phe Trp Gly Gln Leu Tyr Val Ile Asn Tyr Val Leu 50 55 60 ggc atc gcc acc ggc ctg ctc atg gag ttc cag ttc ggg ctg aac tgg Gly Ile Ala Thr Gly Leu Leu Met Glu Phe Gln Phe Gly Leu Asn Trp 65 70 75 80 agc ggc ctg tcg cgc tac gtc ggc aac gtc ttc ggc gcc ccg ctg gcg Ser Gly Leu Ser Arg Tyr Val Gly Asn Val Phe Gly Ala Pro Leu Ala	240

ctg Leu	tgg Trp 130	ggc Gly	gtg Val	gcg Ala	ctg Leu	acc Thr 135	gcg Ala	tac Tyr	gcc Ala	tcg Ser	gcg Ala 140	ttc Phe	tgg Trp	gtc Val	atg Met	432
gtg Val 145	gcg Ala	aac Asn	gcc Ala	tgg Trp	ctg Leu 150	cag Gln	aac Asn	ccg Pro	gtc Val	ggc Gly 155	tac Tyr	gag Glu	gtg Val	cgc Arg	gac Asp 160	480
						gac Asp										528
ttc Phe	ggc Gly	ctg Leu	gcc Ala 180	ttc Phe	999 999	cac His	gtg Val	gtc Val 185	gcc Ala	gcc Ala	gcc Ala	ctg Leu	ctc Leu 190	acc Thr	ggc Gly	576
						gtg Val										624
						cgc Arg 215										672
gcg Ala 225	gcg Ala	gtc Val	tcg Ser	atc Ile	agc Ser 230	ctg Leu	gtg Val	cag Gln	ggc Gly	ttc Phe 235	ggc Gly	ttc Phe	gcc Ala	cag Gln	ttc Phe 240	720
						cag Gln										768
						gaa Glu										816
						gcc Ala										864
						tgt Cys 295										912
						ctg Leu										960
gcg Ala	ctg Leu	ccg Pro	ctg Leu	ccc Pro 325	ttc Phe	gtc Val	gcg Ala	gtg Val	atc Ile 330	ctc Leu	ggc Gly	tgg Trp	atc Ile	gcc Ala 335	cgt Arg	1008
						tgg Trp										1056
cgg Arg	gcg Ala	gtc Val 355	tcg Ser	ccg Pro	gtc Val	gcg Ala	ccc Pro 360	Gly 999	gtg Val	atg Met	ctc Leu	gcc Ala 365	tcg Ser	ctg Leu	atc Ile	1104
ggc Gly	ttc Phe 370	acc Thr	ctg Leu	ctg Leu	ctc Leu	ggc Gly 375	gly ggg	ctc Leu	gcc Ala	gtc Val	gcc Ala 380	aac Asn	tgg Trp	gtg Val	ctg Leu	1152

1248

tte gee egg tae gee gee egg gga gee gee gat eee gee eta gge ege Phe Ala Arg Tyr Ala Ala Arg Gly Ala Ala Asp Pro Ala Leu Gly Arg egg eee gge eea gee gee gae gag tee egt eee gte eee gte ete gge Arg Pro Gly Pro Ala Ala Asp Glu Ser Arg Pro Val Pro Val Leu Gly 410 <210> 145 <211> 416 <212> PRT <213> Micromonospora carbonacea <220> <223> evcB <400> 145 Met Asp Gln Leu Leu Ala Arg Leu Gln Phe Ala Thr Thr Ser Leu His Phe Leu Phe Val Val Val Thr Leu Gly Leu Val Thr Leu Leu 25 Val Gly Leu Gln Thr Ala Trp Thr Ile Thr Gly Asn Pro Val His Glu Arg Leu Thr Arg Phe Trp Gly Gln Leu Tyr Val Ile Asn Tyr Val Leu Gly Ile Ala Thr Gly Leu Leu Met Glu Phe Gln Phe Gly Leu Asn Trp 70 Ser Gly Leu Ser Arg Tyr Val Gly Asn Val Phe Gly Ala Pro Leu Ala Ile Glu Thr Leu Val Ala Phe Phe Leu Glu Ser Thr Phe Leu Gly Met Trp Ile Phe Gly Trp His Arg Leu Arg Arg Gly Val His Leu Ala Leu 120 Leu Trp Gly Val Ala Leu Thr Ala Tyr Ala Ser Ala Phe Trp Val Met Val Ala Asn Ala Trp Leu Gln Asn Pro Val Gly Tyr Glu Val Arg Asp Gly Val Ala His Leu Thr Asp Phe Gly Ala Leu Leu Thr Asn Pro Thr 165 170 Phe Gly Leu Ala Phe Gly His Val Val Ala Ala Leu Leu Thr Gly Gly Met Leu Met Ala Ala Val Ser Ala Trp His Leu Ile Arg Arg Thr Pro Asp His Ala Leu Phe Arg Thr Ser Leu Arg Ile Gly Leu Val Thr 215 Ala Ala Val Ser Ile Ser Leu Val Gln Gly Phe Gly Phe Ala Gln Phe 225 Gly Pro Val Gly Gln Thr Gln Pro Thr Lys Phe Gly Gly Gly Ala Gln

250

```
Arg Asp Ala Leu Val Ala Glu Trp Thr Ser Arg Phe Gly Pro Gly Asp
                                  265
Tyr Thr Pro Pro Val Leu Ala Asp Val Gly Leu Gly Phe Met Ile Leu
Ile Gly Leu Leu Gly Cys Leu Trp Leu Leu Pro Leu Leu Trp
                         295
Arg Asp Trp Phe Ile Arg Leu Arg Phe Pro Leu Trp Leu Ile Leu Leu
Ala Leu Pro Leu Pro Phe Val Ala Val Ile Leu Gly Trp Ile Ala Arg
                325
                                      330
Glu Val Gly Arg Gln Pro Trp Val Ala Tyr Gly Leu Leu Ser Thr Glu
Arg Ala Val Ser Pro Val Ala Pro Gly Val Met Leu Ala Ser Leu Ile
Gly Phe Thr Leu Leu Gly Gly Leu Ala Val Ala Asn Trp Val Leu
                         375
Phe Ala Arg Tyr Ala Ala Arg Gly Ala Ala Asp Pro Ala Leu Gly Arg
Arg Pro Gly Pro Ala Ala Asp Glu Ser Arg Pro Val Pro Val Leu Gly
<210> 146
<211> 1005
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1005)
<220>
<223> evcC
<400> 146
gtg gaa ctc gcc tgg tac gcc ctg ctc ggg ctc ttc ctc gcc ggc tac
Val Glu Leu Ala Trp Tyr Ala Leu Leu Gly Leu Phe Leu Ala Gly Tyr
                                      10
ctg gtc ctc ggc ggc tac gac tac ggc gtc ggc ctg ctc gcc cgg
                                                                     96
Leu Val Leu Gly Gly Tyr Asp Tyr Gly Val Gly Leu Leu Leu Ala Arg
gge gge eeg eeg gee ege ege egg geg gee ete ace gee gtg gge eeg
                                                                     144
Gly Gly Pro Pro Ala Arg Arg Ala Ala Leu Thr Ala Val Gly Pro
                                                                     192
tte tte ete gge aac gag gte tgg etg gtg geg ace gte gge att etg
Phe Phe Leu Gly Asn Glu Val Trp Leu Val Ala Thr Val Gly Ile Leu
ttc ggc gcg ttc ccc acc ctg gag ggg gaa ctg ctg tcc ggc ttc tac
                                                                     240
```

Phe Gly Ala Phe Pro Thr Leu Glu Gly Glu Leu Leu Ser Gly Phe Tyr

75

70

			gcg Ala							288
			cgc Arg							336
			gcc Ala							384
			ctg Leu							432
			ggc Gly 150							480
			gcc Ala							528
			gcc Ala							576
			gtg Val							624
			gat Asp							672
			ccg Pro 230							720
			cgg Arg							768
			ctg Leu							816
			tcc Ser							864
			agc Ser							912
	_	_	ccg Pro 310	_			_	 _	_	 960
			cga Arg							1005

```
<210> 147
<211> 335
<212> PRT
<213> Micromonospora carbonacea
<223> evcC
<400> 147
Val Glu Leu Ala Trp Tyr Ala Leu Leu Gly Leu Phe Leu Ala Gly Tyr
Leu Val Leu Gly Gly Tyr Asp Tyr Gly Val Gly Leu Leu Leu Ala Arg
Gly Gly Pro Pro Ala Arg Arg Arg Ala Ala Leu Thr Ala Val Gly Pro
Phe Phe Leu Gly Asn Glu Val Trp Leu Val Ala Thr Val Gly Ile Leu
Phe Gly Ala Phe Pro Thr Leu Glu Gly Glu Leu Leu Ser Gly Phe Tyr
Pro Val Val Ala Ala Ala Leu Ala Gly Val Ile Met Val Thr Val Gly
Val Gln Leu Arg Ser Arg Pro Thr Asp Glu Pro Thr Arg Ala Ala Trp
Asp Arg Met Val Ala Ala Gly Ser Leu Leu Ala Ala Phe Gly Trp Gly
                            120
Ala Leu Leu Ala Gly Leu Leu Gln Gly Val Pro Leu Ala Ala Asp Gly
His Val Thr Gly Val Gly His Val Ala Thr Pro Phe Ala Ala Leu Ala
145
                    150
Gly Leu Ala Met Thr Ala Leu Val Ala Val His Gly Ala Thr Phe Leu
                                    170
Thr Leu Arg Leu Ser Ala Ala Asp Ala Ala Pro Leu Ala Arg Thr Ala
                                185
Arg Arg Leu Val Ala Val Ala Leu Ala Ala Val Ala Leu Ala Ala Val
                            200
Ala Gly Ala Leu Ser Asp Arg Val Arg Ala Ala Thr Gln Arg Pro Leu
Pro Ala Val Leu Leu Pro Leu Val Leu Val Ala Ala Leu Leu Val Ala
                    230
                                        235
Arg Ala Ala His Ala Arg His Leu Pro Gly Val Ala Phe Ala Ala Thr
Ser Ala Ala Leu Ala Leu Pro Val Ala Gly Val Gly Ala Ala Leu Trp
Pro Tyr Ala Leu Val Ser Thr Val Ala Pro Thr Ala Ser Leu Ser Val
                            280
```

Thr Asp Ala Ala Ala Ser Gly Pro Thr Leu Thr Val Leu Gly Trp Leu

295

290

Ala Leu Pro Leu Leu Pro Ala Leu Leu Gly Phe Gln Ala Met Cys Trp Trp Val Phe Arg Gly Arg Thr Asp Gly Arg Ala Pro Val Tyr Trp 325 330 <210> 148 <211> 1683 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1683) <220> <223> evcD <400> 148 gtg ctc gcg gtg ctc ggc ggg ctg acg gcg ctg ctg gtc gtg ggg cag 48 Val Leu Ala Val Leu Gly Gly Leu Thr Ala Leu Leu Val Val Gly Gln gcc acc gcg ctg gcc acg gtg ctg gcc gcc gcg ctc gac ggg cgg ttg 96 Ala Thr Ala Leu Ala Thr Val Leu Ala Ala Ala Leu Asp Gly Arg Leu Ala Arg Pro Ala Leu Ala Gly Phe Leu Ala Ala Val Val Gly Arg Ala 35 40 ctg gtc gcc tgg gcc cag ggc acg gtg gcg gcg gcc gcc gcg acg 192 Leu Val Ala Trp Ala Gln Gly Thr Val Ala Ala Arg Ala Ala Ala Thr gtc aag gcg gcg ctg cgg gcc gac ctg ctc gcc gcc gtc ggc cgg cac 240 Val Lys Ala Ala Leu Arg Ala Asp Leu Leu Ala Ala Val Gly Arg His ggt ccc ggc tgg gtc gcc ggg cag cgg gcc ggg cag ctc gcc acc ctq Gly Pro Gly Trp Val Ala Gly Gln Arg Ala Gly Gln Leu Ala Thr Leu 90 gcc ggg cgg ggg ctg gac gcc ctg gac gcc tac ttc acc ggg tac ctt 336 Ala Gly Arg Gly Leu Asp Ala Leu Asp Ala Tyr Phe Thr Gly Tyr Leu 100 105 110 ccg cag ctc gtg ctc agc gtc acc gtc ccg gtg gcc gtg ctg gcc cgg 384 Pro Gln Leu Val Leu Ser Val Thr Val Pro Val Ala Val Leu Ala Arg 115 120 ate ace tte gee gae tgg gge teg gee gte ate gte geg etg ace etg 432 Ile Thr Phe Ala Asp Trp Gly Ser Ala Val Ile Val Ala Leu Thr Leu 130 135 ccg ctg atc ccg gtc ttc ggg gcg ctg ctc ggc tgg cag gcg cag gcc 480 Pro Leu Ile Pro Val Phe Gly Ala Leu Leu Gly Trp Gln Ala Gln Ala 145 150 160 gcc acc gag cgg cag tgg cgg ctg tcg acg ctc ggc ggg cac ttc 528

Ala Thr Glu Arg Gln Trp Arg Arg Leu Ser Thr Leu Gly Gly His Phe

165 170 175 ctc gac atg gtc gcc ggc ctg ccc acg ctg cgc gcg ttc ggc cgg gcc 576 Leu Asp Met Val Ala Gly Leu Pro Thr Leu Arg Ala Phe Gly Arg Ala 180 egg ggc cag gtc gag gtg gtc cgc cgg atg gcc gac ggg cac cgc gcc 624 Arg Gly Gln Val Glu Val Val Arg Arg Met Ala Asp Gly His Arg Ala 205 gcg acg atg cgc acg ctg cgg atc gcg ttc ctg tcc gcg ctg gtq ctq 672 Ala Thr Met Arg Thr Leu Arg Ile Ala Phe Leu Ser Ala Leu Val Leu 215 gag ctg gtc gcc acc ctg tcg gtg gcg ctg gtc gcg gtg ccg gtg ggc Glu Leu Val Ala Thr Leu Ser Val Ala Leu Val Ala Val Pro Val Gly 720 230 235 ate egg etg ete gge gge ggg etg geg etg tee ace geg etg etg gtg 768 Ile Arg Leu Leu Gly Gly Gly Leu Ala Leu Ser Thr Ala Leu Leu Val 250 ctg ctg ctc acc ccg gag gcg tac ctg ccg ctg cgg gcg gcc ggc agc 816 Leu Leu Leu Thr Pro Glu Ala Tyr Leu Pro Leu Arg Ala Ala Gly Ser 265 egg tte cae gee age atg gag ggg etg gee geg etg gae gag gea etg 864 Arg Phe His Ala Ser Met Glu Gly Leu Ala Ala Leu Asp Glu Ala Leu 280 285 912 295 300 ccc gtc ccc gac ggg cgc gcc gag atc cgg ttc gag ggc gtg acc gtc 960 Pro Val Pro Asp Gly Arg Ala Glu Ile Arg Phe Glu Gly Val Thr Val 310 gcg tac gag cgg acc gtg gcg cta cgg gac gtc acg ctg aca atc cgg 1008 Ala Tyr Glu Arg Thr Val Ala Leu Arg Asp Val Thr Leu Thr Ile Arg 325 330 ccc ggc gag cgg atc gcg atc gtc ggg ccg agc ggc gcg ggc aag agc 1056 Pro Gly Glu Arg Ile Ala Ile Val Gly Pro Ser Gly Ala Gly Lys Ser 340 acc ctg ctc aac ctg ctc ctc ggc ttc gtc gcc ccg acg cag ggc cgg 1104 Thr Leu Leu Asn Leu Leu Gly Phe Val Ala Pro Thr Gln Gly Arg 355 gtc acc gtg ggt ggc gtc gac ctg gcc ggc gcg gac ccg gac ggc tgg 1152 Val Thr Val Gly Gly Val Asp Leu Ala Gly Ala Asp Pro Asp Gly Trp egg egt cag gte gee tgg gtg eeg caa egg gee cae ete tte gee gee 1200 Arg Arg Gln Val Ala Trp Val Pro Gln Arg Ala His Leu Phe Ala Ala 385 teg etg acc gac aac atc egg etc ggt gec eec ggc acg eec gac gec 1248 Ser Leu Thr Asp Asn Ile Arg Leu Gly Ala Pro Gly Thr Pro Asp Ala geg etc gec ggc geg gtc gec gec geg etg gac gag gtg gtc gec 1296 Ala Leu Ala Gly Ala Val Ala Ala Ala Leu Asp Glu Val Val Ala

425

gcc ctg ccc gac ggg ctc gac acc gtg ctc ggt gag cgc ggg cac ggc Ala Leu Pro Asp Gly Leu Asp Thr Val Leu Gly Glu Arg Gly His Gly 435 440 445	1344
ctg tcc agc ggc cag cgg cag cgg gtc gcc ctg gcc cgg gcg ttc ctg Leu Ser Ser Gly Gln Arg Gln Arg Val Ala Leu Ala Arg Ala Phe Leu 450 455 460	1392
cgg gac gcg ccg gtg gtg ctg ctg gac gag ccg acc gcg cgg ctg gac Arg Asp Ala Pro Val Val Leu Leu Asp Glu Pro Thr Ala Arg Leu Asp 465 470 475 480	1440
acc gcc agc gag gcc ggg gtg ctg gcc gcc acc cgc cgg ctc gtc gcc Thr Ala Ser Glu Ala Gly Val Leu Ala Ala Thr Arg Arg Leu Val Ala 485 490 495	1488
ggg cga acc gcc ctg ttg gtg gcc cac cgg ccg gcg ctg ctc tcc gac Gly Arg Thr Ala Leu Leu Val Ala His Arg Pro Ala Leu Leu Ser Asp 500 505 510	1536
gcc gac cgg atc ctg cgg gtc gag gaa ggc cgg gtc acc gag ctg acc Ala Asp Arg Ile Leu Arg Val Glu Glu Gly Arg Val Thr Glu Leu Thr 515 520 525	1584
acc acc ccg gcc aca ggg gtg acc ccc ggc ccc ggc gag gcg gct gcc Thr Thr Pro Ala Thr Gly Val Thr Pro Gly Pro Gly Glu Ala Ala Ala 530 535 540	1632
gga ccg gcc ggg cag gtc gcc ccc gcc ccg gcc gga gag ggg gcc Gly Pro Ala Gly Gln Val Ala Pro Ala Pro Ala Gly Glu Gly Ala Ala 545 550 555 560	1680
cga Arg	1683
-	1683
Arg <210> 149 <211> 561 <212> PRT	1683
<pre>Arg <210> 149 <211> 561 <212> PRT <213> Micromonospora carbonacea <220></pre>	1683
Arg <210> 149 <211> 561 <212> PRT <213> Micromonospora carbonacea <220> <223> evcD <400> 149 Val Leu Ala Val Leu Gly Gly Leu Thr Ala Leu Leu Val Val Gly Gln	1683
<pre>Arg <210> 149 <211> 561 <212> PRT <213> Micromonospora carbonacea <220> <223> evcD <400> 149 Val Leu Ala Val Leu Gly Gly Leu Thr Ala Leu Leu Val Val Gly Gln</pre>	1683
<pre>Arg <210> 149 <211> 561 <212> PRT <213> Micromonospora carbonacea <220> <223> evcD <400> 149 Val Leu Ala Val Leu Gly Gly Leu Thr Ala Leu Leu Val Val Gly Gln</pre>	1683
<pre> <210> 149 <211> 561 <212> PRT <213> Micromonospora carbonacea <220> <223> evcD <400> 149 Val Leu Ala Val Leu Gly Gly Leu Thr Ala Leu Leu Val Val Gly Gln</pre>	1683
<pre></pre>	1683

100 105 110 Pro Gln Leu Val Leu Ser Val Thr Val Pro Val Ala Val Leu Ala Arg 120 Ile Thr Phe Ala Asp Trp Gly Ser Ala Val Ile Val Ala Leu Thr Leu 135 Pro Leu Ile Pro Val Phe Gly Ala Leu Leu Gly Trp Gln Ala Gln Ala Ala Thr Glu Arg Gln Trp Arg Arg Leu Ser Thr Leu Gly Gly His Phe Leu Asp Met Val Ala Gly Leu Pro Thr Leu Arg Ala Phe Gly Arg Ala 185 Arg Gly Gln Val Glu Val Val Arg Arg Met Ala Asp Gly His Arg Ala Ala Thr Met Arg Thr Leu Arg Ile Ala Phe Leu Ser Ala Leu Val Leu Glu Leu Val Ala Thr Leu Ser Val Ala Leu Val Ala Val Pro Val Gly 230 235 Ile Arg Leu Leu Gly Gly Gly Leu Ala Leu Ser Thr Ala Leu Leu Val Leu Leu Thr Pro Glu Ala Tyr Leu Pro Leu Arg Ala Ala Gly Ser Arg Phe His Ala Ser Met Glu Gly Leu Ala Ala Leu Asp Glu Ala Leu 280 Thr Leu Ser Ala Ala Asp Pro Thr Ala Thr Ala Thr Ala Gly Ser Arg 295 Pro Val Pro Asp Gly Arg Ala Glu Ile Arg Phe Glu Gly Val Thr Val Ala Tyr Glu Arg Thr Val Ala Leu Arg Asp Val Thr Leu Thr Ile Arg Pro Gly Glu Arg Ile Ala Ile Val Gly Pro Ser Gly Ala Gly Lys Ser 345 Thr Leu Leu Asn Leu Leu Gly Phe Val Ala Pro Thr Gln Gly Arg Val Thr Val Gly Gly Val Asp Leu Ala Gly Ala Asp Pro Asp Gly Trp Arg Arg Gln Val Ala Trp Val Pro Gln Arg Ala His Leu Phe Ala Ala 395 Ser Leu Thr Asp Asn Ile Arg Leu Gly Ala Pro Gly Thr Pro Asp Ala 405 410 Ala Leu Ala Gly Ala Val Ala Ala Ala Leu Asp Glu Val Val Ala 425 Ala Leu Pro Asp Gly Leu Asp Thr Val Leu Gly Glu Arg Gly His Gly

```
Leu Ser Ser Gly Gln Arg Gln Arg Val Ala Leu Ala Arg Ala Phe Leu
                        455
Arg Asp Ala Pro Val Val Leu Leu Asp Glu Pro Thr Ala Arg Leu Asp
Thr Ala Ser Glu Ala Gly Val Leu Ala Ala Thr Arg Arg Leu Val Ala
                                    490
Gly Arg Thr Ala Leu Leu Val Ala His Arg Pro Ala Leu Leu Ser Asp
                                505
Ala Asp Arg Ile Leu Arg Val Glu Glu Gly Arg Val Thr Glu Leu Thr
Thr Thr Pro Ala Thr Gly Val Thr Pro Gly Pro Gly Glu Ala Ala Ala
                        535
Gly Pro Ala Gly Gln Val Ala Pro Ala Pro Ala Gly Glu Gly Ala Ala
                                        555
Arg
<210> 150
<211> 1839
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1) .. (1839)
<220>
<223> evcE
<400> 150
atg age ace ggt eee gee gae gee tte gee ate eeg etg eeg gee
Met Ser Thr Gly Pro Ala Asp Asp Ala Phe Ala Ile Pro Leu Pro Ala
gac ggg gcc ccg gtg gcc ggc ggc agc gtc cgg gcc gcc gag cgg gcc
Asp Gly Ala Pro Val Ala Gly Gly Ser Val Arg Ala Ala Glu Arg Ala
                                 25
gtg ctc cgg ctg gcc cgg ccg tac ctg ggc cgg ctg gtc ggc gcg ggt
                                                                   144
Val Leu Arg Leu Ala Arg Pro Tyr Leu Gly Arg Leu Val Gly Ala Gly
                             40
ctg ctc gcc gcc acc gag ttc gcc ggg ctg gcc ctg atg gcc acc
                                                                   192
Leu Leu Ala Ala Ala Thr Glu Phe Ala Gly Leu Ala Leu Met Ala Thr
gcc acc tgg ctg ctg atg agc gcc gcc ggt cgg cca cca ctg gac cgg
                                                                   240
Ala Thr Trp Leu Leu Met Ser Ala Ala Gly Arg Pro Pro Leu Asp Arg
65
                     70
ctc acc gtg gcg atc gtc gcg gtc cgg gcg ctg gcg atc agc cga ggc
                                                                   288
Leu Thr Val Ala Ile Val Ala Val Arg Ala Leu Ala Ile Ser Arg Gly
                 85
                                     90
gtg ttc cgc tac acc gag cgc ctc gcc ggc cac gat gcc gtg ctg cgg
```

Val Phe Arg Tyr Thr Glu Arg Leu Ala Gly His Asp Ala Val Leu Arg

100 105 110 atg atc acc gac gtc egg gcc ggg gtc ttc gcc gcc ctg gcc gcc egg 384 Met Ile Thr Asp Val Arg Ala Gly Val Phe Ala Ala Leu Ala Arg 115 120 cgc gac gcc cgg cag cgc acc ggg gac gcg ctg agc cgg ctc gtg 432 Arg Asp Ala Ala Arg Gln Arg Thr Gly Asp Ala Leu Ser Arg Leu Val tcc gac gtg gag gcc gtg cag gac ctg ctg ctg cgg gtg ctc gtc ccg 480 Ser Asp Val Glu Ala Val Gln Asp Leu Leu Leu Arg Val Leu Val Pro 150 ggg gcc gcc gcc acg gtg gtc agc gtg ctg gcc gtg gcc ggg gcc acc 528 Gly Ala Ala Ala Thr Val Val Ser Val Leu Ala Val Ala Gly Ala Thr 165 170 acc atc tcg ctc ccc gcc gcc ggg gtg ctg gcg ctg ggc ctg etc gtc 576 Thr Ile Ser Leu Pro Ala Ala Gly Val Leu Ala Leu Gly Leu Leu Val gee ggg gtg gee etg eeg ete geg gee ace geg etg ace egg eac gee 624 Ala Gly Val Ala Leu Pro Leu Ala Ala Thr Ala Leu Thr Arg His Ala 200 gee gae egg gtg gee eeg etg ege geg ete gee aeg gae gee gtg 672 Ala Asp Arg Val Ala Pro Leu Arg Gly Ala Leu Ala Thr Asp Ala Val 215 gac ctt gtc cac ggc gcc gcc gcc ctg gcc gcg ttc ggt gcc acc ggg 720 Asp Leu Val His Gly Ala Ala Asp Leu Ala Ala Phe Gly Ala Thr Gly 230 235 tac qcg ctg gac gcc gcc gcc gat cgg gcc cgc cgg ctg gcc cgg ctg 768 Tyr Ala Leu Asp Ala Ala Ala Asp Arg Ala Arg Leu Ala Arg Leu 245 gaa cga cgg ctc gcc gcc acc ggc ttc gcc gtg gac gcc gcc ggg gcg 816 Glu Arg Arg Leu Ala Ala Thr Gly Phe Ala Val Asp Ala Ala Gly Ala 260 265 270 ctc gtc gcc ggg gtg acc gcc ggc acg gtg gtg gtc acc gcg ctg cgc 864 Leu Val Ala Gly Val Thr Ala Gly Thr Val Val Thr Ala Leu Arg 275 gac ggc gtc ggc ggg gtg ctg gtc ggg gtg ctg ggc gtc ggt tcc ctg 912 Asp Gly Val Gly Val Leu Val Gly Val Leu Ala Val Gly Ser Leu 290 295 300 gee gee gte gag gtg geg etg geg etg gte ggg gee gee egg eag ege 960 Ala Ala Val Glu Val Ala Leu Ala Leu Val Gly Ala Ala Arg Gln Arg 305 1008 Thr Gln Leu Arg Ala Gly Leu Val Arg Val Ala Ala Leu Leu Thr Ala ccg cag gcc gac gcg ccc gcc gcc acc ccg ccc ggt gcc gcc cgt gcc 1056 Pro Gln Ala Asp Ala Pro Ala Ala Thr Pro Pro Gly Ala Ala Arg Ala gcc gcc gtc ggt gcc ggc ccg cac gac gtg cgc ttc gac gcg gtc acc 1104 Ala Ala Val Gly Ala Gly Pro His Asp Val Arg Phe Asp Ala Val Thr 355 360

gtg cgg tac cgg Val Arg Tyr Arg 370					.52
gac ctg ccg gcc Asp Leu Pro Ala 385	ggc cgc cgg Gly Arg Arg 390	gtc gcc gtg Val Ala Val	gtc ggg ccg a Val Gly Pro S 395	gc ggc gcc 12 er Gly Ala 400	00
ggc aag agc acc Gly Lys Ser Thr					48
cag ggc cgg gtc Gln Gly Arg Val 420			Leu Ser Ala T		96
gag gaa ctg ccc Glu Glu Leu Pro 435					44
ttc cac gcc acg Phe His Ala Thr 450					92
gac gag gcg gag Asp Glu Ala Glu 465					40
tgg gtg cac gcc Trp Val His Ala					88
ggc gga cag ctc Gly Gly Gln Leu 500			Arg Leu Ala L		36
gcg ctg ctc gcc Ala Leu Leu Ala 515					84
ggg ctc gac ccg Gly Leu Asp Pro 530					32
gcg acc ccc gcc Ala Thr Pro Ala 545					80
ggg ctc gcc gac Gly Leu Ala Asp					28
gtc cag cgt ggc Val Gln Arg Gly 580			Ala Ala Pro G		76
cgg gac cag tgg Arg Asp Gln Trp 595					24
ctg acg ccc cgc Leu Thr Pro Arg 610				18	39

```
<210> 151
<211> 613
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evcE
<400> 151
Met Ser Thr Gly Pro Ala Asp Asp Ala Phe Ala Ile Pro Leu Pro Ala
Asp Gly Ala Pro Val Ala Gly Gly Ser Val Arg Ala Ala Glu Arg Ala
Val Leu Arg Leu Ala Arg Pro Tyr Leu Gly Arg Leu Val Gly Ala Gly
Leu Leu Ala Ala Ahr Glu Phe Ala Gly Leu Ala Leu Met Ala Thr
Ala Thr Trp Leu Leu Met Ser Ala Ala Gly Arg Pro Pro Leu Asp Arg
Leu Thr Val Ala Ile Val Ala Val Arg Ala Leu Ala Ile Ser Arg Gly
Val Phe Arg Tyr Thr Glu Arg Leu Ala Gly His Asp Ala Val Leu Arg
Met Ile Thr Asp Val Arg Ala Gly Val Phe Ala Ala Leu Ala Ala Arg
Arg Asp Ala Ala Arg Gln Arg Thr Gly Asp Ala Leu Ser Arg Leu Val
Ser Asp Val Glu Ala Val Gln Asp Leu Leu Leu Arg Val Leu Val Pro
Gly Ala Ala Ala Thr Val Val Ser Val Leu Ala Val Ala Gly Ala Thr
Thr Ile Ser Leu Pro Ala Ala Gly Val Leu Ala Leu Gly Leu Leu Val
                                185
Ala Gly Val Ala Leu Pro Leu Ala Ala Thr Ala Leu Thr Arg His Ala
Ala Asp Arg Val Ala Pro Leu Arg Gly Ala Leu Ala Thr Asp Ala Val
Asp Leu Val His Gly Ala Ala Asp Leu Ala Ala Phe Gly Ala Thr Gly
                                        235
Tyr Ala Leu Asp Ala Ala Ala Asp Arg Ala Arg Leu Ala Arg Leu
                                    250
```

Glu Arg Arg Leu Ala Ala Thr Gly Phe Ala Val Asp Ala Ala Gly Ala

Leu Val Ala Gly Val Thr Ala Gly Thr Val Val Thr Ala Leu Arg

Asp Gly Val Gly Gly Val Leu Val Gly Val Leu Ala Val Gly Ser Leu

	290					295					300				
Ala 305	Ala	Val	Glu	Val	Ala 310	Leu	Ala	Leu	Val	Gly 315	Ala	Ala	Arg	Gln	Arg 320
Thr	Gln	Leu	Arg	Ala 325	Gly	Leu	Val	Arg	Val 330	Ala	Ala	Leu	Leu	Thr 335	Ala
Pro	Gln	Ala	Asp 340	Ala	Pro	Ala	Ala	Thr 345	Pro	Pro	Gly	Ala	Ala 350	Arg	Ala
Ala	Ala	Val 355	Gly	Ala	Gly	Pro	His 360	Asp	Val	Arg	Phe	Asp 365	Ala	Val	Thr
Val	Arg 370	Tyr	Arg	Ala	Gly	Thr 375	Ala	Pro	Ala	Leu	Asp 380	Arg	Val	Thr	Leu
Asp 385	Leu	Pro	Ala	Gly	Arg 390	Arg	Val	Ala	Val	Val 395	Gly	Pro	Ser	Gly	Ala 400
Gly	Lys	Ser	Thr	Leu 405	Ala	Ala	Val	Leu	Thr 410	Gly	Thr	Val	Arg	Pro 415	Glu
Gln	Gly	Arg	Val 420	Thr	Leu	Asp	Gly	Ala 425	Asp	Leu	Ser	Ala	Tyr 430	Pro	Val
Glu	Glu	Leu 435	Pro	Arg	Ala	Val	Gly 440	Gly	Leu	Leu	Ala	Glu 445	Ala	Tyr	Val
Phe	His 450	Ala	Thr	Val	Arg	Glu 455	Asn	Leu	Leu	Leu	Gly 460	Arg	Pro	Ala	Ala
Asp 465	Glu	Ala	Glu	Leu	Thr 470	Ala	Ala	Thr	Arg	Ala 475	Ala	Gly	Leu	Leu	Asp 480
Trp	Val	His	Ala	Gln 485	Pro	Ala	Gly	Trp	Asp 490	Thr	Val	Val	Gly	Glu 495	Glu
Gly	Gly	Gln	Leu 500	Ser	Gly	Gly	Gln	Arg 505	Gln	Arg	Leu	Ala	Leu 510	Ala	Arg
Ala	Leu	Leu 515	Ala	Ala	Pro	Gly	Val 520	Leu	Val	Leu	Asp	Glu 525	Pro	Thr	Glu
Gly	Leu 530	Asp	Pro	Ser	Ala	Ala 535	Asp	Ala	Val	Leu	Ala 540	Ser	Ala	Leu	Ala
Ala 545	Thr	Pro	Ala	Gly	His 550	Ser	Val	Leu	Leu	Ile 555	Ser	His	Arg	Leu	Ser 560
Gly	Leu	Ala	Asp	Leu 565	Asp	Glu	Ile	Val	Val 570	Leu	Asp	Ala	Gly	Arg 575	Val
Val	Gln	Arg	Gly 580	Arg	His	Asp	Glu	Leu 585	Val	Ala	Ala	Pro	Gly 590	Trp	Tyr
Arg	Asp	Gln 595	Trp	Leu	Leu	Gln	Glu 600	Ala	Ala	Glu	Arg	Gly 605	Tyr	Leu	Ala
Leu	Thr 610	Pro	Arg	Pro											

```
<211> 687
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(687)
<220>
<223> evcF
<400> 152
atg gtg cgc tgc gac gac gta ctc gtg aag gag cgg ctg cgc gag ttg
                                                                 48
Met Val Arg Cys Asp Asp Val Leu Val Lys Glu Arg Leu Arg Glu Leu
age gac egg etg cac gge eeg gea egg ete aag gee gac etg etg qee
                                                                 96
Ser Asp Arg Leu His Gly Pro Ala Arg Leu Lys Ala Asp Leu Leu Ala
gag gee ege cae geg ttg eag gae gee gte gag geg tae egg gae gge
                                                                 144
Glu Ala Arg His Ala Leu Gln Asp Ala Val Glu Ala Tyr Arg Asp Gly
                            40
ggg ctg ccg gcg gcg gag gcc gag cgg cgg gca gtg gcc gag ttc ggc
                                                                 192
Gly Leu Pro Ala Ala Glu Ala Glu Arg Arg Ala Val Ala Glu Phe Gly
                        55
                                            60
gag ccg gcc cgg ctc gcc ccg gcg tac cag gcg gag ctg gcg gcc ggg
                                                                 240
Glu Pro Ala Arg Leu Ala Pro Ala Tyr Gln Ala Glu Leu Ala Ala Gly
                    70
                                        75
teg etg ege gge etg tee etg egg gtg ete geg gte gee gge gte etg
                                                                288
Ser Leu Arg Gly Leu Ser Leu Arg Val Leu Ala Val Ala Gly Val Leu
gtc gtc gcg ggc gat ctg acc tgg cag ggg tcg agc tgg agc ggc ggc
                                                                336
Val Val Ala Gly Asp Leu Thr Trp Gln Gly Ser Ser Trp Ser Gly Gly
           100
ccc ggc ccg ccg gcc tac cgc ctg ctg tcc gcc tcg gtg gac ggc
                                                                 384
Pro Gly Pro Pro Ala Ala Tyr Arg Leu Leu Ser Ala Ser Val Asp Gly
432
Ile Trp Leu Gly Ala Val Val Leu Ser Val Ala Gly Leu Leu Val
   130
gcc gcc tcg gcc cgg tgg gcg cac ccg gcc ctg ccc cgg ctc gcc cgg
                                                                 480
Ala Ala Ser Ala Arg Trp Ala His Pro Ala Leu Pro Arg Leu Ala Arg
                                       155
ctg acc ggt ctc ggg ctc acc gcc acg ctc gtc ctg ggc gtg gcg acc
                                                                 528
Leu Thr Gly Leu Gly Leu Thr Ala Thr Leu Val Leu Gly Val Ala Thr
ggc gcg gcc ctg tac gcc tgg tcg atc ggg ctc tgg gag gcg gcc cgc
                                                                 576
Gly Ala Ala Leu Tyr Ala Trp Ser Ile Gly Leu Trp Glu Ala Ala Arg
                               185
ace tgg eeg eeg atg ete gtg gge geg etg gte tge gge geg ggg tte
                                                                 624
Thr Trp Pro Pro Met Leu Val Gly Ala Leu Val Cys Gly Ala Gly Phe
                           200
                                               205
ttc tgg atc ggt cgg gcc cgg tcc tgg ctc tcg gca cgc cga
```

Phe Trp Ile Gly Arg Ala Ala Arg Ser Trp Leu Leu Ser Ala Arg Arg

215 ccg gcc gga ccg gcg Pro Ala Gly Pro Ala 225 <210> 153 <211> 229 <212> PRT <213> Micromonospora carbonacea <220> <223> evcF <400> 153 Met Val Arg Cys Asp Asp Val Leu Val Lys Glu Arg Leu Arg Glu Leu Ser Asp Arg Leu His Gly Pro Ala Arg Leu Lys Ala Asp Leu Leu Ala Glu Ala Arg His Ala Leu Gln Asp Ala Val Glu Ala Tyr Arg Asp Gly Gly Leu Pro Ala Ala Glu Ala Glu Arg Arg Ala Val Ala Glu Phe Gly Glu Pro Ala Arg Leu Ala Pro Ala Tyr Gln Ala Glu Leu Ala Ala Gly Ser Leu Arg Gly Leu Ser Leu Arg Val Leu Ala Val Ala Gly Val Leu Val Val Ala Gly Asp Leu Thr Trp Gln Gly Ser Ser Trp Ser Gly Gly Pro Gly Pro Pro Ala Ala Tyr Arg Leu Leu Ser Ala Ser Val Asp Gly 120 Ile Trp Leu Gly Ala Val Val Leu Ser Val Ala Gly Leu Leu Val Ala Ala Ser Ala Arg Trp Ala His Pro Ala Leu Pro Arg Leu Ala Arg 155 Leu Thr Gly Leu Gly Leu Thr Ala Thr Leu Val Leu Gly Val Ala Thr 165 Gly Ala Ala Leu Tyr Ala Trp Ser Ile Gly Leu Trp Glu Ala Ala Arg 185 Thr Trp Pro Pro Met Leu Val Gly Ala Leu Val Cys Gly Ala Gly Phe Phe Trp Ile Gly Arg Ala Ala Arg Ser Trp Leu Leu Ser Ala Arg Arg 215 220 Pro Ala Gly Pro Ala 225

```
<211> 333
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1) . . (333)
<220>
<223> evcG
<400> 154
atg aag gee cag geg etg cac gga cac ete gae geg etg ete geg
                                                                   48
Met Lys Ala Gln Ala Leu His Gly His Leu Asp Ala Leu Leu Ala
                                     10
gtg ctg gaa cgg ggc gcg ctg cac ggc tac gcc atc atc gag gcg ctg
                                                                   96
Val Leu Glu Arg Gly Ala Leu His Gly Tyr Ala Ile Ile Glu Ala Leu
ege geg ege age gag gge age ete gat etg eet ace ggg acg ate tae
                                                                   144
Arg Ala Arg Ser Glu Gly Ser Leu Asp Leu Pro Thr Gly Thr Ile Tyr
                             40
ccg gcg ctg cgc cgg ctg gag cgg gcg ggg cac gtg gtc agc agt tgg
                                                                   192
Pro Ala Leu Arg Arg Leu Glu Arg Ala Gly His Val Val Ser Ser Trp
age ace gte aae gge ege gag ege ege ace tae gag etg ace gae tee
                                                                   240
Ser Thr Val Asn Gly Arg Glu Arg Arg Thr Tyr Glu Leu Thr Asp Ser
                     70
ggc cgc cgg gcc ctc gcc ggg gaa cgg gcc ggc tgg cgg gag ttc agc
                                                                   288
Gly Arg Arg Ala Leu Ala Gly Glu Arg Ala Gly Trp Arg Glu Phe Ser
gcg acc gtc ggc cag ttc ctc ggc gac acc ccc gcc acg ccg gcc
                                                                   333
Ala Thr Val Gly Gln Phe Leu Gly Asp Thr Pro Ala Thr Pro Ala
            100
                                105
<210> 155
<211> 111
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evcG
<400> 155
Met Lys Ala Gln Ala Leu His Gly His Leu Asp Ala Leu Leu Ala
Val Leu Glu Arg Gly Ala Leu His Gly Tyr Ala Ile Ile Glu Ala Leu
Arg Ala Arg Ser Glu Gly Ser Leu Asp Leu Pro Thr Gly Thr Ile Tyr
         35
Pro Ala Leu Arg Arg Leu Glu Arg Ala Gly His Val Val Ser Ser Trp
Ser Thr Val Asn Gly Arg Glu Arg Arg Thr Tyr Glu Leu Thr Asp Ser
```

Gly Arg Arg Ala Leu Ala Gly Glu Arg Ala Gly Trp Arg Glu Phe Ser 85 90 95

Ala Thr Val Gly Gln Phe Leu Gly Asp Thr Pro Ala Thr Pro Ala 100 105 110

<210> 156 <211> 909 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(909) <220> <223> evcH <400> 156 gtg ggc agc ccg aag cac acg gag gtc agc gtg gcc cgc cag tcg ccc Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro caa cgg ccc gac gcc gac gag cct gag ctc gac gag acc gac ggc acc Gln Arg Pro Asp Ala Asp Glu Pro Glu Leu Asp Glu Thr Asp Gly Thr gcc gca gag gtc gaa gag gac ggc gcg cgc ccg tcg gcg cag gac gcc 144 Ala Ala Glu Val Glu Glu Asp Gly Ala Arg Pro Ser Ala Gln Asp Ala 35 gac ege geg ete tgg gac gag etg ege ate gac eeg gte gag ate gee 192 Asp Arg Ala Leu Trp Asp Glu Leu Arg Ile Asp Pro Val Glu Ile Ala etg eee gee gge ace gge tae aeg etg egg geg tae egg eeg gea egg 240 Leu Pro Ala Gly Thr Gly Tyr Thr Leu Arg Ala Tyr Arg Pro Ala Arg gag ttg acc ccg acc gac gtc gcc gag cgc gac cag gac gac ccg ttc 288 Glu Leu Thr Pro Thr Asp Val Ala Glu Arg Asp Gln Asp Asp Pro Phe 90 ctg gcc cgc cgg cag gcg gtc gag acc gac gag gac gag gtc 336 Leu Ala Arg Arg Gln Ala Val Glu Thr Asp Glu Asp Glu Asp Glu Val 100 105 ate ate ete gae gag gag gtg gee gee gag tte gee gag geg gae geg 384 Ile Ile Leu Asp Glu Glu Val Ala Ala Glu Phe Ala Glu Ala Asp Ala 115 gag gag gcc ggc ggg aag tcc cgc tcc cgc aag ccc cgc gcc gac gcg 432 Glu Glu Ala Gly Gly Lys Ser Arg Ser Arg Lys Pro Arg Ala Asp Ala 130 135 gac tee gac gac gee gga gee gee aca gac geg gac geg gag gag 480 Asp Ser Asp Asp Ala Gly Ala Ala Thr Asp Ala Asp Ala Glu Glu Glu 145 150 eeg gae tee gae gag gae gag gee gae gag gag gtt eeg gte tte 528 Pro Asp Ser Asp Glu Asp Glu Ala Gly Asp Glu Glu Val Pro Val Phe 165 170

ctc agc cac cgg ggc agg ctg ctg ctg ttc aag acg ccc gaa tcc ctc Leu Ser His Arg Gly Arg Leu Leu Leu Phe Lys Thr Pro Glu Ser Leu 180 185 190	576
gtc agc ttc gtc cgg tcc ggc gca ccc aac gac atg tct caa ctg gac Val Ser Phe Val Arg Ser Gly Ala Pro Asn Asp Met Ser Gln Leu Asp 195 200 205	624
agc tgg aat gaa ctg tcc gaa cgg gtg gag ccg gcc gac atc gtc ccg Ser Trp Asn Glu Leu Ser Glu Arg Val Glu Pro Ala Asp Ile Val Pro 210 215 220	672
ctc gac gag gac acc tac gag ctg gac ctg gtc gtg gag aac ctg cgg Leu Asp Glu Asp Thr Tyr Glu Leu Asp Leu Val Val Glu Asn Leu Arg 225 230 230 235	720
ggt ggg cac gac acc tgg gac tcg gcg ctg ctg atc gag ccg gcg agg Gly Gly His Asp Thr Trp Asp Ser Ala Leu Leu Ile Glu Pro Ala Arg 245 250 255	768
tgg ccc ggg acg tcg cgt atg ccc tgc gtc tgc ccg ccg tgt tgg aca Trp Pro Gly Thr Ser Arg Met Pro Cys Val Cys Pro Pro Cys Trp Thr 260 265 270	816
tgc tct ccg ccg gct cca gcc tcg acg acc tgg acg agg cgc tgc gcg Cys Ser Pro Pro Ala Pro Ala Ser Thr Thr Trp Thr Arg Arg Cys Ala 275 280 285	864
cca cgg cca acg gcg ggc tcg ggg gct tcc tcg gcc gcc g	909
<210> 157 <211> 303 <212> PRT <213> Micromonospora carbonacea	
<211> 303 <212> PRT	
<211> 303 <212> PRT <213> Micromonospora carbonacea <220>	
<211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro	
<pre><211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro</pre>	
<pre><211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro</pre>	
<pre><211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro 1</pre>	
<pre><211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro 1</pre>	
<pre><211> 303 <212> PRT <213> Micromonospora carbonacea <220> <223> evcH <400> 157 Val Gly Ser Pro Lys His Thr Glu Val Ser Val Ala Arg Gln Ser Pro</pre>	

```
Glu Glu Ala Gly Gly Lys Ser Arg Ser Arg Lys Pro Arg Ala Asp Ala
    130
                        135
Asp Ser Asp Asp Ala Gly Ala Ala Thr Asp Ala Asp Ala Glu Glu Glu
                                        155
Pro Asp Ser Asp Glu Asp Glu Ala Gly Asp Glu Glu Val Pro Val Phe
Leu Ser His Arg Gly Arg Leu Leu Phe Lys Thr Pro Glu Ser Leu
Val Ser Phe Val Arg Ser Gly Ala Pro Asn Asp Met Ser Gln Leu Asp
                            200
Ser Trp Asn Glu Leu Ser Glu Arg Val Glu Pro Ala Asp Ile Val Pro
                        215
Leu Asp Glu Asp Thr Tyr Glu Leu Asp Leu Val Val Glu Asn Leu Arg
                    230
Gly Gly His Asp Thr Trp Asp Ser Ala Leu Leu Ile Glu Pro Ala Arg
Trp Pro Gly Thr Ser Arg Met Pro Cys Val Cys Pro Pro Cys Trp Thr
                                265
Cys Ser Pro Pro Ala Pro Ala Ser Thr Thr Trp Thr Arg Arg Cys Ala
                            280
Pro Arg Pro Thr Ala Gly Ser Gly Ala Ser Ser Ala Ala Gly Gly
                        295
<210> 158
<211> 2073
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(2073)
<220>
<223> evcI
atg cag tee geg eeg gee gag egg egg gee ggg etg gee egg geg
                                                                   48
Met Gln Ser Ala Pro Ala Glu Arg Arg Ala Val Gly Leu Ala Arg Ala
ctc cag gcc ggc gcg ctc tcg gcg gtc acc ctc ccg gcg ccc cgg gat
                                                                   96
Leu Gln Ala Gly Ala Leu Ser Ala Val Thr Leu Pro Ala Pro Arg Asp
             20
                                                     30
cte gee gge tae aag eag gte ete teg geg eae gee geg ete gee age
                                                                   144
Leu Ala Gly Tyr Lys Gln Val Leu Ser Ala His Ala Ala Leu Ala Ser
         35
ggc cgg cac tcc gcc gcc gtg gcg ctg cgc gag gtg ctg cgg gag ctc
                                                                   192
Gly Arg His Ser Ala Ala Val Ala Leu Arg Glu Val Leu Arg Glu Leu
```

60

tac Tyr 65	ccg Pro	gcc Ala	gcc Ala	ctg Leu	cgc Arg 70	gcg Ala	tac Tyr	ccg Pro	gac Asp	ccg Pro 75	gcc Ala	gag Glu	ccg Pro	gtc Val	gcc Ala 80	240
ctg Leu	gcc Ala	gtg Val	ttg Leu	gac Asp 85	gcc Ala	ctg Leu	ccc Pro	gag Glu	ccc Pro 90	ggc Gly	atg Met	ctg Leu	ggc Gly	999 Gly 95	acg Thr	288
											gac Asp					336
											aag Lys					384
gtg Val	acc Thr 130	gcg Ala	ctg Leu	cgg Arg	gtc Val	gcc Ala 135	atc Ile	gcc Ala	gag Glu	acc Thr	ccc Pro 140	cgc Arg	cgc Arg	gcg Ala	gcg Ala	432
gtc Val 145	agc Ser	cgg Arg	gcg Ala	ctc Leu	acc Thr 150	tcc Ser	gcc Ala	gtg Val	gcg Ala	gag Glu 155	acg Thr	gtc Val	cgt Arg	cag Gln	gcg Ala 160	480
gtg Val	gcc Ala	tcg Ser	gtg Val	cga Arg 165	gca Ala	tgc Cys	gac Asp	gcg Ala	ggc Gly 170	tgc Cys	gag Glu	gcc Ala	ctg Leu	gtc Val 175	ggc Gly	528
gcg Ala	ctc Leu	gac Asp	gcc Ala 180	cgg Arg	gtc Val	acc Thr	acc Thr	ccc Pro 185	acc Thr	ccg Pro	gtg Val	ccg Pro	ggc Gly 190	cgg Arg	cgg Arg	576
											ttg Leu					624
											gtc Val 220					672
agc Ser 225	cgt Arg	ccc Pro	gag Glu	ccg Pro	gtc Val 230	ccc Pro	ggc Gly	ggc Gly	agc Ser	ctg Leu 235	ccc Pro	gcc Ala	cag Gln	ccc Pro	cgc Arg 240	720
											gtc Val					768
											gcc Ala					816
											atc Ile					864
											ccg Pro 300					912
											ccg Pro					960
ggt	gag	ccg	ttc	cgg	ccc	acg	ctg	acc	acc	gcc	gcg	atc	cag	aac	gcg	1008

Gly	Glu	Pro	Phe	Arg 325	Pro	Thr	Leu	Thr	Thr 330	Ala	Ala	Ile	Gln	Asn 335	Ala	
														acg Thr		1056
														gac Asp		1104
agc Ser	gtc Val 370	ccg Pro	gtg Val	ccg Pro	acc Thr	ccg Pro 375	cgt Arg	ccc Pro	ggc Gly	cag Gln	gag Glu 380	tcc Ser	gct Ala	ccc Pro	ccc Pro	1152
														ccc Pro		1200
														gat Asp 415		1248
														gcc Ala		1296
														gag Glu		1344
														gca Ala		1392
														ccg Pro		1440
														ccc Pro 495		1488
														ccg Pro	ctg Leu	1536
														cgg Arg		1584
														acc Thr		1632
														gcc Ala		1680
														gac Asp 575		1728
														gcc Ala		1776

580 585 590 ccg gcg gtg ggc gcc gat acc aag gcc ggg ttg ccc aag cgg gtg ccg 1824 Pro Ala Val Gly Ala Asp Thr Lys Ala Gly Leu Pro Lys Arg Val Pro 595 600 cag gcc aac ctg gtt ccg ggc tcc ccc ctg cgc gag gag cgt ccc cta 1872 Gln Ala Asn Leu Val Pro Gly Ser Pro Leu Arg Glu Glu Arg Pro Leu egg ata gtc ege gae geg gec age etc gee gag aac aeg aec gge tae 1920 Arg Ile Val Arg Asp Ala Ala Ser Leu Ala Glu Asn Thr Thr Gly Tyr 630 635 ttc cgg ggc tgg cgt cgc ggg cag gag atc ggc ggg ttc gcc gtc ggc 1968 Phe Arg Gly Trp Arg Arg Gly Gln Glu Ile Gly Gly Phe Ala Val Gly 645 650 gge egg eeg gge ege gag geg gee gge tgg gae tte acc egg gae 2016 Gly Arg Pro Gly Arg Glu Ala Ala Gly Gly Trp Asp Phe Thr Arg Asp 665 acc ggc gac cga gac gac ggc cgg gag tac gag tac cgg tcc gcc ggc 2064 Thr Gly Asp Arg Asp Asp Arg Glu Tyr Glu Tyr Arg Ser Ala Gly 680 685 tac cgc tcc 2073 Tyr Arg Ser 690 <210> 159 <211> 691 <212> PRT <213> Micromonospora carbonacea <220> <223> evcI <400> 159 Met Gln Ser Ala Pro Ala Glu Arg Arg Ala Val Gly Leu Ala Arg Ala Leu Gln Ala Gly Ala Leu Ser Ala Val Thr Leu Pro Ala Pro Arg Asp Leu Ala Gly Tyr Lys Gln Val Leu Ser Ala His Ala Ala Leu Ala Ser Gly Arg His Ser Ala Ala Val Ala Leu Arg Glu Val Leu Arg Glu Leu Tyr Pro Ala Ala Leu Arg Ala Tyr Pro Asp Pro Ala Glu Pro Val Ala Leu Ala Val Leu Asp Ala Leu Pro Glu Pro Gly Met Leu Gly Gly Thr Ile Ala Arg Gly Arg Glu Val Ser Val Ala Ala Asp Ala Ile Ala Ala His Leu Ala Ala Asp Gly Val Ala Asp Glu Gly Lys Ile Asn Asp Ala 120 Val Thr Ala Leu Arg Val Ala Ile Ala Glu Thr Pro Arg Arg Ala Ala

	130					135					140				
Val 145	Ser	Arg	Ala	Leu	Thr 150	Ser	Ala	Val	Ala	Glu 155	Thr	Val	Arg	Gln	Ala 160
Val	Ala	Ser	Val	Arg 165	Ala	Cys	Asp	Ala	Gly 170	Cys	Glu	Ala	Leu	Val 175	Gly
Ala	Leu	Asp	Ala 180	Arg	Val	Thr	Thr	Pro 185	Thr	Pro	Val	Pro	Gly 190	Arg	Arg
Ala	Ala	Ala 195	Ārg	Arg	Gly	Glu	Pro 200	Val	Ala	Glu	Leu	Pro 205	Gly	Ala	Gly
Leu	Arg 210	Ala	Leu	Arg	Pro	Thr 215	Glu	Pro	Glu	Pro	Val 220	Pro	Gly	Arg	Arg
Ser 225	Arg	Pro	Glu	Pro	Val 230	Pro	Gly	Gly	Ser	Leu 235	Pro	Ala	Gln	Pro	Arg 240
Pro	Leu	Gly	Pro	Pro 245	Pro	Val	Ala	Pro	Glu 250	Pro	Val	Ala	Pro	Pro 255	Pro
Val	Ala	Pro	Arg 260	Pro	Ile	Thr	Pro	Ala 265	Ala	Ser	Ala	Thr	Pro 270	Pro	Val
Ser	Gly	Pro 275	Pro	Ser	Pro	Glu	Pro 280	Arg	Arg	Leu	Ile	Asp 285	Asn	Pro	Ala
Asn	Arg 290	Pro	Val	Ser	Ala	Pro 295	Pro	Pro	Pro	Pro	Pro 300	Gly	Ile	Thr	Pro
Ile 305	Ala	Pro	Ser	Gln	Arg 310	Glu	Arg	Gly	Ser	Val 315	Pro	Pro	Ala	Glu	Ala 320
Gly	Glu	Pro	Phe	Arg 325	Pro	Thr	Leu	Thr	Thr 330	Ala ,	Ala	Ile	Gln	Asn 335	Ala
Arg	Ala	Glu	Arg 340	Gln	Arg	Thr	Ile	Ile 345	Pro	Pro	Arg	Pro	Lys 350	Thr	Thr
Gly	Glu	Ser 355	Ala	Pro	Pro	Pro	Thr 360	Gly	Gly	Phe	Ser	Ala 365	Thr	Asp	Leu
Ser	Val 370	Pro	Val	Pro	Thr	Pro 375	Arg	Pro	Gly	Gln	Glu 380	Ser	Ala	Pro	Pro
Gly 385	Ser	Arg	Ala	Asn	Trp 390	Pro	Leu	Val	Asn	Asn 395	Pro	Glu	Asp	Pro	Ala 400
Asp	Ser	Ser	Pro	Asn 405	Asn	Pro	Val	Ala	Arg 410	Arg	Pro	Leu	Glu	Asp 415	Arg
Ala	Lys	Arg	Gln 420	Ile	Asp	Ala	Pro	Thr 425	Gln	Val	Val	Pro	Pro 430	Ala	Glu
Gly	Arg	Val 435	Thr	Pro	Pro	Trp	Leu 440	Ala	Asp	Asp	Leu	Pro 445	Gln	Glu	Pro
Pro	Met 450	Leu	Arg	Leu	Val	Glu 455	Pro	Pro	Pro	Leu	Ala 460	Asp	Arg	Ala	Leu
Arg	Asp	Gly	Pro	Gly	Gln	Ala	Ala	Asp	Pro	Arg	Leu	Glu	Pro	Pro	Pro

Leu Arg Leu Val Asp Arg Gly Glu Ala Ala Arg Ala Gly Arg Pro Ala

```
Pro Glu Pro Arg Pro Glu Arg Ala Pro Ala Glu His Arg Ser Pro Leu
            500
                                505
Gly Gln Arg Val Pro Leu Glu Glu Arg Pro Asp Met Glu His Arg Thr
Ala Pro Pro Gln Pro Ser Arg Ser Ala Pro Met Glu Arg Arg Thr Pro
                        535
Pro Ile Ser Asp Glu Gly Asp Gly Asp Leu Leu Ile Phe Ala Ala Ala
                                        555
Lys Ser Ala Trp Phe Val Gly His Gly Asp Glu Ser Glu Met Asp Trp
Ser Ser Thr Ala Asp Thr Gly Trp Gln Ala Ala Glu Gln Ala Ala Arg
Pro Ala Val Gly Ala Asp Thr Lys Ala Gly Leu Pro Lys Arg Val Pro
                            600
Gln Ala Asn Leu Val Pro Gly Ser Pro Leu Arg Glu Glu Arg Pro Leu
Arg Ile Val Arg Asp Ala Ala Ser Leu Ala Glu Asn Thr Thr Gly Tyr
                                        635
Phe Arg Gly Trp Arg Arg Gly Gln Glu Ile Gly Gly Phe Ala Val Gly
                645
Gly Arg Pro Gly Arg Glu Ala Ala Gly Gly Trp Asp Phe Thr Arg Asp
Thr Gly Asp Arg Asp Asp Asp Glu Tyr Glu Tyr Arg Ser Ala Gly
Tyr Arg Ser
   690
<210> 160
<211> 591
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(591)
<220>
<223> evcJ
<400> 160
atg teg cae ege eet gte eeg age ggg ege gtg aeg teg geg aag
                                                                   48
Met Ser His Arg Pro Pro Val Pro Ser Gly Arg Val Thr Ser Ala Lys
ate gtt ate gee ggt ggg tte gge gte gge aag aeg etg gte gge
                                                                   96
Ile Val Ile Ala Gly Gly Phe Gly Val Gly Lys Thr Thr Leu Val Gly
             20
                                 25
```

tcg gtc tcg Ser Val Ser 35												144
gcc ggc gtg Ala Gly Val 50	ggc gtc Gly Val	gac g Asp A	gac acc Asp Thr 55	cgg Arg	cag Gln	gtg Val	ccg Pro 60	ggc Gly	gag Glu	acg Thr	acg Thr	192
acc acg gtg Thr Thr Val 65												240
atc ctg tac Ile Leu Tyr	ctg ttc Leu Phe 85	Gly 1	acc ccc Thr Pro	ggc Gly	cag Gln 90	acc Thr	cgg Arg	ttc Phe	tgg Trp	ttc Phe 95	atg Met	288
tgg gac gag Trp Asp Glu												336
acc cgg cgg Thr Arg Arg 115												384
cgg cgg ctg Arg Arg Leu 130	-	Leu V				_		_		_	_	432
tac cac gac Tyr His Asp 145												480
gtg ccg gtg Val Pro Val												528
gtg ctg atc Val Leu Ile												576
gcg gtc gcg Ala Val Ala 195												591
<210> 161 <211> 197 <212> PRT <213> Micro	monospor	a carb	oonacea									
<220> <223> evcJ												
<400> 161 Met Ser His 1	Arg Pro	Pro V	Val Pro	Ser	Gly 10	Arg	Val	Thr	Ser	Ala 15	Lys	
Ile Val Ile	Ala Gly 20	Gly F	Phe Gly	Val 25	Gly	Lys	Thr	Thr	Leu 30	Val	Gly	
Ser Val Ser 35	Glu Ile	Thr F	Pro Leu 40	Thr	Thr	Glu	Ala	Ile 45	Met	Thr	Ser	
Ala Gly Val 50	Gly Val	Asp A	Asp Thr 55	Arg	Gln	Val	Pro 60	Gly	Glu	Thr	Thr	

Thr Thr Val Ala Met Asp Phe Gly Arg Ile Ser Ile Asp Arg Asp Leu Ile Leu Tyr Leu Phe Gly Thr Pro Gly Gln Thr Arg Phe Trp Phe Met Trp Asp Glu Leu Val Arg Gly Ala Ile Gly Ala Val Leu Val Asp Thr Arg Arg Leu Ala Asp Cys Phe Ala Ala Ile Asp Phe Phe Glu His Arg Arg Leu Pro Tyr Leu Val Ala Ile Asn Cys Phe Asp Gly Met Gln 135 Tyr His Asp Pro Gln Asp Val Arg Asp Ala Leu Ala Ile Ser His Asp Val Pro Val Val Ala Cys Asp Ala Arg Asn Arg Glu Ser Thr Lys His Val Leu Ile Ser Leu Val Glu Tyr Val Leu Thr Met Arg Arg Ser Arg 180 185 Ala Val Ala Pro Ala 195 <210> 162 <211> 402 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(402) <220> <223> evcJ2 <400> 162 gtg tcg ggg acg aag gag gtg agc ggc gac atg gat cgt gac gag ccg Val Ser Gly Thr Lys Glu Val Ser Gly Asp Met Asp Arg Asp Glu Pro act ggc gcg ttg gtc cgt ccg tac gcc gtc acc cgc ggt cgt acc cgc 96 Thr Gly Ala Leu Val Arg Pro Tyr Ala Val Thr Arg Gly Arg Thr Arg 20 25 cct cgg ctg gac atc gcg ttg gag gcg ctc gtc gag acg acg gtg cgc 144 Pro Arg Leu Asp Ile Ala Leu Glu Ala Leu Val Glu Thr Thr Val Arg ggt cgg gcc gct gcc agt agc aac ggt ggc cag ggc cga gag cac cag 192 Gly Arg Ala Ala Ala Ser Ser Asn Gly Gly Gln Gly Arg Glu His Gln tac atc gcc gcg ctg tgc gac gga cgc gtg cag tcg ctt gcc gag atc 240 Tyr Ile Ala Ala Leu Cys Asp Gly Arg Val Gln Ser Leu Ala Glu Ile 70 gcg gcg cgg atg cag ctc ccg ctc ggc gtg gct agg gtg ctc atc gcc 288 Ala Ala Arg Met Gln Leu Pro Leu Gly Val Ala Arg Val Leu Ile Ala

90

```
gac atg gcg acg gac ggc ctg gtc gca gtc cac gag ccg acc atc ctg
                                                                   336
Asp Met Ala Thr Asp Gly Leu Val Ala Val His Glu Pro Thr Ile Leu
gac gac tcc gac gac gcg gtg ggc act gaa ctg ctg gag agg gtg ctg
                                                                   384
Asp Asp Ser Asp Asp Ala Val Gly Thr Glu Leu Leu Glu Arg Val Leu
                            120
agt gga ctt cgc agg ctc
                                                                   402
Ser Gly Leu Arg Arg Leu
    130
<210> 163
<211> 134
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> evcJ2
<400> 163
Val Ser Gly Thr Lys Glu Val Ser Gly Asp Met Asp Arg Asp Glu Pro
Thr Gly Ala Leu Val Arg Pro Tyr Ala Val Thr Arg Gly Arg Thr Arg
Pro Arg Leu Asp Ile Ala Leu Glu Ala Leu Val Glu Thr Thr Val Arg
Gly Arg Ala Ala Ser Ser Asn Gly Gly Gln Gly Arg Glu His Gln
Tyr Ile Ala Ala Leu Cys Asp Gly Arg Val Gln Ser Leu Ala Glu Ile
Ala Ala Arg Met Gln Leu Pro Leu Gly Val Ala Arg Val Leu Ile Ala
Asp Met Ala Thr Asp Gly Leu Val Ala Val His Glu Pro Thr Ile Leu
Asp Asp Ser Asp Asp Ala Val Gly Thr Glu Leu Leu Glu Arg Val Leu
                            120
Ser Gly Leu Arg Arg Leu
   130
<210> 164
<211> 351
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(351)
<220>
<223> evcK
```

<400> 164

gtg ccc ggt Val Pro Gly 1												48
ctg gcg tcg Leu Ala Ser					Āsp							96
gcg atc gcg Ala Ile Ala 35	tcc ggg Ser Gly	ctg c	Val S	gc cto er Lev 40	acg Thr	cag Gln	gga Gly	gcg Ala 45	gca Ala	cgc Arg	tgc Cys	144
ttc gag ggc Phe Glu Gly 50												192
ttc ctg ttc Phe Leu Phe 65												240
gcc gcc cgt Ala Ala Arg												288
ctg gtc gac Leu Val Asp					Thr							336
gtg ggg atg Val Gly Met 115												351
<210> 165 <211> 117 <212> PRT <213> Micror	monospor	a carb	bonace	ea								
<211> 117 <212> PRT	nonospor	a cark	bonace	ea								
<211> 117 <212> PRT <213> Micror					Val 10	Ser	Ala	Asp	Gly	Leu 15	Leu	
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly	Val Ala 5	His A	Ala V	al Ala	10 Asp			_	_	15		
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly 1	Val Ala 5 Ser Arg 20	His A	Ala Va Leu Pi Val Sa	al Ala ro Arç 25	10 Asp	Arg	Ala	Asp	Gln 30	15 Leu	Ala	
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly 1 Leu Ala Ser Ala Ile Ala	Val Ala 5 Ser Arg 20 Ser Gly	His A	Ala Va Leu P: Val Se	al Ala ro Arg 25 er Leu 40	10 Asp Thr	Arg Gln	Ala Gly	Asp Ala 45	Gln 30 Ala	15 Leu Arg	Ala Cys	
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly 1 Leu Ala Ser Ala Ile Ala 35 Phe Glu Gly	Val Ala 5 Ser Arg 20 Ser Gly Gly Ala	His A	Ala Va Leu Pr Val Se Leu G	al Alaro Arco 25 er Leu 40 ln Thr	10 Asp Thr	Arg Gln Val	Ala Gly Glu 60	Asp Ala 45	Gln 30 Ala Asp	15 Leu Arg Asn	Ala Cys Gly	
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly 1 Leu Ala Ser Ala Ile Ala 35 Phe Glu Gly 50 Phe Leu Phe	Val Ala 5 Ser Arg 20 Ser Gly Gly Ala Leu Met	His A Asp I Leu V Val I Ser I 70	Ala Va Leu Pr Val Se Leu G 55	al Alaro Arc 25 er Leu 40 ln Thr	10 Asp Thr Val	Arg Gln Val Ser 75	Ala Gly Glu 60 Ser	Asp Ala 45 Met	Gln 30 Ala Asp	15 Leu Arg Asn Val	Ala Cys Gly Leu 80	
<211> 117 <212> PRT <213> Micror <220> <223> evcK <400> 165 Val Pro Gly 1 Leu Ala Ser Ala Ile Ala 35 Phe Glu Gly 50 Phe Leu Phe 65	Val Ala 5 Ser Arg 20 Ser Gly Gly Ala Leu Met Ser Cys 85	His AAsp I Leu V Val I Ser I 70 Asp V	Ala Va Leu P: Val Se 55 Ile Se Val G:	al Alaro Arco 25 er Leu 40 ln Thr er Asp	10 Asp Thr Val Gly Val 90 Thr	Arg Gln Val Ser 75 Gly	Ala Gly Glu 60 Ser	Asp Ala 45 Met Phe Glu	Gln 30 Ala Asp Ala Met	Leu Arg Asn Val Ala 95	Ala Cys Gly Leu 80 Leu	

```
<210> 166
<211> 3435
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(3435)
<220>
<223> evcL
<400> 166
atg ccg atc tgg tcc aag ctc ggt ctc atc atg atc gtg ccg acc atc
                                                                   48
Met Pro Ile Trp Ser Lys Leu Gly Leu Ile Met Ile Val Pro Thr Ile
gcc acg gtc gtc ggc acc agt ggc ctc gtc gac aac ctg gaa acg
                                                                   96
Ala Thr Val Val Val Gly Thr Ser Gly Leu Val Asp Asn Leu Glu Thr
             20
ctg aac aac gcc aac cgc tcc ggc gac ctg gcc aat ctg gtg ggc tac
                                                                   144
Leu Asn Asn Ala Asn Arg Ser Gly Asp Leu Ala Asn Leu Val Gly Tyr
                             40
teg gge gae etg gte aae age ete eag gae gaa ege ace tee geg gtg
                                                                   192
Ser Gly Asp Leu Val Asn Ser Leu Gln Asp Glu Arg Thr Ser Ala Val
                         55
ttg ctg ctc ggg gcg agc ggc gac cag gcc aag gcg cag tac cag gag
                                                                   240
Leu Leu Gly Ala Ser Gly Asp Gln Ala Lys Ala Gln Tyr Gln Glu
                                                                   288
gcg tac aac cgg gtc aac atc cgg gtc gac cag gac aag gtg ccg tac
Ala Tyr Asn Arg Val Asn Ile Arg Val Asp Gln Asp Lys Val Pro Tyr
                                     90
                 85
ctg caa cag cgg ggg gag gtc gac ggc ctg ccg agc agc ctg gag ggc
                                                                   336
Leu Gln Gln Arg Gly Glu Val Asp Gly Leu Pro Ser Ser Leu Glu Gly
            100
                                105
ctc ctc gac ggg atc gac cag aac ctg aag gac ctc ccc ggc acc cgc
                                                                   384
Leu Leu Asp Gly Ile Asp Gln Asn Leu Lys Asp Leu Pro Gly Thr Arg
        115
age cag gte tte aac gge aag ttg aag ate ate gae gee atg cag geg
                                                                   432
Ser Gln Val Phe Asn Gly Lys Leu Lys Ile Ile Asp Ala Met Gln Ala
tac gag ggc ctg atc aac gac ctg ctg tcc atc cgc gac tcc gcc acc
                                                                   480
Tyr Glu Gly Leu Ile Asn Asp Leu Leu Ser Ile Arg Asp Ser Ala Thr
145
cac ctc gcc ggt gac aac gac ctg agc gac cgg atg cgg gcc gcg gca
                                                                   528
His Leu Ala Gly Asp Asn Asp Leu Ser Asp Arg Met Arg Ala Ala Ala
gcc gtc gcc cgg gag aag gaa tac ctc tcg gtc cgc cgg gtc gtg gtg
                                                                   576
Ala Val Ala Arg Glu Lys Glu Tyr Leu Ser Val Arg Arg Val Val
                                185
cac cgg gcg ctg atc cag cgc gag ttg acc ccc atc ctg cgc acc gac
                                                                   624
```

His	Arg	Ala 195	Leu	Ile	Gln	Arg	Glu 200	Leu	Thr	Pro	Ile	Leu 205	Arg	Thr	Asp	
	atc Ile 210															672
	gtg Val															720
	ggc Gly															768
	acc Thr															816
	gcg Ala															864
	ctc Leu 290															912
gta Val 305	cag Gln	cgc Arg	acg Thr	gtg Val	ttc Phe 310	ctc Leu	cag Gln	acc Thr	ggc Gly	ctg Leu 315	ctg Leu	ctc Leu	ggc Gly	atg Met	ctg Leu 320	960
	ctg Leu															1008
tcg Ser	ctg Leu	cgc Arg	gac Asp 340	ctg Leu	cgc Arg	cag Gln	ggt Gly	gcg Ala 345	ctc Leu	agc Ser	atc Ile	gcc Ala	cag Gln 350	tac Tyr	ggt Gly	1056
ttg Leu	ccc Pro	cag Gln 355	gcc Ala	gtt Val	gcc Ala	cgg Arg	ctg Leu 360	cgc Arg	gat Asp	ccg Pro	cag Gln	ttt Phe 365	tcc Ser	agc Ser	cag Gln	1104
	tcc Ser 370															1152
	agc Ser															1200
cac His	ctg Leu	gag Glu	gcc Ala	gta Val 405	cgg Arg	acg Thr	gcg Ala	gcg Ala	gag Glu 410	cag Gln	gcc Ala	gcg Ala	ctg Leu	cgc Arg 415	gcc Ala	1248
	gtc Val															1296
	gac Asp															1344
	ccg Pro															1392

450			455			460			
		aac Asn							1440
		cag Gln 485							1488
		gag Glu							1536
		atc Ile							1584
		gag Glu							1632
		atg Met							1680
		gac Asp 565							1728
		cgc Arg							1776
		ggc Gly							1824
		gag Glu							1872
		ccc Pro							1920
		ccc Pro 645							1968
		ggc Gly							2016
		ccg Pro							2064
		gta Val							2112
		ggc Gly							2160

					ctg Leu											2208
					tcg Ser											2256
					gac Asp											2304
gcc Ala	atc Ile 770	ccc Pro	cga Arg	cag Gln	ctg Leu	ccg Pro 775	agc Ser	agc Ser	ccg Pro	gag Glu	gcc Ala 780	cgg Arg	ggc Gly	tgg Trp	acc Thr	2352
_		_	_	_	gtg Val 790	_	_			_	_	_	_		_	2400
					cag Gln											2448
ccg Pro	ttc Phe	ggc Gly	acg Thr 820	ccc Pro	gtc Val	tcc Ser	ggt Gly	cag Gln 825	ccg Pro	ttc Phe	ggc Gly	acg Thr	ccc Pro 830	gtg Val	tcc Ser	2496
					gcg Ala											2544
					gcg Ala											2592
					ccg Pro 870											2640
					ccc Pro											2688
					acg Thr											2736
					cgg Arg											2784
					gag Glu											2832
					acg Thr 950											2880
					aac Asn											2928

gac gtc acc ggc cgg ccc gtc cag aca cca gca ccc ggg acg aca ggt Asp Val Thr Gly Arg Pro Val Gln Thr Pro Ala Pro Gly Thr Thr Gly 980 985 990	2976
aac gca ccg atg gca gac acc ccg atg gcc gga gga atg ccg cgc gac Asn Ala Pro Met Ala Asp Thr Pro Met Ala Gly Gly Met Pro Arg Asp 995 1000 1005	3024
aac ggg tcg ccg acc aac ggt ggc acc cgc ccc ggt ccc gcc gag ggc Asn Gly Ser Pro Thr Asn Gly Gly Thr Arg Pro Gly Pro Ala Glu Gly 1010 1015 1020	3072
ttc gcc ggc cgg cgc cac acg ccg cag gcc cac gcc tgg cag act gcc Phe Ala Gly Arg Arg Pro Thr Pro Gln Ala His Ala Trp Gln Thr Ala 1025 1030 1035 1040	3120
gcg gac gac ggc tgg cgg gcc gcc tcg gcg gcc acc gag gtc ccg gtg Ala Asp Asp Gly Trp Arg Ala Ala Ser Ala Ala Thr Glu Val Pro Val 1045 1050	3168
gcg gag acc acc cgc aag ggc ctg ccg aag cgg gtg ccg atg gcc caa Ala Glu Thr Thr Arg Lys Gly Leu Pro Lys Arg Val Pro Met Ala Gln 1060 1065 1070	3216
ctc gtg cct ggc ggg gtg gag aag ccc acc acg tcg gtc cag cgc cgt Leu Val Pro Gly Gly Val Glu Lys Pro Thr Thr Ser Val Gln Arg Arg 1075 1080 1085	3264
acg ccg gag ggc gtc cgc ggt ctg ctc tcg gca tac cat cga ggc gtg Thr Pro Glu Gly Val Arg Gly Leu Leu Ser Ala Tyr His Arg Gly Val 1090 1095 1100	3312
cag cgt ggg cgt acc gag ccc gac ggc aac ccg acc aac ccg gag gca Gln Arg Gly Arg Thr Glu Pro Asp Gly Asn Pro Thr Asn Pro Glu Ala 1105 1110 1115 1120	3360
gct ccg ggt ggg cag caa tcc tcg cag tct ggc tca ggc ccg gtg gcc Ala Pro Gly Gln Gln Ser Ser Gln Ser Gly Ser Gly Pro Val Ala 1125 1130 1135	3408
ggg agc ggg cag aag gag caa caa gga Gly Ser Gly Gln Lys Glu Gln Gln Gly 1140 1145	3435
<210> 167 <211> 1145 <212> PRT <213> Micromonospora carbonacea	
<220> <223> evcL	
<400> 167 Met Pro Ile Trp Ser Lys Leu Gly Leu Ile Met Ile Val Pro Thr Ile 1 5 10 15	
Ala Thr Val Val Val Gly Thr Ser Gly Leu Val Asp Asn Leu Glu Thr 20 25 30	
Leu Asn Asn Ala Asn Arg Ser Gly Asp Leu Ala Asn Leu Val Gly Tyr 35 40 45	
Ser Gly Asp Leu Val Asn Ser Leu Gln Asp Glu Arg Thr Ser Ala Val 50 55 60	

Leu Leu Gly Ala Ser Gly Asp Gln Ala Lys Ala Gln Tyr Gln Glu Ala Tyr Asn Arg Val Asn Ile Arg Val Asp Gln Asp Lys Val Pro Tyr Leu Gln Gln Arg Gly Glu Val Asp Gly Leu Pro Ser Ser Leu Glu Gly Leu Leu Asp Gly Ile Asp Gln Asn Leu Lys Asp Leu Pro Gly Thr Arg Ser Gln Val Phe Asn Gly Lys Leu Lys Ile Ile Asp Ala Met Gln Ala Tyr Glu Gly Leu Ile Asn Asp Leu Leu Ser Ile Arg Asp Ser Ala Thr His Leu Ala Gly Asp Asn Asp Leu Ser Asp Arg Met Arg Ala Ala Ala Ala Val Ala Arg Glu Lys Glu Tyr Leu Ser Val Arg Arg Val Val Val 185 His Arg Ala Leu Ile Gln Arg Glu Leu Thr Pro Ile Leu Arg Thr Asp 200 Tyr Ile Ala Ser Gly Thr Gly Gln Gln Ala Leu Gln Ser Phe Lys Ala Val Ala Ser Leu Asp Glu Ser Asp Leu His Asp Gln Thr Val Ala 235 Gly Gly Asp Arg Arg Glu Ala Gln Asn Tyr Thr Gly Trp Leu Asp Gly Asn Thr Asn Gly Ser Met Ala Asn Ala Pro Phe Gly Pro Asp Gln Trp 260 265 Asp Ala Ala Met Val Ala Ser Ala Lys Leu Ile Arg Thr Val Glu Ala 280 Lys Leu Asp Gly Asn Val Val Lys Gln Ala Asp Ala Leu Arg Ser Asp 295 Val Gln Arg Thr Val Phe Leu Gln Thr Gly Leu Leu Leu Gly Met Leu 310 315 Leu Leu Ala Ile Leu Phe Ala Tyr Leu Val Ala Arg Ser Met Ala Arg Ser Leu Arg Asp Leu Arg Gln Gly Ala Leu Ser Ile Ala Gln Tyr Gly 345 Leu Pro Gln Ala Val Ala Arg Leu Arg Asp Pro Gln Phe Ser Ser Gln 360 Leu Ser Pro Val Gln Ala Ala Asn Gln Ile Ala Glu Pro Leu Pro Val Arg Ser Lys Asp Glu Phe Gly Gln Val Thr Glu Ala Phe Asn Ala Val 395 His Leu Glu Ala Val Arg Thr Ala Ala Glu Gln Ala Ala Leu Arg Ala

405 410 415 Ser Val Ala Thr Met Phe Val Asn Leu Ala Arg Arg Ser Gln Ile Leu Val Asp Arg Leu Ile Gly His Leu Asp Arg Leu Glu Arg Gly Glu Glu 435 440 Asp Pro Asp Arg Leu Ala Glu Leu Phe Gln Leu Asp His Leu Ala Thr 455 Arg Met Arg Arg Asn Asp Glu Asn Leu Leu Val Leu Ala Gly Ala Asp Ser Thr Arg Val Gln Arg Glu Pro Ala Ala Leu Ile Asp Val Leu Arg 490 Ala Ala Gln Ser Glu Val Glu His Tyr Thr Arg Ile Glu Phe Gly Val 505 Ile Asp Arg Asp Ile Glu Val Ala Ala His Ala Val Asn Asp Leu Val 515 520 His Leu Val Ala Glu Leu Phe Asp Asn Ala Thr Ala Phe Ser Pro Pro 535 Asp Ser Gln Val Met Val Glu Ala Arg Arg Val Gly Asp Arg Ala Asn Leu Tyr Val Glu Asp Arg Gly Ile Gly Ile Ser Ala Glu Gln Leu His Asp Leu Asn Asp Arg Leu Ala Ser Pro Pro Gln Val Asp Val Ala Val 585 Ser Arg Met Met Gly Leu Val Val Val Ala Arg Leu Ala Ser Arg His Gly Val Lys Val Glu Leu Arg Pro Gly Thr Asp Arg Gly Thr Val Ala 615 Asp Val Thr Leu Pro Thr Thr Val Leu Val Pro Arg Ala Leu Ser Gly Arg Phe Gln Gln Pro Gly Ala Leu Pro Ala Pro Pro Ala Ser Leu Thr 650 Ser Ser Gln Pro Gly Gly Ala Pro Pro Ala Leu Gly Ala Phe Ala Ala 660 665 Phe Gly Asn Asn Pro Ala Thr Pro Ala Pro Thr Gln Arg Pro Gly His Ser Gly Asn Gln Val Thr Leu Gly Gly Arg Ser Phe Asp Pro Ala Ser Arg Asn Gly His Gly Thr Pro Ala Ser Thr Gly Ser Met Arg Ser Met 710 715 Pro Ala Trp Ser Asp Leu Thr Gly Ala Ser Gly Thr Ala Gly Gly Ala 730 Ala Ala Gly Arg Thr Ser Asn Gly Gln Ser Ser Asp Pro Leu Pro Gln

Arg Arg Ala Ser Gly Asp Gly Asp Pro Ala Ser Ser Gly Gln Gln Pro 760 Ala Ile Pro Arg Gln Leu Pro Ser Ser Pro Glu Ala Arg Gly Trp Thr 775 Pro Pro Val Ser Val Pro Pro Val Ser Ala Pro Pro Val Ser Val Phe Pro Val Ser Gly Gln Pro Val Ser Ala Ala Pro Val Ser Gly Gln 810 Pro Phe Gly Thr Pro Val Ser Gly Gln Pro Phe Gly Thr Pro Val Ser 825 Gly Gln Pro Tyr Ser Ala Gln Pro Leu Pro Ser Arg Pro Val Pro Ser Ala Gln Ala Pro Val Ala Pro Pro Ala Trp Pro Pro Val Ala Ala Pro 855 Glu Pro Val Thr Pro Pro Val Pro Glu Arg Leu Ala Ala Ala Leu Asp 870 875 Met Thr Glu Leu Pro Arg Val Pro Ser Thr Glu Val Pro Ser Thr Pro Ala Thr Gln Pro Thr Thr Pro Pro Thr Pro Ala Arg Ser Thr Pro 905 Val Gln Ala Gln Asn Arg Gln Gln Arg Tyr Ala Asp Glu Thr Met Glu 920 Leu Pro Ile Phe Arg Glu Leu Glu Ser Ala Trp Phe Arg Thr Arg Arg 935 Ser Gly Ser Glu Glu Thr Ala Gly Val Ala Gln Arg Ala Thr Asn Gly 950 Ala Gly Ser Pro Ala Asn Ala Ala Val Thr Gln Gln Phe Ser Ala Val 965 970 Asp Val Thr Gly Arg Pro Val Gln Thr Pro Ala Pro Gly Thr Thr Gly 985 Asn Ala Pro Met Ala Asp Thr Pro Met Ala Gly Gly Met Pro Arg Asp Asn Gly Ser Pro Thr Asn Gly Gly Thr Arg Pro Gly Pro Ala Glu Gly 1015 Phe Ala Gly Arg Arg Pro Thr Pro Gln Ala His Ala Trp Gln Thr Ala 1030 1035 Ala Asp Asp Gly Trp Arg Ala Ala Ser Ala Ala Thr Glu Val Pro Val 1045 Ala Glu Thr Thr Arg Lys Gly Leu Pro Lys Arg Val Pro Met Ala Gln 1065 Leu Val Pro Gly Gly Val Glu Lys Pro Thr Thr Ser Val Gln Arg Arg 1075 Thr Pro Glu Gly Val Arg Gly Leu Leu Ser Ala Tyr His Arg Gly Val

1095

Gln Arg Gly Arg Thr Glu Pro Asp Gly Asn Pro Thr Asn Pro Glu Ala 1105 1110 Ala Pro Gly Gly Gln Gln Ser Ser Gln Ser Gly Ser Gly Pro Val Ala 1130 Gly Ser Gly Gln Lys Glu Gln Gln Gly <210> 168 <211> 603 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(603) <220> <223> evcM <400> 168 atg gat cac ccc cac cgc ctc gtc ctg ctc gcc ggc cct tcg ggc tcc Met Asp His Pro His Arg Leu Val Leu Leu Ala Gly Pro Ser Gly Ser 10 gga aag tcg tac ata gcc caa caa acc ggg ctt cct gtt ctt tgt ctg 96 Gly Lys Ser Tyr Ile Ala Gln Gln Thr Gly Leu Pro Val Leu Cys Leu 20 25 gac gac ttc tac aag gat ggt gat gac cct acg tta ccg cgc caa aac 144 Asp Asp Phe Tyr Lys Asp Gly Asp Pro Thr Leu Pro Arg Gln Asn ggt ctt gtg gac tgg gac tca ccc cag tcg tgg gac gcc ggg gcg gcc 192 Gly Leu Val Asp Trp Asp Ser Pro Gln Ser Trp Asp Ala Gly Ala Ala 55 gtg gaa acg att gcc cgg ctg gcg cgg gac ggc aag gcc gaa gtg ccg 240 Val Glu Thr Ile Ala Arg Leu Ala Arg Asp Gly Lys Ala Glu Val Pro gtt tat gcg atc ggc gcg gac cgg cgg gtg gcc acc cgg aca ttc gag 288 Val Tyr Ala Ile Gly Ala Asp Arg Arg Val Ala Thr Arg Thr Phe Glu 85 90 gtc gcc gga tcg cca ctt ttc gtc gcc gaa ggg att ttc gcc gcc gag 336 Val Ala Gly Ser Pro Leu Phe Val Ala Glu Gly Ile Phe Ala Ala Glu atc gtc gag gaa tgc cga cgg cga ggg ctg ctc gcc ggg gcg tac gcg 384 Ile Val Glu Glu Cys Arg Arg Gly Leu Leu Ala Gly Ala Tyr Ala 115 ctg cgc cgg ccg cgc ggc acc acc ttt ttc cgg cgg ctc gcc cgc gac 432 Leu Arg Arg Pro Arg Gly Thr Thr Phe Phe Arg Arg Leu Ala Arg Asp 130

ctg gcc gag cag cgc aag gct ccc ggg atg ctg ctg cgc ggc ctg

Leu Ala Glu Gln Arg Lys Ala Pro Gly Met Leu Leu Arg Arg Gly Leu

145

gcc ctg ctg cgc gcg gag ccg gcg gtg ctg cgc cgc cag gcg ggg ctc 528 Ala Leu Leu Arg Ala Glu Pro Ala Val Leu Arg Arg Gln Ala Gly Leu 165 ggc gct cac ccg gcc ccg gcc cgc gag gtg ctg cgc cgg gtg gcc gac 576 Gly Ala His Pro Ala Pro Ala Arg Glu Val Leu Arg Arg Val Ala Asp 180 185 190 ctg ctc gcc ggc cac ccg cac cac ccc 603 Leu Leu Ala Gly His Pro His His Pro 195 <210> 169 <211> 201 <212> PRT <213> Micromonospora carbonacea <220> <223> evcM Met Asp His Pro His Arg Leu Val Leu Leu Ala Gly Pro Ser Gly Ser 15 Gly Lys Ser Tyr Ile Ala Gln Gln Thr Gly Leu Pro Val Leu Cys Leu Asp Asp Phe Tyr Lys Asp Gly Asp Pro Thr Leu Pro Arg Gln Asn Gly Leu Val Asp Trp Asp Ser Pro Gln Ser Trp Asp Ala Gly Ala Ala Val Glu Thr Ile Ala Arg Leu Ala Arg Asp Gly Lys Ala Glu Val Pro Val Tyr Ala Ile Gly Ala Asp Arg Arg Val Ala Thr Arg Thr Phe Glu Val Ala Gly Ser Pro Leu Phe Val Ala Glu Gly Ile Phe Ala Ala Glu 105 Ile Val Glu Glu Cys Arg Arg Gly Leu Leu Ala Gly Ala Tyr Ala 115 Leu Arg Arg Pro Arg Gly Thr Thr Phe Phe Arg Arg Leu Ala Arg Asp 135 Leu Ala Glu Gln Arg Lys Ala Pro Gly Met Leu Leu Arg Arg Gly Leu 155 Ala Leu Leu Arg Ala Glu Pro Ala Val Leu Arg Arg Gln Ala Gly Leu 170 Gly Ala His Pro Ala Pro Ala Arg Glu Val Leu Arg Arg Val Ala Asp 180 185 190 Leu Leu Ala Gly His Pro His His Pro 195

<210> 170 <211> 1074

```
<212> DNA
<213> Micromonospora carbonacea
<221> CDS
<222> (1)..(1074)
<220>
<223> evcN
<400> 170
atg gtc gca atc tca tac gag gac atc gtc aag gtc ccc aag gcg ctg
                                                                   48
Met Val Ala Ile Ser Tyr Glu Asp Ile Val Lys Val Pro Lys Ala Leu
                                     10
ctg cac gac cac ctc gac ggc ggc ctg cgg ccg gcg acg atc gtc gag
                                                                   96
Leu His Asp His Leu Asp Gly Gly Leu Arg Pro Ala Thr Ile Val Glu
ctg gcc gcc gag gtc ggc cac gag ctg ccc acc acc gac ccg gaa gcg
                                                                   144
Leu Ala Ala Glu Val Gly His Glu Leu Pro Thr Thr Asp Pro Glu Ala
         35
ctc ggc cgc tgg ttc gtc gcg gcg gcg aac tcc ggc tcg ctg gag cgc
                                                                   192
Leu Gly Arg Trp Phe Val Ala Ala Ala Asn Ser Gly Ser Leu Glu Arg
     50
tac ctg gag acg ttc gcc cac acc gtg gcg gtc atg cag acc gcg ccc
                                                                   240
Tyr Leu Glu Thr Phe Ala His Thr Val Ala Val Met Gln Thr Ala Pro
gca ctg cgg cgg gtg gcc cag gag tgc gcg ctg gac ctg gcc gcc gac
                                                                   288
Ala Leu Arg Arg Val Ala Gln Glu Cys Ala Leu Asp Leu Ala Ala Asp
ggg gtc gtc tac gcc gag gtg cgg ttc gcc ccc gag cag cac ctg gag
                                                                   336
Gly Val Val Tyr Ala Glu Val Arg Phe Ala Pro Glu Gln His Leu Glu
egg gae etg ace etg gae gag gte gte gag geg gte gee ggg tte
                                                                   384
Arg Asp Leu Thr Leu Asp Glu Val Val Glu Ala Val Val Ala Gly Phe
                            120
                                                125
gee gag gge geg geg etc gee gee gee gge eat eeg ate egg gte
                                                                   432
Ala Glu Gly Ala Ala Leu Ala Ala Asp Ala Gly His Pro Ile Arg Val
                        135
gge ace etg etc ace gec atg egg cac gec egg teg eag gag atc
                                                                   480
Gly Thr Leu Leu Thr Ala Met Arg His Ala Ala Arg Ser Gln Glu Ile
                    150
gee gaa etg geg gtg egg eac ege gae gee gge gtg gtg gge tte gae
                                                                   528
Ala Glu Leu Ala Val Arg His Arg Asp Ala Gly Val Val Gly Phe Asp
atc gcc ggg gcg gag gcg gga ttc ccg ccc acc cgg cac ctg gac gcc
                                                                   576
Ile Ala Gly Ala Glu Ala Gly Phe Pro Pro Thr Arg His Leu Asp Ala
            180
                                185
ttc gag tac ctg cag cqq gag aac ttc cac ttc acc att cac qcc qqc
                                                                   624
Phe Glu Tyr Leu Gln Arg Glu Asn Phe His Phe Thr Ile His Ala Gly
        195
gag gcg ttc ggg ctg ccg tcg atc tgg cag gcc atc cag tgg tgc ggc
Glu Ala Phe Gly Leu Pro Ser Ile Trp Gln Ala Ile Gln Trp Cys Gly
```

210		215	2	220		
gcg gac cgc cf Ala Asp Arg Le 225						720
ggc gac ccg cc Gly Asp Pro Pi						768
cgg atc ccg ct Arg Ile Pro Le 20						816
gcg gcg tcg at Ala Ala Ser II 275		_				864
ttc cgg gtg ac Phe Arg Val Th 290			Arg Leu M			912
atg tcc cgg ga Met Ser Arg G 305						960
aag gag ctc ca Lys Glu Leu G						1008
ccg ttc gac ga Pro Phe Asp G 34						1056
tac ggg aag c Tyr Gly Lys Le 355						1074
<210> 171 <211> 358 <212> PRT <213> Micromon	nospora car	bonacea				
<220> <223> evcN						
<400> 171 Met Val Ala II 1	le Ser Tyr 5	Glu Asp Ile	Val Lys V	/al Pro Lys	Ala Leu 15	
Leu His Asp H	is Leu Asp 20	Gly Gly Leu 25	Arg Pro A	Ala Thr Ile 30	Val Glu	
Leu Ala Ala G 35	lu Val Gly	His Glu Leu 40	Pro Thr T	Thr Asp Pro 45	Glu Ala	
Leu Gly Arg Tr 50	rp Phe Val	Ala Ala Ala 55	Asn Ser G	Gly Ser Leu 60	Glu Arg	
Tyr Leu Glu Tl 65	70		75		80	
Ala Leu Arg A	rg Val Ala	Gln Glu Cve	Ala Leu A	Asp Leu Ala	Ala Asp	

Gly Val Val Tyr Ala Glu Val Arg Phe Ala Pro Glu Gln His Leu Glu Arg Asp Leu Thr Leu Asp Glu Val Val Glu Ala Val Val Ala Gly Phe 120 Ala Glu Gly Ala Ala Leu Ala Ala Asp Ala Gly His Pro Ile Arg Val Gly Thr Leu Leu Thr Ala Met Arg His Ala Ala Arg Ser Gln Glu Ile 150 Ala Glu Leu Ala Val Arg His Arg Asp Ala Gly Val Val Gly Phe Asp 165 Ile Ala Gly Ala Glu Ala Gly Phe Pro Pro Thr Arg His Leu Asp Ala Phe Glu Tyr Leu Gln Arg Glu Asn Phe His Phe Thr Ile His Ala Gly Glu Ala Phe Gly Leu Pro Ser Ile Trp Gln Ala Ile Gln Trp Cys Gly 215 Ala Asp Arg Leu Gly His Gly Val Arg Ile Val Asp Asp Ile Thr Pro Gly Asp Pro Pro Val Leu Gly Arg Leu Ala Ala Tyr Val Arg Asp Lys 245 Arg Ile Pro Leu Glu Leu Cys Pro Ser Ser Asn Val Gln Thr Gly Ala 265 Ala Ala Ser Ile Ala Glu His Pro Ile Gly Leu Leu Arg Asp Leu Arg Phe Arg Val Thr Val Asn Thr Asp Asn Arg Leu Met Ser Gly Thr Ser 295 Met Ser Arg Glu Met Ala Leu Leu Ala Glu Ala Phe Gly Tyr Gly Trp 310 315 Lys Glu Leu Gln Trp Phe Thr Ile Asn Ala Met Lys Ser Ala Phe Ile 325 Pro Phe Asp Glu Arg Leu Ala Ile Ile Asp Glu Val Ile Lys Pro Ala 345 Tyr Gly Lys Leu Leu Gly 355

```
<210> 172
<211> 960
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(960)
<220>
<223> evrMR
```

0> 1								
		atc Ile 5						48
		gcc Ala						96
		ttc Phe						144
		ccg Pro						192
		ctc Leu						240
		gcg Ala 85						288
		tcg Ser						336
		gct Ala						384
		ctg Leu						432
		ctg Leu						480
		ccg Pro 165						528
		ctc Leu						576
		gtg Val						624
		gtg Val						672
		cac His						720
		gac Asp 245						768

cac ttc gag (His Phe Glu (
acc ggc cgg (Thr Gly Arg (275											
cac acc gac of His Thr Asp 1 290											
ccg gtc cgg g Pro Val Arg 3	Val Thr										
<210> 173 <211> 320 <212> PRT <213> Microme	onospora	carbona	acea								
<220> <223> evrMR											
<400> 173 Met Asp Pro 1	Arg Ile 5	Val Asp	Arg	Leu	Arg 10	Cys	Pro	Val	Cys	Ala 15	Glu
Pro Leu Thr	Glu Ala 20	Ala Ala	Gly	Thr 25	Thr	Arg	Ala	Leu	Arg 30	Cys	Pro
Arg Arg His 35	Ser Phe	Asp Val	Ala 40	Arg	Gln	Gly	Tyr	Val 45	Asp	Leu	Leu
Ala Gly Arg	Ala Pro	His Val 55	Gly	Asp	Thr	Ala	Glu 60	Met	Val	Ala	Ala
Arg Ala Asp : 65	Phe Leu	Ala Ala 70	Gly	His	Tyr	Asp 75	Thr	Leu	Ser	Ala	Ala 80
Leu Ala Ala	Ala Ala 85	Leu Ala	Ala	Leu	Ser 90	His	Pro	Pro	Glu	Ala 95	Pro
Gly Ala Asp	Ala Ser 100	Ala Gly	Lys	Asp 105	Gly	Gln	Asp	Ala	Gln 110	Ala	Gly
Arg Asp Ala 115	Ser Ala	Gly His	Asp 120	Ala	Ser	Ala	Gly	Gln 125	Pro	Ala	Val
Gly Thr Tyr	Pro Leu	Val Val 135	Asp	Ala	Gly	Ala	Gly 140	Thr	Gly	Arg	His
Leu Ala Ala 145	Val Leu	Ala Ala 150	Leu	Pro	Asp	Ala 155	Val	Gly	Leu	Ala	Leu 160
Asp Val Ser	Lys Pro 165	Ala Leu	Arg	Arg	Ala 170	Ala	Arg	Ala	His	Pro 175	Arg
Ala Ala Ala	Ala Leu 180	Ala Asp	Thr	Trp 185	Arg	Arg	Leu	Pro	Leu 190	Ala	Asp
Ala Ser Val	Ala Val	Leu Leu	Asp 200	Val	Phe	Ala	Pro	Arg 205	Asn	Gly	Ala

210	Arg Val	Leu His 215	Pro Ala	Gly A	la Leu 220	Leu	Val	Val	Thr	
Pro Ala Glu . 225		Leu Ala 230	Glu Leu		sp Ser 35	Leu	Asp	Leu	Leu 240	
Lys Val Asp	Pro Asp 245	Lys Ala	Asp Arg	Val A 250	la Gly	Ser	Leu	Ala 255	Gly	
His Phe Glu	Gln Thr 260	Ala Glu	Ser Val 265		rg Ala	Arg	Leu 270	Glu	Leu	
Thr Gly Arg	Gln Val	Ala Thr	Leu Val 280	Gly M	et Gly	Pro 285	Ser	Ala	Trp	
His Thr Asp	Pro Ala	Thr Leu 295	Ala Ala	Arg I	le Ala 300	Ala	Leu	Pro	Glu	
Pro Val Arg		Leu Ala 310	Val Arg		ly Val 15	Tyr	Arg	Pro	Arg 320	
<210> 174 <211> 579 <212> DNA <213> Microm	onospora	carbona	acea							
<220> <221> CDS <222> (1)(579)									
<220> <223> evrMR2										
	ccg ggc									48
<223> evrMR2 <400> 174 gtg tgg gag Val Trp Glu	ccg ggc Pro Gly 5	Asp Glu gtg ctg	Ile Glu	Leu A	rg Pro	Thr cgg	Val tgt	Glu 15 ttc	Ile ggc	48 96
<223> evrMR2 <400> 174 gtg tgg gag Val Trp Glu 1 gag gcg cgc	ccg ggc Pro Gly 5 atc gcc Ile Ala 20 cag gcg	Asp Glu gtg ctg Val Leu gcg atg	cac gtg His Val 25	Leu A 10 atc c Ile L	rg Pro tg gcc eu Ala tc aac	Thr cgg Arg	tgt Cys 30	Glu 15 ttc Phe	Ile ggc Gly gtc	
<223> evrMR2 <400> 174 gtg tgg gag Val Trp Glu 1 gag gcg cgc Glu Ala Arg atg ccg gcg Met Pro Ala	ccg ggc Pro Gly 5 atc gcc Ile Ala 20 cag gcg Gln Ala acc ccg	Asp Glu gtg ctg Val Leu gcg atg Ala Met ccg gag	cac gtg His Val 25 agc tgg Ser Trp 40 tgg cag	Leu A 10 atc c Ile L ctg c Leu L	rg Pro tg gcc eu Ala tc aac eu Asn tg atg	Thr cgg Arg tcc ser 45	tgt Cys 30 cac His	Glu 15 ttc Phe ctg Leu	ggc Gly gtc Val	96
<223> evrMR2 <400> 174 gtg tgg gag Val Trp Glu 1 gag gcg cgc Glu Ala Arg atg ccg gcg Met Pro Ala 35 gac ctg gtc Asp Leu Val	ccg ggc Pro Gly 5 atc gcc Ile Ala 20 cag gcg Gln Ala acc ccg Thr Pro	Asp Glu gtg ctg Val Leu gcg atg Ala Met ccg gag Pro Glu 55 gtg ctg	cac gtg His Val 25 agc tgg Ser Trp 40 tgg cag Trp Gln cac cac	ttc g Phe V gac g Asp A	rg Pro tg gcc eu Ala tc aac eu Asn tg atg al Met 60 cg ctg	Thr cgg Arg tcc Ser 45 ggc Gly ttc	tgt Cys 30 cac His ggc Gly	Glu 15 ttc Phe ctg Leu cgg Arg	ggc Gly gtc Val ggc Gly	96 144
<223> evrMR2 <400> 174 gtg tgg gag Val Trp Glu 1 gag gcg cgc Glu Ala Arg atg ccg gcg Met Pro Ala 35 gac ctg gtc Asp Leu Val 50 gac cac cgg Asp His Arg	ccg ggc Pro Gly 5 atc gcc Ile Ala 20 cag gcg Gln Ala acc ccg Thr Pro tcg ttc Ser Phe	Asp Glu gtg ctg Val Leu gcg atg Ala Met ccg gag Pro Glu 55 gtg ctg Val Leu 70 gcc aag	cac gtg His Val 25 agc tgg Ser Trp 40 tgg cag Trp Gln cac cac His His	ttc g Phe V gac gac gac gac c	rg Pro tg gcc eu Ala tc aac eu Asn tg atg al Met 60 cg ctg la Leu 75 cg acg	Thr cgg Arg tcc Ser 45 ggc Gly ttc Phe ctg	tgt Cys 30 cac His ggc Gly tcg ser	Glu 15 ttc Phe ctg Leu cgg Arg ctg Leu	ggc Gly gtc Val ggc Gly gcc Ala 80	96 144 192

Gln Gln Ti	gg cgc cp Arg 15													384
gcg gcg gc Ala Ala Al 130														432
gag ctg ga Glu Leu G 145														480
gcg atc gg Ala Ile G														528
ggg ccc ta Gly Pro Ty														576
acc Thr														579
<210> 175 <211> 193 <212> PRT <213> Micro	comonos	spora	ı car	bona	ıcea									
<220> <223> evr	IR2													
<400> 175 Val Trp Gl	lu Pro	Gly 5	Asp	Glu	Ile	Glu	Leu 10	Arg	Pro	Thr	Val	Glu 15	Ile	
Val Trp G		5	_				10					15		
Val Trp Gl 1 Glu Ala An Met Pro Al	rg Ile 20	5 Ala	Val	Leu	His	Val 25	10 Ile	Leu	Ala	Arg	Cys 30	15 Phe	Gly	
Val Trp Gl 1 Glu Ala An Met Pro Al	rg Ile 20 la Gln 35	5 Ala Ala	Val Ala	Leu Met	His Ser 40	Val 25 Trp	10 Ile Leu	Leu Leu	Ala Asn	Arg Ser 45	Cys 30 His	15 Phe Leu	Gly Val	
Val Trp Gl 1 Glu Ala An Met Pro Al Asp Leu Va	rg Ile 20 la Gln 35	5 Ala Ala Pro	Val Ala Pro	Leu Met Glu 55	His Ser 40 Trp	Val 25 Trp Gln	10 Ile Leu Phe	Leu Leu Val	Ala Asn Met 60	Arg Ser 45 Gly	Cys 30 His	15 Phe Leu Arg	Gly Val Gly	
Val Trp Glad And And Met Pro And	rg Ile 20 la Gln 35 al Thr	Ala Ala Pro Phe	Val Ala Pro Val 70	Leu Met Glu 55 Leu	His Ser 40 Trp	Val 25 Trp Gln His	10 Ile Leu Phe Asp	Leu Leu Val Ala 75	Ala Asn Met 60 Leu	Arg Ser 45 Gly Phe	Cys 30 His Gly Ser	15 Phe Leu Arg Leu	Gly Val Gly Ala 80	
Val Trp Gl 1 Glu Ala An Met Pro Al Asp Leu Va 50 Asp His An 65	rg Ile 20 la Gln 35 al Thr rg Ser	Ala Ala Pro Phe Leu 85	Val Ala Pro Val 70 Ala	Leu Met Glu 55 Leu Lys	His Ser 40 Trp His	Val 25 Trp Gln His	10 Ile Leu Phe Asp Asp 90	Leu Val Ala 75 Pro	Ala Asn Met 60 Leu Thr	Arg Ser 45 Gly Phe Leu	Cys 30 His Gly Ser	15 Phe Leu Arg Leu Val 95	Gly Val Gly Ala 80 Asp	
Val Trp Gland Reserved Reserve	Ile 20 la Gln 35 al Thr rg Ser eu Gly eu Val	Ala Ala Pro Phe Leu 85 Glu	Val Ala Pro Val 70 Ala Arg	Leu Met Glu 55 Leu Lys	His Ser 40 Trp His Gln	Val 25 Trp Gln His Leu	10 Ile Leu Phe Asp Asp 90 Ile	Leu Leu Val Ala 75 Pro	Ala Asn Met 60 Leu Thr	Arg Ser 45 Gly Phe Leu Gly	Cys 30 His Gly Ser Pro	15 Phe Leu Arg Leu Val 95 Ser	Gly Val Gly Ala 80 Asp	
Val Trp Gland Reserved Reserve	rg Ile 20 la Gln 35 al Thr rg Ser eu Gly eu Val 100 rp Arg	Ala Ala Pro Phe Leu 85 Glu Ser	Val Ala Pro Val 70 Ala Arg	Leu Met Glu 55 Leu Lys Leu Ile	His Ser 40 Trp His Gln Pro Leu 120	Val 25 Trp Gln His Leu His 105	10 Ile Leu Phe Asp 90 Ile Ala	Leu Leu Val Ala 75 Pro Ala Pro	Ala Asn Met 60 Leu Thr Gly	Arg Ser 45 Gly Phe Leu Gly His 125	Cys 30 His Gly Ser Pro Glu 110	15 Phe Leu Arg Leu Val 95 Ser Ala	Gly Val Gly Ala 80 Asp Phe Asp	
Val Trp Gland And And And And And And And And And A	rg Ile 20 la Gln 35 al Thr rg Ser eu Gly 100 rp Arg 15	Ala Ala Pro Phe Leu 85 Glu Ser Leu	Val Ala Pro Val 70 Ala Arg Arg	Leu Met Glu 55 Leu Lys Leu Ile Leu 135	His Ser 40 Trp His Gln Pro Leu 120 His	Val 25 Trp Gln His Leu His 105 Ala	10 Ile Leu Phe Asp 90 Ile Ala Cys	Leu Leu Val Ala 75 Pro Ala Pro Leu	Ala Asn Met 60 Leu Thr Gly Gln Asp 140	Arg Ser 45 Gly Phe Leu Gly His 125 Trp	Cys 30 His Gly Ser Pro Glu 110 Pro	15 Phe Leu Arg Leu Val 95 Ser Ala Tyr	Gly Val Gly Ala 80 Asp Phe Asp	

Gly Pro Tyr His Glu Glu Pro Pro Gly Trp Glu Glu Val Asp Leu Ser 180 185 190

Thr

<210> 176 <211> 1176 <212> DNA <213> Micromonospora carbonacea <220> <221> CDS <222> (1)..(1176) <400> 176 gtg tgg atc gag aag aac ggg ccc gtc tac cgc att cgg gac ctc gtt Val Trp Ile Glu Lys Asn Gly Pro Val Tyr Arg Ile Arg Asp Leu Val cgc ggt aaa aag gtc acc att cag acc ggt tat ccg acg aag acc agc Arg Gly Lys Lys Val Thr Ile Gln Thr Gly Tyr Pro Thr Lys Thr Ser gcc aag aat gcg atg gtg cag ttc cgt gcg gag cag ttg cag ggc aac Ala Lys Asn Ala Met Val Gln Phe Arg Ala Glu Gln Leu Gln Gly Asn 40 gcg ctc atg ccg cgc ggt cag att acc ctc gcc gat ttc gtg ggg 192 Ala Leu Met Pro Arg Gly Gly Gln Ile Thr Leu Ala Asp Phe Val Gly 55 gag tgg tgg ccg agc tac gaa aag acg ctg aaa ccg acc gcc gtg aac 240 Glu Trp Trp Pro Ser Tyr Glu Lys Thr Leu Lys Pro Thr Ala Val Asn 288 teg gag gge aac egg ate ege aac eac ete etg eee ata ete gge eat Ser Glu Gly Asn Arg Ile Arg Asn His Leu Leu Pro Ile Leu Gly His 85 90 95 etc acc ett gac gag etg gac ggg cag gtc acc cag cag tgg gtc aac 336 Leu Thr Leu Asp Glu Leu Asp Gly Gln Val Thr Gln Gln Trp Val Asn 100 gac ctg gag gcc ggc gtc ggc ccg tgg ccg gag tcc acg cgg ggt cgt 384 Asp Leu Glu Ala Gly Val Gly Pro Trp Pro Glu Ser Thr Arg Gly Arg 115 120 125 cgg aag ccg ctg gca gcg aag acg atc agc aac tgc cac ggc ctg ctg 432 Arg Lys Pro Leu Ala Ala Lys Thr Ile Ser Asn Cys His Gly Leu Leu 480 cac acg atc tgc ggc gcg gcg atc gcg gcg aaa cgg atc agg ctc aac His Thr Ile Cys Gly Ala Ala Ile Ala Ala Lys Arg Ile Arg Leu Asn 150 ccg tgc tct tcg acg atg ctg ccc cgg cgc gag ccg aaa gag atg aag 528 Pro Cys Ser Ser Thr Met Leu Pro Arg Arg Glu Pro Lys Glu Met Lys 170 ttc ctg agc gac ccg gag atc ggt cgg ctt atc acg gcg ctt ccg ccg 576 Phe Leu Ser Asp Pro Glu Ile Gly Arg Leu Ile Thr Ala Leu Pro Pro 180 185 190

cac tgg His Tr															624
ggt gag Gly Glu 210	ı Ala														672
cgg ccc Arg Pro 225															720
gga gag Gly Gli															768
gtc agt Val Se															816
gga aag Gly Lys															864
gta agg Val Arg 290	Thr	_							_	_		_		_	912
gcc ggg Ala Gly 305															960
gcg ato Ala Ile															1008
ctc ggt Leu Gly															1056
cgt gag Arg Gli															1104
gcc ggc Ala Gly 370	/ Val	cgg Arg	gct Ala	gag Glu	gac Asp 375	ctg Leu	gag Glu	gcg Ala	gaa Glu	ctc Leu 380	gac Asp	gag Glu	gag Glu	ctg Leu	1152
acg gad Thr Asp 385															1176
<210> 1 <211> 3 <212> 1 <213> 1	92 PRT	mono	spora	a ca	rbona	acea									
<400> 1 Val Trp 1		Glu	Lys 5	Asn	Gly	Pro	Val	Tyr 10	Arg	Ile	Arg	Asp	Leu 15	Val	

Arg Gly Lys Lys Val Thr Ile Gln Thr Gly Tyr Pro Thr Lys Thr Ser 20 25 30

Ala Lys Asn Ala Met Val Gln Phe Arg Ala Glu Gln Leu Gln Gly Asn Ala Leu Met Pro Arg Gly Gly Gln Ile Thr Leu Ala Asp Phe Val Gly Glu Trp Trp Pro Ser Tyr Glu Lys Thr Leu Lys Pro Thr Ala Val Asn Ser Glu Gly Asn Arg Ile Arg Asn His Leu Leu Pro Ile Leu Gly His Leu Thr Leu Asp Glu Leu Asp Gly Gln Val Thr Gln Gln Trp Val Asn 100 105 Asp Leu Glu Ala Gly Val Gly Pro Trp Pro Glu Ser Thr Arg Gly Arg Arg Lys Pro Leu Ala Ala Lys Thr Ile Ser Asn Cys His Gly Leu Leu 135 His Thr Ile Cys Gly Ala Ala Ile Ala Ala Lys Arg Ile Arg Leu Asn 150 155 Pro Cys Ser Ser Thr Met Leu Pro Arg Glu Pro Lys Glu Met Lys 170 Phe Leu Ser Asp Pro Glu Ile Gly Arg Leu Ile Thr Ala Leu Pro Pro His Trp Arg Pro Leu Val Met Leu Leu Val Ala Thr Gly Leu Arg Trp 200 Gly Glu Ala Ile Gly Leu Arg Ala Gly Arg Val Asp Leu Leu Ala Ala Arg Pro Arg Leu Thr Val Val Glu Gln Leu Gln Glu Leu Ala Ser Thr Gly Glu Leu Val Phe Gln Ser Pro Lys Thr Ala Lys Gly Arg Arg Thr 250 245 Val Ser Phe Thr Thr Lys Val Ala Leu Leu Leu Thr Pro Leu Ile Ala 265 Gly Lys Lys Ser Asp Glu Val Val Phe Thr Ala Pro Lys Gly Gly Met 280 Val Arg Thr Arg Asn Phe Arg Arg Ile Trp Val Lys Ala Cys Glu Glu 295 Ala Gly Leu Pro Gly Leu Arg Ile His Asp Leu Arg His Thr His Ala 310 315 Ala Ile Leu Ile Ser Ala Gly Arg Pro Leu Ser Ala Ile Ser Arg Arg 325 Leu Gly His Ser Ser Ile Ala Val Thr Asp Leu Leu Tyr Gly His Leu Arg Glu Glu Val Asp Glu Gly Ile Leu Ala Ala Ile Glu Glu Ala Met

Ala Gly Val Arg Ala Glu Asp Leu Glu Ala Glu Leu Asp Glu Glu Leu

```
370
                        375
                                             380
Thr Asp Val Leu Ala Asp Ala Ala
                    390
<210> 178
<211> 26
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 178
ccctcgagat gtccagcaag atccta
                                                                    26
<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 179
cgaattctca ggcagactgc tctg
                                                                    24
<210> 180
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
<400> 180
ccctcgagaa tgtccagcaa gatccta
                                                                    27
<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
<400> 181
cgaattcaga ctgctctgcc gccgc
                                                                    25
<210> 182
<211> 12152
<212> DNA
<213> Micromonospora carbonacea
<400> 182
gtcttcgggg aacgccacgg gaacctcctc gccagaaccg gacgagctga ccgtaaccgg 60
tgggcacccg cgcgcggatc aaccggtgcg gtggttccca ggttccggcc gcgcggcccc 120
gacgcaccgc ccccggtgtg agaaggggac ccatctctac cgtaggcgtt aacaaggggc 180
```

```
cetteettte accgeaggtg caggaegtet eetgeggega gggtgegegg geeegeeegg 240
gtgtcgacca gcagccggcc gtcggcgtcc acgccggtcg ccacgccggt cacctccgca 300
ccgccgggca gcagcacccg caccggtctg ccgaccgtcg cgcaggccgc caggtacgcg 360
tegegeagee egetggeeac egegtegeeg eeggegtgge geeageggte gtaceagteg 420
gcgacagagc gcagcagtgc gcgcagcagc gggtcccggt cggtggcgac ggccccggcg 480
agetggageg aggtggeegg caggeeggte gggttegeeg geagetegte ggegegeagg 540
accgcctcgg ccaggatgcc cgcgcacttg gcgtcgccga tcagcaggtc gttgggccac 660
ttgagggcgg cgtccagctc ggccagccgg gccaccgcct cgaccagcgc gacgccggcg 720
agcaggggca gccagccgta cccggtcgcg ggggccggcg gccagtcgcg ctccgcgaca 780
gcctcgcccg gccgcagcag cacgctggtc gcgattccgg cgcggggcgg cgactgccag 840
acceggeege geeggeeceg geeggeggte tgeegetegg egateaceae gaggeeetee 900
ggctcgccgg atcgggccgc ctccgccacg tccgcgttgg tcgagccggt ctcggcgcgt 960
agetecagee gggeeeaggg geegtgeggg geggteageg ceeggegeag eegggeegee 1020
gacageggeg ggegatecag gteggtgtae ggegageegg geatecegee ageetaegge 1080
ccgcccggac gcggcggcgg gtgccggcgt tgcccgagcc cggtgaggtt gctgaggcgt 1140
actgcacacc gtcggccacc tgaaccatcg ttatattccg tgggtgacta ccgagaccgg 1200
gatcaacatc cacagcacgg cgggcaagct ggcggacctg gagcgacggg tcgacgaggc 1260
ggtgcacgcc ggatcggcgc gtgcggtgtc caagcagcac gcccggggca agaagacggc 1320
gegggagegg ategggetge tgetegaega ggggteette gtegagetgg aegggttege 1380
ccggcaccgg tccaccaact tcggcctgga ccgcacccgc ccgtacggcg acggggtgat 1440
caccggctac ggcacggtcg acgggcggca ggtctgcgtc ttcgcgcagg acttcacggt 1500
cttcggcggc tccctcggcg aggtgttcgg cgaaaagatc gtcaaggtga tggacctggc 1560
catgaagatc ggctgcccgg tcgtcggcat caacgactcc ggcggcgccc gcatccagga 1620
gggcgtggcg tccctcgggc tctacggcga gatcttcttc cgcaacgtgc gggccagcgg 1680
cgtcatcccg cagatctccc tgatcatggg cccgtgcgcg ggcggcgcgg tctattctcc 1740
ggcggtcacc gacttcaccg tgatggtcga ccagacctcg cacatgttca tcaccggccc 1800
cgacgtgatc aagacggtca ccggcgagga cgtcgggatg gaggaactgg gcggtgcccg 1860
cacccacaac gcgcgcagcg gcaacgcgca ctacctcggc accgacgagg aggacgcgat 1920
cgagtacgtc aaggegetge tgtegtacet geegtegaac aacetggaeg ageegeeggt 1980
cttcgacgcc ccggccgacg tggcgatcag cgacgccgac cgggagctgg acagcctcgt 2040
cccggactcg gcgaaccagc cgtacgacat gcaccgggtc atcgagcacg tgctggacga 2100
cggggagttc ctggaggtcc agccgctgta cgcgcagaac atggtggtcg gcttcggtcg 2160
aatcgaggga cgaccggtcg gcgtggtggc caaccagccg atgcacctcg ccggcacgct 2220
ggacategee gegteggaga aggeegeeeg gttegtgege acetgegaeg egtteaacat 2280
ccccgtgctg accttcgtgg acgtgcccgg gttcctaccc ggcaccggcc aggagtggga 2340
eggcateate eggegeggeg egaageteat etaegegtae geegaggega eegteeegaa 2400
ggtcaccgtg atcacccgca aggcgtacgg cggggcgtac gacgtgatgg gctccaagca 2460
cctgggcgcg gatctgaact tcgcctggcc gaccgcgcag atcgcggtga tgggcgcgca 2520
gggcgcggtg aacatectgt accggcagga gctggccgcc gccgaggacc cggccgccgt 2580
gcgcgcgag aagatcgccg agtacgagga caccctggcc aacccgtacg tcgccgccga 2640
gcgcgggtac gtcgactcgg tgatcccgcc gcacgagacg cgtacccaga tcgtccgggc 2700
gttgcgggtg ctgcgcacca agcgcgagac gctcccggcg aagaagcacg gcaacatccc 2760
gctctaggcg cggtgcaggg aggggcccct gtcacgcgat ccgtgcagca gggccccctc 2820
ccgacgccgg aggagccggc gggcccggca gccgggcgcc ggtcagcacg ccgggttggc 2880
ggcgaggcac atccgccggg cggccgtgcg gcccagttcg agcagctccg cgtcgctggt 2940
ctegeggggg cegteeggee egtegaegee caaceegege tegggeaega tgaeggtgae 3000
caggtcgccg acccggacga tcatccgggt ttccggcggg taccccacgt cgaggggctt 3060
gcccgtcgtg gggtccaccg gggacatcac ggtgtgccgc aacacgaccg cctcgtcgcc 3120
ggcgaagtcg cgggcgatcg tctgccaggt gtgggccacc gagatcgcgc cacggccgtc 3180
gtccaggggc cgaaccgccg tgtcgctcca gcgggcgcag gtggtcgccg cccggtccag 3240
gtcggcgagc agccggccgg ccggggcggg gtcgaggcgg tagacgtcct gggtgaggac 3300
ggggacggcc atcgacccgt cctggcccga cgtgtcgtcc aggagcagcg tctgggatcg 3360
cgagtagcga gacaccggcg gccccgccc cggctccttg cccacggcgc acgactggag 3420
cagcgggtcc acccggacct gctcctgaag cccagagtcc cccagtcgta cgttgctcgg 3480
caegeceagg teggeegggt ceageaggge eteetggeeg ateteggtee ggeeggaeeg 3540
ctccggctcg gtagacgcgc gccacccgtc gacccaggac atcggcggcg cgaggtgccc 3600
geeggeeegg eegeegaeeg eeaeggegaa gaeegagagt aeggeeagea eggeegegge 3660
cgccgccatc gccgtacgcc ggctgcggcg gcgggcccgg gcgcggatgt ccgccggctc 3720
gggccaacgg acgtcccgca ggtcccggtg catccgttcg gcgaacgtca ggtcgtcacg 3780
categgegge etectecagg teagagaegg egageageee ggegagegeg geaegeeeee 3840
gggagagacg ggctttcacg gtgccgaccg gggcggcggt ctcccgtgcc acctcggcca 3900
ccggcatgcc gagcaggtag tgcagggcga tggcggtgcg ctgcgcctcg ggcagccggc 3960
gtagegeege caccacetee agegtegegg tgeteggege ggggaegete teeggegeae 4020
cgtgccgcag gtacgcccgc gcccggctac gcatgctgcg ccaccggctc accgcgatcc 4080
```

```
ggctcgccac cacgcgcagc cagccctccg gatcgtcgta cccgcgtacg gtcggccagc 4140
gctgccatgc gcggatgtac gcctcctgca cggcgtcctg cgcctcggcc aggtttccgg 4200
tgatcatgta cacgaaaccc agcaatcgtt gccggctgcc ccggtagaac tcgtcgaacc 4260
cctcggcgtc cggcatccgc cacctccccg tgtcgcaggg gacacgcctg gcgggtggtc 4320
cccggttgcc cgaccggccg gcttcttccc tccccggggg tccccggcgg gttcctcccg 4380 gggtctcccg gcgggcccgt cacgtcacgg ccggcgcgc gggctcgtca cgtcacggcc 4440
ggcgcggcgg gccttcggca gcgaacagcg accgtccgag aatcgggtgc cggccggagt 4500
ggtcgaggc gcgggtgggc ggtggtcaga ccgtgagccc ggcgtcggtg aggatcgggc 4560
cggcgagcag cagggcgccg acggcgaggc cggccaggca gacgaccagg aagacaccga 4620
cccagaacag gggcgggaac ggcgtcaacc gggcgagctg gtcggcgtcg gactccggca 4680
teeggeeacg getgegeage egetgeaact egateacegg acgeaegeeg cegaacagea 4740
ggaaccagac cgaggtccag gcgaacgcgg cctgcacctg cggcggggcg taccaggaga 4800
cggcgaagac cagaccgccg gtggcgagca gcgacagtgc cccgtagacg ttgcggatca 4860
tegecageat ggecageage ageaceaceg tgacegagag cageatggtg ateeggttee 4920
cggcgagcag ccacgccccg gccagcccga gcagggtcgg ggcgacgtac ccggcgaaca 4980
gggtgaggat catgcccagc ccggtggggc ggccggccga cagggtgagc ccggaggtgt 5040
ccgagtgcag ccggatgccg cgcagcttcc gcccggtgag cagggcggcc agcgcatgac 5100
egecetegtg ggegatggte acegegttac gegegaceeg ceagggeace eggqtqqcqa 5160
ccaccgccag cgcgacggcg gcggtggcca ggaccagcag cggtggcggg tcgggttgcg 5220
cgccgacgag ttcgttccag acgacgctca ggccgtcgat caggtccacg gggccgcagc 5280
ggcccggtcg accagcgccg gggcgcacgc ccgccgctga ccggcacccg gtcaggtcgc 5400
gggcaccccg gtcaggtcgc ctgcgacgaa gaaggccgcc gctctggtgc ccacccgcaa 5460
ccgccgccga gggcggacct caccgaccgg cggcaccttg cgtccacgta ggaccacggc 5520
gagcaccccg gtcggcgca gcacggaagc gaccctggtc agcatcccgg gcaggccctc 5580
cccggcccgc tccccctgcc agctcgtctg ctccccgtac ggcaggtcgg tcacgaccag 5640
gtegggggte atgeeegega eggeeteggt gagggeeaeg eggtegaaea egteggeeeg 5700
cegeacegeg taeggeageg ggeegeetge egegteeaga egggegegea geeggtggge 5760
ggcggcggcc gcctccgcgt agtgcggctt gtcgaacgcc tcggcgcgtt gcgccagctc 5820
gegggeeege gtgtegagee eggegeeggt eageaggeeg aggttggeee gageaaggte 5880
gagggccgcc tcgtcgacgt cggaggcgag cagcccggca aggctcggcc ggtgcagcag 5940
cgcgagcacc gtcagcaggt agccgctgcc gcagcacggg tcccagacgg tggccggggc 6000
ggacgtcggg cgcaactcca gcgcggtttg caggacctcg gaggcgagcc gcaccgggaa 6060
cgccgggaag cccggcgccg agcgcaacac ggcgccactg gccaggtcgc cgtacgcacc 6120
gegtaeggtt tegtgeeggt aagteacatg ceeteeegg egeaceetae caateeggea 6180
ccgccgggcc gggtcaggca ggccgggact cgatccagtg gaagtcggtg ggaggcagcg 6240
gegtgaegte etceagggae ageeeegeet tgeegeaeag eegtteeagg tegeeteggg 6300
tccgctccag gccctgcccg ttgaccagca tccccacgtc ggtcaggtac gccagcgcgt 6360
tggccgccgg gccgaccacg tccggcagca cgtggtcgat catgacgatc cggccgcccg 6420
gggcgaccgc ctcggcacag tgccggagga ttcccgtcgc ccggccgtcg ccccaaccgt 6480
ggatcacact tttgagcagg tagaggtcgg cgtcggcggg gaccctctcg aagaagtcac 6540
cgctgccgct ggcgctgtcg tagagcacgc cccgcacgcc ggggttcgcg gcgagcacgg 6660
eggecageag ggtgeegtet eegeegeeca egtegaeeae egteegeaeg eeggeeaggt 6720
cggtacgctc ggcaacggcc gccgcgacgc tgtgggtcac ctggctcatc gccgcgttgt 6780
acagetegga aaggtegggt egeeegeeea egtagetgaa gaagteggtg eegaagatge 6840
cgtcgaaggc cggctcgccg gtgcggacgc tgtgcgccag gccgtcccag gccgtggtca 6900
tggccgggtc ggtcagcatc cgggccagcg ggcgcagcgt gccgggtcgg tccccacgca 6960 gcagcgccc catcggggcg agcgcgaacc ggccgggtgt ggtctcggtg agcacccgca 7020
gegeggeeag ggegegeage acceggaaca tggtgteege tegggegteg tacegeageg 7080
ccaactcctg cggggtgcgc tcgtcgtcgc cgatcgcgtc gggcagcccc agccggacgc 7140
agtagcegae cageeggetg gecateeege egaacaceaa eegeateage teeggeeagg 7200
cgtccgtgtc cgggacggtc atcggaccgg ctcggcggcc ggcaggccca gcccgatgcg 7320
caeggcecgt tegaceggeg agtagtegee gteegggegg teeaggteea getegeeeae 7380
cggctgcagg ctcggctggg ccatgaaccg gggccgcgtg ccggtgttgg ccaccggggt 7440
gtgcaccagg aacgggtggc acaggtagac gtcaccggcg cgtccggtgg cggaggcgag 7500 cgggcggtcc cggccgacgt cgcccacgtc gaggtaggtg ccctccgggc cgtacggttc 7560
gagcagcggc ggcacgtcca ggtgggagcc gaccctgacc agcgtcggcg cctcccgctc 7620
gtcggtgtcg gagaagagga acagcagcag cagggcccgc ccccgcgacc ggaggttgca 7680
gcggaagacc tccgcgtagt tgggcgggac caggtccagc tcgccctccc agttctgggg 7740
gcccagccgc tgcgcgtcgt cggccaggaa actggcgtcg atgtgccagc cgtagtcctc 7800
ggtctgctcc gggcgcttgg gcaccgggaa ccggaccggg aaggtgccga tccggtccaa 7860
eggettecag egececacce egacgagetg gtegaaggeg gegtgeagee ggggegtggt 7920
ggcgctgcgc acgaagggct cggcgtcctg gaggcccagc cggaccacct cgcgggacca 7980
```

ggtgctccgg tcctcggggt ccatgccgag ttgccgccac agcagttcgc gaccctgctg 8040 cgcgagctcg gccgggaacg ccgcctccaa cttcacgaac ccgtcggaga cgaaccgctc 8100 gacctgctcg tcgctgagga cctgggcgct catcgcactc cttcccgccg gttcccgccg 8160 aggeggageg agaeggtege accegegetg accggacegg gegaegegee tegteaagat 8220 tegecaggtt gaatggtaga caageegeca cegteaggga etaaegtttt ceteageate 8280 gtccgggcca ccgcgagagc gccgcacccc ccgctccacc acccgcaacc atcggctctc 8340 cccgggtgcg gcgatgccgt cgagccgggc gcgggcctcc tccggcagcg gccggtcggc 8400 cgccgccagc gccgccggg cctggtccag cgtgcgggg ccgacgaccg tgctggtcac 8460 ccccggcgcg tcgtagaccc aggcgtgcgc caggtccggc agggacaggc ccagctcgac 8520 ggccacette gccaacegge ccagggteeg ccacacegge tgccagtgeg ggcccgatgg 8580 ggcgtaccag gcggtgaacc gggcgtcgcg gggcggctcg ccgtcggcga accggtcgga 8640 gagcagaccc atcgccagcg ggctgtaggt gaacaggccg aggccgtact ccgcgcacag 8700 eggeageacg tecegetega tetegegtte cageaggttg taeggegaet geteggeeae 8760 caccggggcg gcgccccggg actgcgccgt gcgcagcagg tcgacgatcc gccagctggg 8820 caccgtgccc agccggggct ggtcggccag ctcgtatgcc gtgggcacgg tggaggtgcc 8880 cacgtagegg accttgeegg ageggaceag gtegtegagg geggacaeeg teteeteeac 8940 cggagtgtcc gggtcgtgac ggtgcaggta gagcaggtcg atgtggtcgg tacccagccg 9000 gegeaacgae egetegeact ceegetteag ggegtacgee gaggtgeece ggtegttegg 9060 tecegggeeg aceggattga agatettggt ggeeageagg aegtegteec ggeageteeg 9120 caeggeegeg cegaegatet cetegetgeg geegteetgg tagaegttgg cegtgtegae 9180 gaggttgact cccgcttcga cggccgtggc gacgatcctg gcggcctcct ccggcccggt 9240 cgggccgccg aagttgaacg cccccaggga caccttggac acccgcagtc cacaccggcc 9300 caactgtcgg tactccacgc tgccctcccc tgcggtggtg gtcgccggcc accccgtcgt 9360 geggeeggtg etecceggag eeggggagtg geegateteg atgggggage etagtacege 9420 gegggtgeet eggeegtggt actageagaa etgetagage ateegtegag eegeegggeg 9480 gccgggcggc agccggtacg gtgtgcctga acccaccacg ggccggcgcc ggacgaccgg 9540 tegacgageg ategagetga teggegggga geggatgage gacaagtaeg geegeagtge 9600 cttcaagtcg agcgacgtca actacaagct cgccctctgg gatccccggg tcagcggggt 9720 cegetacetg aagaegetea tetteaacet ggeegagaac etgggegagg egaaceggge 9780 ccggttgcgc cggatcgcca accgggacgt cggcgacccc atctccgtcg tctgggacgg 9840; egaceggate tgeatggaet atetecagge ggtgetggag etggagttet tetecegeea 9900 cgtgccactg gacggcgcga cggtgctgga gatcggcgcg ggctacggcc gcacctgtca 9960 egeogtgete tecaaceaeg aegtegeege gtaceaegtg gtegacetge egaacteeet 10020 cgctctggcc cgccgctacc tgggcacggt gctcaccgcc gagcagttgg cgagggtcca 10080° cttccacggc gtcggcgagg tggacgggcc gctgagcgag ctgcgctacg acctcgtgat 10140 caacatcgac tcgttcgcgg agatgacggc ggagacggtg cgcgcgtacc tcgccttcgt 10200 cgccaccagg gcccgccacc tgtacgtcaa caaccccgtc gggaagtacc tcgacaagag 10260 cctggacggg cacttccagg gcgaggccgt ggtcaacctt gcgctgagca ccggcctgct 10320 gegegaegte ategaeatee aegaeaacea ggeegtgegg eggeagteee gggegtteet 10380 cgacgcgtac cggccggggc cgggctgggc ctgcgtggcg gagagccgga cgatcccgtg 10440 gagctactac tggcaggcgc tctaccgggc cggcgaggcg gccccggcac ccgggcggga 10500 ttgaggtgac cggccgagcg ggcgagcccg ccgaccggcc cgtcgtcgcc gtcctcggcg 10560 ceteeggeet ggteggeace getgtgetgg eegegetege egaceggeg gteacegtee 10620 gggccgtcgc ccgccgggct gccgtgctgc ccgccgcgcc gggccgcgcg gcgtttgagg 10680 tggtacggc cgacctgacc gaccggggag ccctggcggc ggcggtacgc gacgcgacgg 10740 ccgtggtcaa cctcaccctg gacagttccg gctggcgggg cgccgacgac gaccgcagcg 10800 cgcgggtcaa cgtcgagctg acccgggaac tcgtcgggat gctccgccc gggccgggcg 10860 geacgeceae caeactggte ttegeegget cegeeteeca ggtgggeegg cegeecegga 10920 tecegatega eggeacegag eeggaceace eegceacece gtacgacegg eagaageagg 10980 ccgcggagtc gctggtcgtg gcggccaccg gggccggcgt cgtgaacggg gtgtcgctgc 11040 gactgcccac cgtgttcggc ccggtgccgc cgggcgccgg gcccgaccgg ggcgtggtgt 11100 ccacgatgat ccgccgggcg ctgtccggag cgccactgac catgtggcac gacggccggg 11160 tgcaacggca actgctgtac gtggccgacg ccgccgccgc cttcgtggcg gcgctggacc 11220 accccggggc gctgaccggc cggcactggc cgctcggcga cggccggggt gaacggctcg 11280 gggacctgtt ccgcgccatc gccgccctgg tggccgagcg gaccggtcgg ccaccggtgc 11340 cggtgctggc cgtgccccg cccgacgagg cccgggtcag cgacttccac gacatggtcg 11400 ttgacgcctc ggccttccag gcggtcaccg ggtgggcgc ccgggtgccg ttgcgcctcg 11460 cgctggaccg caccgtcgcg gcgctcgccc gcgacgacag cggccccgag gccccgggcg 11520 gcgtcggccc gacgcgggcg gatcaggccc ggaagccgga ctcgatctcc aggcaggtcc 11580 ggtagtcggg cagcaaccca cgggcgagcg cctggtcgaa ggtgatcgcg gtgcggtccc 11640 gctccgacag gatcggttcg acgtcctcgg ggatgggcag gcccagcccg gggtcgagcg 11700 cgtcgagcgc cagttcgttc tcgaagacgt actcctggga caggacgtac gacatgacgg 11760 tgtcgtcggc cagggcgacg aacatgtgcg cgaccccgac cggcaggtag accgcctgga 11820 actecteget gtegageace acgetgtece acttgeegaa egteggtgag eccaecegea 11880

cgtcgaggac caggt gcggggtacg ggtga tctgccgcac gggga gcgagaggaa cacco cgacggtcag cggg	aagtgc agcco aacagc gggta ccccgg tagto	ccgca gcgto cccga ccgto ccgggt agac	cccccg gcg	ggagacg ct caacgag to	gtagctgg gagatacg	12000 12060
<210> 183 <211> 873 <212> DNA <213> Micromonos	spora carbo	nacea				
<220> <221> CDS <222> (1)(873)	ı					
<220> <223> ORF1						
<400> 183 atg ccc ggc tcg Met Pro Gly Ser 1		Asp Leu A				48
gcc cgg ctg cgc Ala Arg Leu Arg 20						96
ctg gag cta cgc Leu Glu Leu Arg 35						144
gcg gcc cga tcc Ala Ala Arg Ser 50		Glu Gly Le				192
cag acc gcc ggc Gln Thr Ala Gly 65						240
cgc gcc gga atc Arg Ala Gly Ile	gcg acc ago Ala Thr Ser 85	. Val Leu Le	tg cgg ccg eu Arg Pro 90	ggc gag g Gly Glu A	ct gtc la Val 95	288
gcg gag cgc gac Ala Glu Arg Asp 100						336
ccc ctg ctc gcc Pro Leu Leu Ala 115	ggc gtc gcg Gly Val Ala	g ctg gtc ga Leu Val G 120	ag gcg gtg lu Ala Val	gcc cgg c Ala Arg L 125	tg gcc eu Ala	384
gag ctg gac gcc Glu Leu Asp Ala 130		Trp Pro A				432
gcc aag tgc gcg Ala Lys Cys Ala 145						480
gac cag ccc ccg Asp Gln Pro Pro		Leu Gly I		Asn Val T		528

cgc gcc gac gag ctg ccg gcg aac ccg acc ggc ctg ccg gcc acc tcg 576

Arg Ala Asp	Glu Leu 180	Pro	Ala	Asn	Pro 185	Thr	Gly	Leu	Pro	Ala 190	Thr	Ser	
ctc cag ctc Leu Gln Leu 195	gcc ggg Ala Gly	gcc (Val 2	gcc Ala 200	acc Thr	gac Asp	cgg Arg	gac Asp	ccg Pro 205	ctg Leu	ctg Leu	cgc Arg	624
gca ctg ctg Ala Leu Leu 210	cgc tct Arg Ser	Val 2	gcc (Ala / 215	gac Asp	tgg Trp	tac Tyr	gac Asp	cgc Arg 220	tgg Trp	cgc Arg	cac His	gcc Ala	672
ggc ggc gac Gly Gly Asp 225													720
tgc gcg acg Cys Ala Thr	gtc ggc Val Gly 245	Arg :	ccg (Pro '	gtg Val	cgg Arg	gtg Val 250	ctg Leu	ctg Leu	ccc Pro	ggc Gly	ggt Gly 255	gcg Ala	768
gag gtg acc Glu Val Thr													816
gtc gac acc Val Asp Thr 275			Pro i										864
cac ctg cgg His Leu Arg 290													873
<210> 184 <211> 291 <212> PRT <213> Micror	nonospor	a carl	bona	cea									
<211> 291 <212> PRT	nonospor	a carl	bonac	cea									
<211> 291 <212> PRT <213> Micron		Tyr '			Leu	Asp 10	Arg	Pro	Pro	Leu	Ser 15	Ala	
<211> 291 <212> PRT <213> Micror <220> <223> ORF1 <400> 184 Met Pro Gly	Ser Pro	Tyr 1	Thr <i>i</i>	Asp		10					15		
<211> 291 <212> PRT <213> Micror <220> <223> ORF1 <400> 184 Met Pro Gly 1	Ser Pro 5 Arg Arg 20	Tyr :	Thr i	Asp Thr	Ala 25	10 Pro	His	Gly	Pro	Trp 30	15 Ala	Arg	
<pre><211> 291 <212> PRT <213> Micron <220> <223> ORF1 <400> 184 Met Pro Gly 1 Ala Arg Leu Leu Glu Leu</pre>	Ser Pro 5 Arg Arg 20 Arg Ala	Tyr 1	Thr i	Asp Thr Gly 40	Ala 25 Ser	10 Pro Thr	His Asn	Gly Ala	Pro Asp 45	Trp 30 Val	15 Ala Ala	Arg Glu	
<211> 291 <212> PRT <213> Micror <220> <223> ORF1 <400> 184 Met Pro Gly 1 Ala Arg Leu Leu Glu Leu 35 Ala Ala Arg	Ser Pro 5 Arg Arg 20 Arg Ala Ser Gly	Tyr f	Thr i	Asp Thr Gly 40 Glu	Ala 25 Ser Gly	10 Pro Thr	His Asn Val	Gly Ala Val 60	Pro Asp 45	Trp 30 Val Ala	15 Ala Ala Glu	Arg Glu Arg	
<pre><211> 291 <212> PRT <213> Micror <220> <223> ORF1 <400> 184 Met Pro Gly 1 Ala Arg Leu Leu Glu Leu 35 Ala Ala Arg 50 Gln Thr Ala</pre>	Ser Pro 5 Arg Arg 20 Arg Ala Ser Gly Gly Arg	Tyr 7 Ala 1 Glu 7 Glu 1 Gly 7 Thr 8	Thr i	Asp Thr Gly 40 Glu Arg	Ala 25 Ser Gly	10 Pro Thr Leu Arg	His Asn Val Val	Gly Ala Val 60 Trp	Pro Asp 45 Ile Gln	Trp 30 Val Ala Ser	15 Ala Ala Glu Pro	Arg Glu Arg Pro 80	
<211> 291 <212> PRT <213> Micror <220> <223> ORF1 <400> 184 Met Pro Gly 1 Ala Arg Leu Leu Glu Leu 35 Ala Ala Arg 50 Gln Thr Ala 65	Ser Pro 5 Arg Arg 20 Arg Ala Ser Gly Gly Arg Ile Ala 85	Tyr S	Thr A Leu 5 Thr (Pro (55 Arg A	Asp Thr Gly 40 Glu Arg Val	Ala 25 Ser Gly Gly Leu	10 Pro Thr Leu Arg Leu 90	His Asn Val Val 75 Arg	Gly Ala Val 60 Trp Pro	Pro Asp 45 Ile Gln Gly	Trp 30 Val Ala Ser Glu	15 Ala Ala Glu Pro Ala 95	Arg Glu Arg Pro 80 Val	

```
Glu Leu Asp Ala Ala Leu Lys Trp Pro Asn Asp Leu Leu Ile Gly Asp
Ala Lys Cys Ala Gly Ile Leu Ala Glu Ala Val Pro Gly Pro Ala Pro
                    150
                                        155
Asp Gln Pro Pro Ala Ile Val Leu Gly Ile Gly Leu Asn Val Thr Leu
Arg Ala Asp Glu Leu Pro Ala Asn Pro Thr Gly Leu Pro Ala Thr Ser
Leu Gln Leu Ala Gly Ala Val Ala Thr Asp Arg Asp Pro Leu Leu Arg
                            200
Ala Leu Leu Arg Ser Val Ala Asp Trp Tyr Asp Arg Trp Arg His Ala
Gly Gly Asp Ala Val Ala Ser Gly Leu Arg Asp Ala Tyr Leu Ala Ala
Cys Ala Thr Val Gly Arg Pro Val Arg Val Leu Leu Pro Gly Gly Ala
                                    250
Glu Val Thr Gly Val Ala Thr Gly Val Asp Ala Asp Gly Arg Leu Leu
Val Asp Thr Arg Ala Gly Pro Arg Thr Leu Ala Ala Gly Asp Val Leu
His Leu Arg
    290
<210> 185
<211> 1581
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(1581)
<220>
<223> ORF2
gtg act acc gag acc ggg atc aac atc cac agc acg gcg ggc aag ctg
                                                                  48
Val Thr Thr Glu Thr Gly Ile Asn Ile His Ser Thr Ala Gly Lys Leu
                                     10
gcg gac ctg gag cga cgg gtc gac gag gcg gtg cac gcc gga tcg gcg
                                                                  96
Ala Asp Leu Glu Arg Arg Val Asp Glu Ala Val His Ala Gly Ser Ala
cgt gcg gtg tcc aag cac gcc cgg ggc aag aag acg gcg cgg gag
                                                                  144
Arg Ala Val Ser Lys Gln His Ala Arg Gly Lys Lys Thr Ala Arg Glu
         35
egg ate ggg etg etc gae gag ggg tee tte gte gag etg gae ggg
Arg Ile Gly Leu Leu Asp Glu Gly Ser Phe Val Glu Leu Asp Gly
     50
tto goo ogg cao ogg too aco aao tto ggo otg gao ogo aco ogo cog
Phe Ala Arg His Arg Ser Thr Asn Phe Gly Leu Asp Arg Thr Arg Pro
```

65					70					75					80	
						acc Thr										288
gtc Val	tgc Cys	gtc Val	ttc Phe 100	gcg Ala	cag Gln	gac Asp	ttc Phe	acg Thr 105	gtc Val	ttc Phe	ggc Gly	ggc Gly	tcc Ser 110	ctc Leu	ggc	336
						atc Ile										384
						ggc Gly 135										432
						ctc Leu										480
						gtc Val										528
						gtc Val										576
						tcg Ser										624
						gag Glu 215										672
						cgc Arg										720
						gag Glu										768
						gag Glu										816
						gac Asp										864
						gac Asp 295										912
						gag Glu										960
						atc Ile										1008

aac cag ccg at Asn Gln Pro Me 34	t His Leu										1056
aag gcc gcc cg Lys Ala Ala Ar 355		_	_	_							1104
ctg acc ttc gt Leu Thr Phe Va 370											1152
tgg gac ggc at Trp Asp Gly Il 385		Arg Gly									1200
gag gcg acc gt Glu Ala Thr Va			Val								1248
ggg gcg tac ga Gly Ala Tyr As 42	p Val Met										1296
ttc gcc tgg cc Phe Ala Trp Pr 435											1344
gtg aac atc ct Val Asn Ile Le 450											1392
gcc gtg cgc gc Ala Val Arg Al 465	c gag aag a Glu Lys 470	atc gcc Ile Ala	gag Glu	tac Tyr	gag Glu 475	gac Asp	acc Thr	ctg Leu	gcc Ala	aac Asn 480	1440
ccg tac gtc gc Pro Tyr Val Al			Tyr								1488
cac gag acg cg His Glu Thr Ar 50	g Thr Gln										1536
aag cgc gag ac Lys Arg Glu Th 515											1581
<210> 186 <211> 527 <212> PRT <213> Micromonospora carbonacea											
<220> <223> ORF2											
<400> 186 Val Thr Thr Gl 1	u Thr Gly 5	Ile Asn	Ile	His 10	Ser	Thr	Ala	Gly	Lys 15	Leu	

Ala Asp Leu Glu Arg Arg Val Asp Glu Ala Val His Ala Gly Ser Ala 20 25 30

Arg Ala Val Ser Lys Gln His Ala Arg Gly Lys Lys Thr Ala Arg Glu Arg Ile Gly Leu Leu Asp Glu Gly Ser Phe Val Glu Leu Asp Gly 55 Phe Ala Arg His Arg Ser Thr Asn Phe Gly Leu Asp Arg Thr Arg Pro Tyr Gly Asp Gly Val Ile Thr Gly Tyr Gly Thr Val Asp Gly Arg Gln 90 Val Cys Val Phe Ala Gln Asp Phe Thr Val Phe Gly Gly Ser Leu Gly 105 Glu Val Phe Gly Glu Lys Ile Val Lys Val Met Asp Leu Ala Met Lys Ile Gly Cys Pro Val Val Gly Ile Asn Asp Ser Gly Gly Ala Arg Ile 135 Gln Glu Gly Val Ala Ser Leu Gly Leu Tyr Gly Glu Ile Phe Phe Arg 150 155 Asn Val Arg Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Pro Cys Ala Gly Gly Ala Val Tyr Ser Pro Ala Val Thr Asp Phe Thr 185 Val Met Val Asp Gln Thr Ser His Met Phe Ile Thr Gly Pro Asp Val 195 200 Ile Lys Thr Val Thr Gly Glu Asp Val Gly Met Glu Glu Leu Gly Gly Ala Arg Thr His Asn Ala Arg Ser Gly Asn Ala His Tyr Leu Gly Thr Asp Glu Glu Asp Ala Ile Glu Tyr Val Lys Ala Leu Leu Ser Tyr Leu 245 250 Pro Ser Asn Asn Leu Asp Glu Pro Pro Val Phe Asp Ala Pro Ala Asp Val Ala Ile Ser Asp Ala Asp Arg Glu Leu Asp Ser Leu Val Pro Asp Ser Ala Asn Gln Pro Tyr Asp Met His Arg Val Ile Glu His Val Leu 295 Asp Asp Gly Glu Phe Leu Glu Val Gln Pro Leu Tyr Ala Gln Asn Met Val Val Gly Phe Gly Arg Ile Glu Gly Arg Pro Val Gly Val Val Ala Asn Gln Pro Met His Leu Ala Gly Thr Leu Asp Ile Ala Ala Ser Glu 345 Lys Ala Ala Arg Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Val 355 Leu Thr Phe Val Asp Val Pro Gly Phe Leu Pro Gly Thr Gly Gln Glu 370 375 380

```
Trp Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Ile Tyr Ala Tyr Ala
Glu Ala Thr Val Pro Lys Val Thr Val Ile Thr Arg Lys Ala Tyr Gly
Gly Ala Tyr Asp Val Met Gly Ser Lys His Leu Gly Ala Asp Leu Asn
Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Gln Gly Ala
Val Asn Ile Leu Tyr Arq Gln Glu Leu Ala Ala Ala Glu Asp Pro Ala
                       455
Ala Val Arg Ala Glu Lys Ile Ala Glu Tyr Glu Asp Thr Leu Ala Asn
Pro Tyr Val Ala Ala Glu Arg Gly Tyr Val Asp Ser Val Ile Pro Pro
His Glu Thr Arg Thr Gln Ile Val Arg Ala Leu Arg Val Leu Arg Thr
                               505
Lys Arg Glu Thr Leu Pro Ala Lys Lys His Gly Asn Ile Pro Leu
                           520
<210> 187
<211> 888
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(888)
<220>
<223> ORF3
<400> 187
atg cac egg gae etg egg gae gte egt tgg eee gag eeg geg gae ate
                                                                48
Met His Arg Asp Leu Arg Asp Val Arg Trp Pro Glu Pro Ala Asp Ile
ege gee egg gee ege ege ege age egg egt aeg geg atg geg gee
                                                                96
Arg Ala Arg Ala Arg Arg Ser Arg Arg Thr Ala Met Ala Ala Ala
            20
144
Ala Ala Val Leu Ala Val Leu Ser Val Phe Ala Val Ala Val Gly Gly
egg gee gge ggg cae ete geg eeg eeg atg tee tgg gte gae ggg tgg
                                                                192
Arg Ala Gly Gly His Leu Ala Pro Pro Met Ser Trp Val Asp Gly Trp
ege geg tet ace gag eeg gag egg tee gge egg ace gag ate gge eag
                                                                240
Arg Ala Ser Thr Glu Pro Glu Arg Ser Gly Arg Thr Glu Ile Gly Gln
```

gag gcc ctg ctg gac ccg gcc gac ctg ggc gtg ccg agc aac gta cga

Glu	Ala	Leu	Leu	Asp 85	Pro	Ala	Asp	Leu	Gly 90	Val	Pro	Ser	Asn	Val 95	Arg	
ctg Leu	ggg Gly	gac Asp	tct Ser 100	gly ggg	ctt Leu	cag Gln	gag Glu	cag Gln 105	gtc Val	cgg Arg	gtg Val	gac Asp	ccg Pro 110	ctg Leu	ctc Leu	336
	tcg Ser															384
	tac Tyr 130															432
gac Asp 145	Gly 999	tcg Ser	atg Met	gcc Ala	gtc Val 150	ccc Pro	gtc Val	ctc Leu	acc Thr	cag Gln 155	gac Asp	gtc Val	tac Tyr	cgc Arg	ctc Leu 160	480
	ccc Pro															528
	acc Thr															576
	cgt Arg															624
gac Asp	ttc Phe 210	gcc Ala	ggc Gly	gac Asp	gag Glu	gcg Ala 215	gtc Val	gtg Val	ttg Leu	cgg Arg	cac His 220	acc Thr	gtg Val	atg Met	tcc Ser	672
	gtg Val															720
	acc Thr															768
_	gag Glu	_		_			_		_	_	-				_	816
	gac Asp															864
_	ctc Leu 290	_	_		_		_									888
	0> 18 1> 29															

<211> 296

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> ORF3

<400> 188

Met His Arg Asp Leu Arg Asp Val Arg Trp Pro Glu Pro Ala Asp Ile
1 5 10 15

Arg Ala Arg Ala Arg Arg Ser Arg Arg Thr Ala Met Ala Ala 20 25 30

Ala Ala Val Leu Ala Val Leu Ser Val Phe Ala Val Ala Val Gly Gly 35 40 45

Arg Ala Gly Gly His Leu Ala Pro Pro Met Ser Trp Val Asp Gly Trp 50 55 60

Arg Ala Ser Thr Glu Pro Glu Arg Ser Gly Arg Thr Glu Ile Gly Gln 65 70 75 80

Glu Ala Leu Leu Asp Pro Ala Asp Leu Gly Val Pro Ser Asn Val Arg 85 90 95

Leu Gly Asp Ser Gly Leu Gln Glu Gln Val Arg Val Asp Pro Leu Leu 100 105 110

Gln Ser Cys Ala Val Gly Lys Glu Pro Gly Ala Gly Pro Pro Val Ser 115 120 125

Arg Tyr Ser Arg Ser Gln Thr Leu Leu Leu Asp Asp Thr Ser Gly Gln 130 135 140

Asp Gly Ser Met Ala Val Pro Val Leu Thr Gln Asp Val Tyr Arg Leu 145 150 155 160

Asp Pro Ala Pro Ala Gly Arg Leu Leu Ala Asp Leu Asp Arg Ala Ala 165 170 175

Thr Thr Cys Ala Arg Trp Ser Asp Thr Ala Val Arg Pro Leu Asp Asp 180 185 190

Gly Arg Gly Ala Ile Ser Val Ala His Thr Trp Gln Thr Ile Ala Arg 195 200 205

Asp Phe Ala Gly Asp Glu Ala Val Val Leu Arg His Thr Val Met Ser 210 225 220

Pro Val Asp Pro Thr Thr Gly Lys Pro Leu Asp Val Gly Tyr Pro Pro 225 230 235 240

Glu Thr Arg Met Ile Val Arg Val Gly Asp Leu Val Thr Val Ile Val
245 250 255

Pro Glu Arg Gly Leu Gly Val Asp Gly Pro Asp Gly Pro Arg Glu Thr
260 265 270

Ser Asp Ala Glu Leu Leu Glu Leu Gly Arg Thr Ala Ala Arg Arg Met 275 280 285

Cys Leu Ala Ala Asn Pro Ala Cys 290 295

<210> 189

<211> 498

<212> DNA

<213> Micromonospora carbonacea

```
<221> CDS
<222> (1) .. (498)
<220>
<223> ORF4
<400> 189
atg ccg gac gcc gag ggg ttc gac gag ttc tac cgg ggc agc cgg caa
                                                                 48
Met Pro Asp Ala Glu Gly Phe Asp Glu Phe Tyr Arg Gly Ser Arg Gln
                                    10
cga ttg ctg ggt ttc gtg tac atg atc acc gga aac ctg gcc gag gcg
                                                                 96
Arg Leu Leu Gly Phe Val Tyr Met Ile Thr Gly Asn Leu Ala Glu Ala
            20
                                25
cag gac gcc gtg cag gag gcg tac atc cgc gca tgg cag cgc tgg ccg
                                                                 144
Gln Asp Ala Val Gln Glu Ala Tyr Ile Arg Ala Trp Gln Arg Trp Pro
acc gta cgc ggg tac gac gat ccg gag ggc tgg ctg cgc gtg gtg gcg
                                                                 192
Thr Val Arg Gly Tyr Asp Asp Pro Glu Gly Trp Leu Arg Val Val Ala
    50
                        55
age egg ate geg gtg age egg tgg ege age atg egt age egg geg egg
                                                                 240
Ser Arg Ile Ala Val Ser Arg Trp Arg Ser Met Arg Ser Arg Ala Arg
                    70
gcg tac ctg cgg cac ggt gcg ccg gag agc gtc ccc gcg ccg agc acc
                                                                 288
Ala Tyr Leu Arg His Gly Ala Pro Glu Ser Val Pro Ala Pro Ser Thr
gcg acg ctg gag gtg gtg gcg cta cgc cgg ctg ccc gag gcg cag
                                                                 336
Ala Thr Leu Glu Val Val Ala Ala Leu Arg Arg Leu Pro Glu Ala Gln
           100
                               105
ege ace gee ate gee etg cae tae etg ete gge atg eeg gtg gee gag
                                                                 384
Arg Thr Ala Ile Ala Leu His Tyr Leu Leu Gly Met Pro Val Ala Glu
gtg gca cgg gag acc gcc gcc ccg gtc ggc acc gtg aaa gcc cgt ctc
                                                                 432
Val Ala Arg Glu Thr Ala Ala Pro Val Gly Thr Val Lys Ala Arg Leu
                       135
480
Ser Arg Gly Arg Ala Ala Leu Ala Gly Leu Leu Ala Val Ser Asp Leu
                   150
gag gag gcc gcc gat gcg
                                                                 498
Glu Glu Ala Ala Asp Ala
               165
<210> 190
<211> 166
<212> PRT
<213> Micromonospora carbonacea
<220>
<223> ORF4
<400> 190
Met Pro Asp Ala Glu Gly Phe Asp Glu Phe Tyr Arg Gly Ser Arg Gln
```

Arg Leu Leu Gly Phe Val Tyr Met Ile Thr Gly Asn Leu Ala Glu Ala

			20					25					30			
Gln	Asp	Ala 35	Val	Gln	Glu	Ala	Tyr 40	Ile	Arg	Ala	Trp	Gln 45	Arg	Trp	Pro	
Thr	Val 50	Arg	Gly	Tyr	Asp	Asp 55	Pro	Glu	Gly	Trp	Leu 60	Arg	Val	Val	Ala	
Ser 65	Arg	Ile	Ala	Val	Ser 70	Arg	Trp	Arg	Ser	Met 75	Arg	Ser	Arg	Ala	Arg 80	
Ala	Tyr	Leu	Arg	His 85	Gly	Ala	Pro	Glu	Ser 90	Val	Pro	Ala	Pro	Ser 95	Thr	
Ala	Thr	Leu	Glu 100	Val	Val	Ala	Ala	Leu 105	Arg	Arg	Leu	Pro	Glu 110	Ala	Gln	
Arg	Thr	Ala 115	Ile	Ala	Leu	His	Tyr 120	Leu	Leu	Gly	Met	Pro 125	Val	Ala	Glu	
Val	Ala 130	Arg	Glu	Thr	Ala	Ala 135	Pro	Val	Gly	Thr	Val 140	Lys	Ala	Arg	Leu	
Ser 145	Arg	Gly	Arg	Ala	Ala 150	Leu	Ala	Gly	Leu	Leu 155	Ala	Val	Ser	Asp	Leu 160	
Glu	Glu	Ala	Ala	Asp 165	Ala											
<210> 191 <211> 840 <212> DNA <213> Micromonospora carbonacea																
	L> CI	os L)	(840))												
<220 <223)> 3> OI	RF5														
gtg		ccc												cgg Arg 15		48
														tgc Cys		96
														ctc Leu		144
														gcc Ala		192
														gcg Ala		240

aac gcg gtg acc atc gcc cac gag ggc ggt cat gcg ctg gcc gcc ctg

Asn A	Ala	Val	Thr	Ile 85	Ala	His	Glu	Gly	Gly 90	His	Ala	Leu	Ala	Ala 95	Leu	
ctc a Leu :																336
ggg (_	_	_		_				_		_			384
acc o																432
gcg t Ala 7 145																480
gtg g Val V																528
gca (Ala 1	_	_	_		_				_	_		_	_			576
tac q Tyr A																624
ttc o																672
cgc a Arg s 225	_	-			-	_			_	_	_	_		_		720
ttg a																768
tgc (Cys)	_				_	_		_	_	_		_		_	_	816
ctc a Leu :																840
<210> 192 <211> 280 <212> PRT <213> Micromonospora carbonacea																
<220: <223:		RF5														
<400: Val 1			Gly	Ala 5	Gly	Arg	Pro	Gly	Pro 10	Gly	Arg	Ala	Pro	Arg 15	Pro	

Trp Arg Ala Arg Gly Ala Arg Thr Gly Pro Gly Pro Leu Gly Cys Gly

20 25 30 Pro Val Asp Leu Ile Asp Gly Leu Ser Val Val Trp Asn Glu Leu Val Gly Ala Gln Pro Asp Pro Pro Pro Leu Leu Val Leu Ala Thr Ala Ala 55 Val Ala Leu Ala Val Val Ala Thr Arg Val Pro Trp Arg Val Ala Arg Asn Ala Val Thr Ile Ala His Glu Gly Gly His Ala Leu Ala Ala Leu Leu Thr Gly Arg Lys Leu Arg Gly Ile Arg Leu His Ser Asp Thr Ser 105 Gly Leu Thr Leu Ser Ala Gly Arg Pro Thr Gly Leu Gly Met Ile Leu Thr Leu Phe Ala Gly Tyr Val Ala Pro Thr Leu Leu Gly Leu Ala Gly 135 Ala Trp Leu Leu Ala Gly Asn Arg Ile Thr Met Leu Leu Ser Val Thr 155 Val Val Leu Leu Ala Met Leu Ala Met Ile Arg Asn Val Tyr Gly Ala Leu Ser Leu Leu Ala Thr Gly Gly Leu Val Phe Ala Val Ser Trp Tyr Ala Pro Pro Gln Val Gln Ala Ala Phe Ala Trp Thr Ser Val Trp Phe Leu Leu Phe Gly Gly Val Arg Pro Val Ile Glu Leu Gln Arg Leu Arg Ser Arg Gly Arg Met Pro Glu Ser Asp Ala Asp Gln Leu Ala Arg Leu Thr Pro Phe Pro Pro Leu Phe Trp Val Gly Val Phe Leu Val Val Cys Leu Ala Gly Leu Ala Val Gly Ala Leu Leu Ala Gly Pro Ile 265 Leu Thr Asp Ala Gly Leu Thr Val 275 280 <210> 193 <211> 753 <212> DNA <213> Micromonospora carbonacea

<220> <221> CDS

<220> <223> ORF6

<400> 193

<222> (1)..(753)

					gaa Glu											48
					cgc Arg											96
					gtc Val											144
					gtc Val											192
_	_				ctg Leu 70	_			_	_		_		_		240
_		_	-	-	gag Glu		_		_		_		_			288
					gcc Ala											336
					ttc Phe											384
					cgc Arg											432
					cgg Arg 150											480
gag Glu	gcc Ala	gtc Val	gcg Ala	ggc Gly 165	atg Met	acc Thr	ccc Pro	gac Asp	ctg Leu 170	gtc Val	gtg Val	acc Thr	gac Asp	ctg Leu 175	ccg Pro	528
					agc Ser											576
					agg Arg											624
ctc Leu	gcc Ala 210	gtg Val	gtc Val	cta Leu	cgt Arg	gga Gly 215	cgc Arg	aag Lys	gtg Val	ccg Pro	ccg Pro 220	gtc Val	ggt Gly	gag Glu	gtc Val	672
					ttg Leu 230											720
					acc Thr											753

<210> 194

<211> 251

<212> PRT

<213> Micromonospora carbonacea

<220>

<223> ORF6

<400> 194

Val Thr Tyr Arg His Glu Thr Val Arg Gly Ala Tyr Gly Asp Leu Ala 1 5 10 15

Ser Gly Ala Val Leu Arg Ser Ala Pro Gly Phe Pro Ala Phe Pro Val 20 25 30

Arg Leu Ala Ser Glu Val Leu Gln Thr Ala Leu Glu Leu Arg Pro Thr 35 40 45

Ser Ala Pro Ala Thr Val Trp Asp Pro Cys Cys Gly Ser Gly Tyr Leu 50 55 60

Leu Thr Val Leu Ala Leu Leu His Arg Pro Ser Leu Ala Gly Leu Leu 65 70 75 80

Ala Ser Asp Val Asp Glu Ala Ala Leu Asp Leu Ala Arg Ala Asn Leu 85 90 95

Gly Leu Leu Thr Gly Ala Gly Leu Asp Thr Arg Ala Arg Glu Leu Ala 100 105 110

Gln Arg Ala Glu Ala Phe Asp Lys Pro His Tyr Ala Glu Ala Ala 115 120 125

Ala Ala His Arg Leu Arg Ala Arg Leu Asp Ala Ala Gly Gly Pro Leu 130 135 140

Pro Tyr Ala Val Arg Arg Ala Asp Val Phe Asp Arg Val Ala Leu Thr 145 150 155 160

Glu Ala Val Ala Gly Met Thr Pro Asp Leu Val Val Thr Asp Leu Pro 165 170 175

Tyr Gly Glu Gln Thr Ser Trp Gln Gly Glu Arg Ala Gly Glu Gly Leu 180 185 190

Pro Gly Met Leu Thr Arg Val Ala Ser Val Leu Pro Pro Thr Gly Val

Leu Ala Val Val Leu Arg Gly Arg Lys Val Pro Pro Val Gly Glu Val 210 215 220

Arg Pro Arg Arg Leu Arg Val Gly Thr Arg Ala Ala Phe Phe 225 230 235 240

Val Ala Gly Asp Leu Thr Gly Val Pro Ala Thr 245 250

<210> 195

<211> 1086

<212> DNA

<213> Micromonospora carbonacea

<221> CDS

<222> (1)..(1086) <220> <223> ORF7 <400> 195 48 Met Thr Val Pro Asp Thr Asp Glu Arg Ala Thr Thr Thr Asp Glu Pro 10 age gee ege egg geg eag ace gge geg gae gee tgg eeg gag etg 96 Ser Ala Arg Arg Ala Gln Thr Gly Ala Asp Ala Ala Trp Pro Glu Leu 25 atg cgg ttg gtg ttc ggc ggg atg gcc agc cgg ctg gtc ggc tac tgc 144 Met Arg Leu Val Phe Gly Gly Met Ala Ser Arg Leu Val Gly Tyr Cys gtc cgg ctg ggg ctg ccc gac gcg atc ggc gac gac gag cgc acc ccg 192 Val Arg Leu Gly Leu Pro Asp Ala Ile Gly Asp Asp Glu Arg Thr Pro 50 cag gag ttg gcg ctg cgg tac gac gcc cga gcg gac acc atg ttc cgg 240 Gln Glu Leu Ala Leu Arg Tyr Asp Ala Arg Ala Asp Thr Met Phe Arg 288 gtg ctg cgc gcc ctg gcc gcg ctg cgg gtg ctc acc gag acc aca ccc Val Leu Arg Ala Leu Ala Ala Leu Arg Val Leu Thr Glu Thr Thr Pro ggc cgg ttc gcg ctc gcc ccg atg ggg gcg ctg ctg cgt ggg gac cga 336 Gly Arg Phe Ala Leu Ala Pro Met Gly Ala Leu Leu Arg Gly Asp Arg 100 ccc ggc acg ctg cgc ccg ctg gcc cgg atg ctg acc gac ccg gcc atg 384 Pro Gly Thr Leu Arg Pro Leu Ala Arg Met Leu Thr Asp Pro Ala Met ace acg gee tgg gac gge etg geg cac age gte ege ace gge gag eeg 432 Thr Thr Ala Trp Asp Gly Leu Ala His Ser Val Arg Thr Gly Glu Pro 135 gcc ttc gac ggc atc ttc ggc acc gac ttc ttc agc tac gtg ggc ggg 480 Ala Phe Asp Gly Ile Phe Gly Thr Asp Phe Phe Ser Tyr Val Gly Gly 150 155 ega eec gae ett tee gag etg tae aac geg geg atg age eag gtg ace 528 Arg Pro Asp Leu Ser Glu Leu Tyr Asn Ala Ala Met Ser Gln Val Thr 165 170 cac age gte geg geg gee gtt gee gag egt ace gae etg gee gge gtg 576 His Ser Val Ala Ala Ala Val Ala Glu Arg Thr Asp Leu Ala Gly Val egg aeg gtg gte gae gtg gge gge gga gae gge aec etg etg gee gee Arg Thr Val Val Asp Val Gly Gly Gly Asp Gly Thr Leu Leu Ala Ala 195 200 205 gtg ctc gcc gcg aac ccc ggc gtg cgg ggc gtg ctc tac gac agc gcc Val Leu Ala Ala Asn Pro Gly Val Arg Gly Val Leu Tyr Asp Ser Ala 210 215 age gge age geg gag geg ggg aac etg ege ege gee ggg gte gge 720

Ser Gly Ser Ala Glu Ala Ala Gly Asn Leu Arg Arg Ala Gly Val Gly

225		230				235					240		
gac cgg tgc Asp Arg Cys	cgg atc Arg Ile 245	gag gt Glu Va	g ggt l Gly	gac Asp	ttc Phe 250	ttc Phe	gag Glu	agg Arg	gtc Val	ccc Pro 255	gcc Ala	768	
gac gcc gac Asp Ala Asp	ctc tac Leu Tyr 260	ctg ct Leu Le	ı Lys	agt Ser 265	gtg Val	atc Ile	cac His	ggt Gly	tgg Trp 270	ggc Gly	gac Asp	816	
ggc cgg gcg Gly Arg Ala 275												864	
ggc ggc cgg Gly Gly Arg 290	atc gtc Ile Val	atg at Met Il 29	e Asp	cac His	gtg Val	ctg Leu	ccg Pro 300	gac Asp	gtg Val	gtc Val	ggc Gly	912	
ccg gcg gcc Pro Ala Ala 305	aac gcg Asn Ala	ctg gc Leu Al 310	g tac a Tyr	ctg Leu	acc Thr	gac Asp 315	gtg Val	gly ggg	atg Met	ctg Leu	gtc Val 320	960	
aac ggg cag Asn Gly Gln												1008	
ggc aag gcg Gly Lys Ala			ı Glu i									1056	
gac ttc cac Asp Phe His 355												1086	
<210> 196 <211> 362 <212> PRT <213> Micromonospora carbonacea													
<220> <223> ORF7												•	
<400> 196 Met Thr Val 1	Pro Asp 5	Thr As	o Glu i	Arg	Ala 10	Thr	Thr	Thr	Asp	Glu 15	Pro	•	
Ser Ala Arg	Arg Ala 20	Gln Th	Gly A	Ala 25	Asp	Ala	Ala	Trp	Pro 30	Glu	Leu		
Met Arg Leu 35	Val Phe	Gly Gl	Met 1	Ala	Ser	Arg	Leu	Val 45	Gly	Tyr	Cys		
			40 Ala					45					
35 Val Arg Leu	Gly Leu	Pro As ₁	40 Ala	Ile	Gly	Asp	Asp 60	45 Glu	Arg	Thr	Pro		
Val Arg Leu 50 Gln Glu Leu	Gly Leu Ala Leu	Pro Asj 59 Arg Ty: 70	40 Ala :	Ile Ala	Gly Arg	Asp Ala 75	Asp 60 Asp	45 Glu Thr	Arg Met	Thr Phe	Pro Arg 80		

Pro Gly Thr Leu Arg Pro Leu Ala Arg Met Leu Thr Asp Pro Ala Met 120 Thr Thr Ala Trp Asp Gly Leu Ala His Ser Val Arg Thr Gly Glu Pro 135 Ala Phe Asp Gly Ile Phe Gly Thr Asp Phe Phe Ser Tyr Val Gly Gly Arg Pro Asp Leu Ser Glu Leu Tyr Asn Ala Ala Met Ser Gln Val Thr 165 His Ser Val Ala Ala Ala Val Ala Glu Arg Thr Asp Leu Ala Gly Val Arg Thr Val Val Asp Val Gly Gly Asp Gly Thr Leu Leu Ala Ala Val Leu Ala Ala Asn Pro Gly Val Arg Gly Val Leu Tyr Asp Ser Ala 215 Ser Gly Ser Ala Glu Ala Ala Gly Asn Leu Arg Arg Ala Gly Val Gly Asp Arg Cys Arg Ile Glu Val Gly Asp Phe Phe Glu Arg Val Pro Ala Asp Ala Asp Leu Tyr Leu Leu Lys Ser Val Ile His Gly Trp Gly Asp 265 Gly Arg Ala Thr Gly Ile Leu Arg His Cys Ala Glu Ala Val Ala Pro Gly Gly Arg Ile Val Met Ile Asp His Val Leu Pro Asp Val Val Gly Pro Ala Ala Asn Ala Leu Ala Tyr Leu Thr Asp Val Gly Met Leu Val Asn Gly Gln Gly Leu Glu Arg Thr Arg Gly Asp Leu Glu Arg Leu Cys 325 330 Gly Lys Ala Gly Leu Ser Leu Glu Asp Val Thr Pro Leu Pro Pro Thr Asp Phe His Trp Ile Glu Ser Arg Pro Ala <210> 197 <211> 852 <212> DNA <213> Micromonospora carbonacea

<212> DNA
<213> Micromonospora carbona
<220>
<221> CDS
<222> (1)..(852)
<220>
<220>
<223> ORF8
<400> 197

atg agc gcc cag gtc ctc agc gac gag cag gtc gag cgg ttc gtc tcc Met Ser Ala Gln Val Leu Ser Asp Glu Gln Val Glu Arg Phe Val Ser

1				5					10					15		
						gag Glu										96
						tgg Trp										144
						gag Glu 55										192
						gcc Ala										240
						ggg Gly										288
						ccg Pro										336
						gac Asp										384
						tgg Trp 135										432
						cgc Arg										480
						ttc Phe										528
						tcc Ser										576
						acc Thr										624
						gcc Ala 215										672
tgc Cys 225	cac His	ccg Pro	ttc Phe	ctg Leu	gtg Val 230	cac His	acc Thr	ccg Pro	gtg Val	gcc Ala 235	aac Asn	acc Thr	ggc Gly	acg Thr	cgg Arg 240	720
						ccg Pro										768
						gac Asp										816

852

atc ggg ctg ggc ctg ccg gcc gcc gag ccg gtc cga

Ile Gly Leu Gly Leu Pro Ala Ala Glu Pro Val Arg 275 280 <210> 198 <211> 284 <212> PRT <213> Micromonospora carbonacea <220> <223> ORF8 <400> 198 Met Ser Ala Gln Val Leu Ser Asp Glu Gln Val Glu Arg Phe Val Ser Asp Gly Phe Val Lys Leu Glu Ala Ala Phe Pro Ala Glu Leu Ala Gln Gln Gly Arg Glu Leu Trp Arg Gln Leu Gly Met Asp Pro Glu Asp Arg Ser Thr Trp Ser Arg Glu Val Val Arg Leu Gly Leu Gln Asp Ala 55 Glu Pro Phe Val Arg Ser Ala Thr Thr Pro Arg Leu His Ala Ala Phe Asp Gln Leu Val Gly Val Gly Arg Trp Lys Pro Leu Asp Arg Ile Gly Thr Phe Pro Val Arg Phe Pro Val Pro Lys Arg Pro Glu Gln Thr Glu 105 Asp Tyr Gly Trp His Ile Asp Ala Ser Phe Leu Ala Asp Asp Ala Gln Arg Leu Gly Pro Gln Asn Trp Glu Gly Glu Leu Asp Leu Val Pro Pro 135 Asn Tyr Ala Glu Val Phe Arg Cys Asn Leu Arg Ser Arg Gly Arg Ala Leu Leu Leu Phe Leu Phe Ser Asp Thr Asp Glu Arg Glu Ala Pro 165 Thr Leu Val Arg Val Gly Ser His Leu Asp Val Pro Pro Leu Leu Glu 180 185 Pro Tyr Gly Pro Glu Gly Thr Tyr Leu Asp Val Gly Asp Val Gly Arg Asp Arg Pro Leu Ala Ser Ala Thr Gly Arg Ala Gly Asp Val Tyr Leu Cys His Pro Phe Leu Val His Thr Pro Val Ala Asn Thr Gly Thr Arg 230 235 Pro Arg Phe Met Ala Gln Pro Ser Leu Gln Pro Val Gly Glu Leu Asp 245 Leu Asp Arg Pro Asp Gly Asp Tyr Ser Pro Val Glu Arg Ala Val Arg

265

260

Ile Gly Leu Gly Leu Pro Ala Ala Glu Pro Val Arg 275 280

<210> 199 <211> 1062 <212> DNA <213> Micromonospora carbonacea														
<220> <221> CDS <222> (1)(1062)														
220> 223> ORF9														
1400> 199 Itg gag tac cga cag ttg ggc cgg tgt gga ctg cgg gtg tcc aag gtg 48 I'al Glu Tyr Arg Gln Leu Gly Arg Cys Gly Leu Arg Val Ser Lys Val 1 5 10 15														
cc ctg ggg gcg ttc aac ttc ggc ggc ccg acc ggg ccg gag gac 96 er Leu Gly Ala Phe Asn Phe Gly Gly Pro Thr Gly Pro Glu Glu Ala 20 25 30														
cc agg atc gtc gcc acg gcc gtc gaa gcg gga gtc aac ctc gtc gac 14. Na Arg Ile Val Ala Thr Ala Val Glu Ala Gly Val Asn Leu Val Asp 35 40 45	4													
ncg gcc aac gtc tac cag gac ggc cgc agc gag gag atc gtc ggc gcg 193 Thr Ala Asn Val Tyr Gln Asp Gly Arg Ser Glu Glu Ile Val Gly Ala 50 55 60	2													
cc gtg cgg agc tgc cgg gac gac gtc ctg ctg gcc acc aag atc ttc 240 cla Val Arg Ser Cys Arg Asp Asp Val Leu Leu Ala Thr Lys Ile Phe 65 70 75 80	0													
at ccg gtc ggc ccg gga ccg aac gac cgg ggc acc tcg gcg tac gcc 288 sn Pro Val Gly Pro Gly Pro Asn Asp Arg Gly Thr Ser Ala Tyr Ala 85 90 95	8													
tg aag cgg gag tgc gag cgg tcg ttg cgc cgg ctg ggt acc gac cac 330 eu Lys Arg Glu Cys Glu Arg Ser Leu Arg Arg Leu Gly Thr Asp His 100 105 110	6													
tc gac ctg ctc tac ctg cac cgt cac gac ccg gac act ccg gtg gag le Asp Leu Leu Tyr Leu His Arg His Asp Pro Asp Thr Pro Val Glu 115 120 125	4													
gag acg gtg tcc gcc ctc gac gac ctg gtc cgc tcg ggc aag gtc cgc 433 Glu Thr Val Ser Ala Leu Asp Asp Leu Val Arg Ser Gly Lys Val Arg 130 135 140	2													
ac gtg ggc acc tcc acc gtg ccc acg gca tac gag ctg gcc gac cag Tyr Val Gly Thr Ser Thr Val Pro Thr Ala Tyr Glu Leu Ala Asp Gln 150 155 160	0													
ccc cgg ctg ggc acg gtg ccc agc tgg cgg atc gtc gac ctg ctg cgc 529 Pro Arg Leu Gly Thr Val Pro Ser Trp Arg Ile Val Asp Leu Leu Arg 165 170 175	8													
ceg geg cag tee egg gge gee gee eeg gtg gtg gee gag eag teg eeg 570 Chr Ala Gln Ser Arg Gly Ala Ala Pro Val Val Ala Glu Gln Ser Pro	6													

180 185 190 tac aac ctg ctg gaa cgc gag atc gag cgg gac gtg ctg ccg ctg tgc 624 Tyr Asn Leu Leu Glu Arg Glu Ile Glu Arg Asp Val Leu Pro Leu Cys 195 200 205 gcg gag tac ggc ctc ggc ctg ttc acc tac agc ccg ctg gcg atg ggt 672 Ala Glu Tyr Gly Leu Gly Leu Phe Thr Tyr Ser Pro Leu Ala Met Gly 210 215 ctg ctc tcc gac cgg ttc gcc gac ggc gag ccg ccc cgc gac gcc cgg 720 Leu Leu Ser Asp Arg Phe Ala Asp Gly Glu Pro Pro Arg Asp Ala Arg 225 230 235 tte ace gee tgg tae gee eea teg gge eeg eac tgg eag eeg gtg tgg 768 Phe Thr Ala Trp Tyr Ala Pro Ser Gly Pro His Trp Gln Pro Val Trp cgg acc ctg ggc cgg ttg gcg aag gtg gcc gtc gag ctg ggc ctg tcc 816 Arg Thr Leu Gly Arg Leu Ala Lys Val Ala Val Glu Leu Gly Leu Ser 260 ctg ccg gac ctg gcg cac gcc tgg gtc tac gac gcg ccg ggg gtg acc 864 Leu Pro Asp Leu Ala His Ala Trp Val Tyr Asp Ala Pro Gly Val Thr 280 age acg gtc gtc ggc ccc cgc acg ctg gac cag gcc cgg gcg gcg ctg 912 Ser Thr Val Val Gly Pro Arg Thr Leu Asp Gln Ala Arg Ala Ala Leu 295 gcg gcg gcc gac cgg ccg ctg ccg gag gag gcc cgc gcc cgg ctc gac 960 Ala Ala Asp Arg Pro Leu Pro Glu Glu Ala Arg Ala Arg Leu Asp 310 315 ggc atc gcc gca ccc ggg gag agc cga tgg ttg cgg gtg gtg gag cgg 1008 Gly Ile Ala Ala Pro Gly Glu Ser Arg Trp Leu Arg Val Val Glu Arg ggg gtg egg ege tet ege ggt gge eeg gae gat get gag ga'a aac gtt 1056 Gly Val Arg Arg Ser Arg Gly Gly Pro Asp Asp Ala Glu Glu Asn Val agt ccc 1062 Ser Pro <210> 200 <211> 354 <212> PRT <213> Micromonospora carbonacea <220> <223> ORF9 Val Glu Tyr Arg Gln Leu Gly Arg Cys Gly Leu Arg Val Ser Lys Val Ser Leu Gly Ala Phe Asn Phe Gly Gly Pro Thr Gly Pro Glu Glu Ala Ala Arg Ile Val Ala Thr Ala Val Glu Ala Gly Val Asn Leu Val Asp Thr Ala Asn Val Tyr Gln Asp Gly Arg Ser Glu Glu Ile Val Gly Ala

	50					55					60				
Ala 65	Val	Arg	Ser	Cys	Arg 70	Asp	Asp	Val	Leu	Leu 75	Ala	Thr	Lys	Ile	Phe 80
Asn	Pro	Val	Gly	Pro 85	Gly	Pro	Asn	Asp	Arg 90	Gly	Thr	Ser	Ala	Tyr 95	Ala
Leu	Lys	Arg	Glu 100	Cys	Glu	Arg	Ser	Leu 105	Arg	Arg	Leu	Gly	Thr 110	Asp	His
Ile	Asp	Leu 115	Leu	Tyr	Leu	His	Arg 120	His	Asp	Pro	Asp	Thr 125	Pro	Val	Glu
Glu	Thr 130	Val	Ser	Ala	Leu	Asp 135	Asp	Leu	Val	Arg	Ser 140	Gly	Lys	Val	Arg
Tyr 145	Val	Gly	Thr	Ser	Thr 150	Val	Pro	Thr	Ala	Tyr 155	Glu	Leu	Ala	Asp	Glr 160
Pro	Arg	Leu	Gly	Thr 165	Val	Pro	Ser	Trp	Arg 170	Ile	Val	Asp	Leu	Leu 175	Arg
Thr	Ala	Gln	Ser 180	Arg	Gly	Ala	Ala	Pro 185	Val	Val	Ala	Glu	Gln 190	Ser	Pro
Tyr	Asn	Leu 195	Leu	Glu	Arg	Glu	Ile 200	Glu	Arg	Asp	Val	Leu 205	Pro	Leu	Cys
Ala	Glu 210	Tyr	Gly	Leu	Gly	Leu 215	Phe	Thr	Tyr	Ser	Pro 220	Leu	Ala	Met	Gly
Leu 225	Leu	Ser	Asp	Arg	Phe 230	Ala	Asp	Gly	Glu	Pro 235	Pro	Arg	Asp	Ala	Arg 240
Phe	Thr	Ala	Trp	Tyr 245	Ala	Pro	Ser	Gly	Pro 250	His	Trp	Gln	Pro	Val 255	Trp
Arg	Thr	Leu	Gly 260	Arg	Leu	Ala	Lys	Val 265	Ala	Val	Glu	Leu	Gly 270	Leu	Ser
Leu	Pro	Asp 275	Leu	Ala	His	Ala	Trp 280	Val	Tyr	Asp	Ala	Pro 285	Gly	Val	Thr
Ser	Thr 290	Val	Val	Gly	Pro	Arg 295	Thr	Leu	Asp	Gln	Ala 300	Arg	Ala	Ala	Leu
Ala 305	Ala	Ala	Asp	Arg	Pro 310	Leu	Pro	Glu	Glu	Ala 315	Arg	Ala	Arg	Leu	Asp 320
Gly	Ile	Ala	Ala	Pro 325	Gly	Glu	Ser	Arg	Trp 330	Leu	Arg	Val	Val	Glu 335	Arg
Gly	Val	Arg	Arg 340	Ser	Arg	Gly	Gly	Pro 345	Asp	Asp	Ala	Glu	Glu 350	Asn	Val
Ser	Pro														

<210> 201 <211> 927

<220>

<212> DNA <213> Micromonospora carbonacea

<221> CDS <222> (1) .. (927) <220> <223> ORF10 <400> 201 atg agc gac aag tac ggc cgc agt gcg ctg tgg gaa cgg tac aac agc 48 Met Ser Asp Lys Tyr Gly Arg Ser Ala Leu Trp Glu Arg Tyr Asn Ser 10 aca cag gtg acc gag gag gcg gcg gac gac ctc acc tcc ttc aag tcg 96 Thr Gln Val Thr Glu Glu Ala Ala Asp Asp Leu Thr Ser Phe Lys Ser 20 25 age gae gte aac tae aag ete gee ete tgg gat eee egg gte age ggg 144 Ser Asp Val Asn Tyr Lys Leu Ala Leu Trp Asp Pro Arg Val Ser Gly gtc cgc tac ctg aag acg ctc atc ttc aac ctg gcc gag aac ctg ggc 192 Val Arg Tyr Leu Lys Thr Leu Ile Phe Asn Leu Ala Glu Asn Leu Gly 50 55 gag geg aac egg gee egg ttg ege egg ate gee aac egg gae gte gge 240 Glu Ala Asn Arg Ala Arg Leu Arg Arg Ile Ala Asn Arg Asp Val Gly gac ccc atc tcc gtc gtc tgg gac ggc gac cgg atc tgc atg gac tat 288 Asp Pro Ile Ser Val Val Trp Asp Gly Asp Arg Ile Cys Met Asp Tyr ctc cag gcg gtg ctg gag ctg gag ttc ttc tcc cgc cac gtg cca ctg 336 Leu Gln Ala Val Leu Glu Leu Glu Phe Phe Ser Arg His Val Pro Leu 100 105 gac ggc gcg acg gtg ctg gag atc ggc gcg ggc tac ggc cgc acc tgt 384 Asp Gly Ala Thr Val Leu Glu Ile Gly Ala Gly Tyr Gly Arg Thr Cys 120 cac gcc gtg ctc tcc aac cac gac gtc gcc gcg tac cac gtg gtc gac 432 His Ala Val Leu Ser Asn His Asp Val Ala Ala Tyr His Val Val Asp 135 ctg ccg aac tcc ctc gct ctg gcc cgc cgc tac ctg ggc acg gtg ctc 480 Leu Pro Asn Ser Leu Ala Leu Ala Arg Arg Tyr Leu Gly Thr Val Leu 150 155 ace gee gag cag ttg geg agg gte cae tte cae gge gte gge gag gtg 528 Thr Ala Glu Gln Leu Ala Arg Val His Phe His Gly Val Gly Glu Val 165 gac ggg ccg ctg agc gag ctg cgc tac gac ctc gtg atc aac atc gac 576 Asp Gly Pro Leu Ser Glu Leu Arg Tyr Asp Leu Val Ile Asn Ile Asp 180 teg tte geg gag atg acg geg gag acg gtg ege geg tae ete gee tte 624 Ser Phe Ala Glu Met Thr Ala Glu Thr Val Arg Ala Tyr Leu Ala Phe 195 200 205 gtc gcc acc agg gcc cgc cac ctg tac gtc aac aac ccc gtc ggg aag Val Ala Thr Arg Ala Arg His Leu Tyr Val Asn Asn Pro Val Gly Lys 210 215 tac ctc gac aag agc ctg gac ggg cac ttc cag ggc gag gcc gtg gtc

Tyr Leu Asp Lys Ser Leu Asp Gly His Phe Gln Gly Glu Ala Val Val

225	2	230		235			240							
aac ctt gcg ct Asn Leu Ala Le														
gac aac cag go Asp Asn Gln Al 26	a Val A													
cgg ccg ggg cc Arg Pro Gly Pr 275														
tgg agc tac ta Trp Ser Tyr Ty 290	c tgg c r Trp G	cag gcg 31n Ala 295	ctc tac Leu Tyr	cgg gcc Arg Ala	ggc gag Gly Glu 300	gcg gcc Ala Ala	ccg 912 Pro							
gca ccc ggg cg Ala Pro Gly Ar 305	_						927							
<210> 202 <211> 309 <212> PRT <213> Micromonospora carbonacea														
<220> <223> ORF10														
<400> 202 Met Ser Asp Ly 1	s Tyr G 5	Gly Arg	Ser Ala	Leu Trp	Glu Arg	Tyr Asn 15	Ser							
Thr Gln Val Th		3lu Ala	Ala Asp 25	Asp Leu	Thr Ser	Phe Lys	Ser							
Ser Asp Val As	n Tyr L	Lys Leu	Ala Leu	Trp Asp	Pro Arg	Val Ser	Gly							
			40		45									
Val Arg Tyr Le	ı Lys T	Thr Leu 55		Asn Leu	45		Gly							
	- g Ala A	55	Ile Phe		45 Ala Glu 60	Asn Leu	-							
50 Glu Ala Asn Ar	g Ala A	55 Arg Leu 70	Ile Phe	Ile Ala 75	Ala Glu 60 Asn Arg	Asn Leu	Gly 80							
50 Glu Ala Asn Ar 65	g Ala A r Val V 85	55 Arg Leu 70 Val Trp	Ile Phe Arg Arg Asp Gly	Ile Ala 75 Asp Arg 90	Ala Glu 60 Asn Arg Ile Cys	Asn Leu Asp Val Met Asp	Gly 80 Tyr							
Glu Ala Asn Ar 65 Asp Pro Ile Se Leu Gln Ala Va	y Ala A val V 85 l Leu G	55 Arg Leu 70 Val Trp Glu Leu	Ile Phe Arg Arg Asp Gly Glu Phe 105	Ile Ala 75 Asp Arg 90 Phe Ser	Ala Glu 60 Asn Arg Ile Cys Arg His	Asn Leu Asp Val Met Asp 95 Val Pro 110	Gly 80 Tyr Leu							
Glu Ala Asn Ar 65 Asp Pro Ile Se Leu Gln Ala Va 10	y Ala A val V 85 Leu G	55 Arg Leu 70 Val Trp Glu Leu Leu Glu	Ile Phe Arg Arg Asp Gly Glu Phe 105 Ile Gly 120	Ile Ala 75 Asp Arg 90 Phe Ser Ala Gly	Ala Glu 60 Asn Arg Ile Cys Arg His Tyr Gly 125	Asn Leu Asp Val Met Asp 95 Val Pro 110 Arg Thr	Gly 80 Tyr Leu Cys							
Glu Ala Asn Ar 65 Asp Pro Ile Se Leu Gln Ala Va Asp Gly Ala Th 115 His Ala Val Le	y Ala A r Val V 85 l Leu G r Val L u Ser A	Arg Leu 70 Val Trp Glu Leu Leu Glu Asn His 135	Ile Phe Arg Arg Asp Gly Glu Phe 105 Ile Gly 120 Asp Val	Ile Ala 75 Asp Arg 90 Phe Ser Ala Gly Ala Ala	Ala Glu 60 Asn Arg Ile Cys Arg His Tyr Gly 125 Tyr His 140	Asn Leu Asp Val Met Asp 95 Val Pro 110 Arg Thr Val Val	Gly 80 Tyr Leu Cys							

```
Asp Gly Pro Leu Ser Glu Leu Arg Tyr Asp Leu Val Ile Asn Ile Asp
                                185
Ser Phe Ala Glu Met Thr Ala Glu Thr Val Arg Ala Tyr Leu Ala Phe
        195
                            200
                                                205
Val Ala Thr Arg Ala Arg His Leu Tyr Val Asn Asn Pro Val Gly Lys
Tyr Leu Asp Lys Ser Leu Asp Gly His Phe Gln Gly Glu Ala Val Val
                    230
Asn Leu Ala Leu Ser Thr Gly Leu Leu Arg Asp Val Ile Asp Ile His
Asp Asn Gln Ala Val Arg Arg Gln Ser Arg Ala Phe Leu Asp Ala Tyr
Arg Pro Gly Pro Gly Trp Ala Cys Val Ala Glu Ser Arg Thr Ile Pro
Trp Ser Tyr Tyr Trp Gln Ala Leu Tyr Arg Ala Gly Glu Ala Ala Pro
                        295
                                            300
Ala Pro Gly Arg Asp
305
<210> 203
<211> 999
<212> DNA
<213> Micromonospora carbonacea
<220>
<221> CDS
<222> (1)..(999)
<220>
<223> ORF11
<400> 203
gtg ctg gcc gcg ctc gcc gac cgg gcg gtc acc gtc cgg gcc gtc gcc
                                                                   48
Val Leu Ala Ala Leu Ala Asp Arg Ala Val Thr Val Arg Ala Val Ala
ege egg get gee gtg etg eee gee geg eeg gge ege geg ttt gag
                                                                   96
Arg Arg Ala Ala Val Leu Pro Ala Ala Pro Gly Arg Ala Ala Phe Glu
             20
gtg gta egg gee gae etg ace gae egg gga gee etg geg geg gta
                                                                   144
Val Val Arg Ala Asp Leu Thr Asp Arg Gly Ala Leu Ala Ala Val
ege gae geg aeg gee gtg gte aac ete aee etg gae agt tee gge tgg
                                                                   192
Arg Asp Ala Thr Ala Val Val Asn Leu Thr Leu Asp Ser Ser Gly Trp
egg gge gee gae gae gge ege age geg egg gte aae gte gag etg ace
                                                                   240
Arg Gly Ala Asp Asp Asp Arg Ser Ala Arg Val Asn Val Glu Leu Thr
egg gaa ete gte ggg atg ete ege eee ggg eeg gge aeg eee aee
                                                                   288
Arg Glu Leu Val Gly Met Leu Arg Pro Gly Pro Gly Gly Thr Pro Thr
```

aca ctg gtc ttc gcc ggc tcc gcc tcc cag gtg ggc cgg ccg ccc cgg

336

Thr	Leu	Val	Phe 100	Ala	Gly	Ser	Ala	Ser 105	Gln	Val	Gly	Arg	Pro 110	Pro	Arg	
atc Ile	ccg Pro	atc Ile 115	gac Asp	ggc Gly	acc Thr	gag Glu	ccg Pro 120	gac Asp	cac His	ccc Pro	gcc Ala	acc Thr 125	ccg Pro	tac Tyr	gac Asp	384
												gcc Ala				432
												gtg Val				480
												tcc Ser				528
cgc Arg	cgg Arg	gcg Ala	ctg Leu 180	tcc Ser	gga Gly	gcg Ala	cca Pro	ctg Leu 185	acc Thr	atg Met	tgg Trp	cac His	gac Asp 190	ggc Gly	cgg Arg	576
												gcc Ala 205				624
gcg Ala	gcg Ala 210	ctg Leu	gac Asp	cac His	ccc Pro	999 Gly 215	gcg Ala	ctg Leu	acc Thr	ggc Gly	cgg Arg 220	cac His	tgg Trp	ccg Pro	ctc Leu	672
												cgc Arg				720
gcc Ala	ctg Leu	gtg Val	gcc Ala	gag Glu 245	cgg Arg	acc Thr	ggt Gly	cgg Arg	cca Pro 250	ccg Pro	gtg Val	ccg Pro	gtg Val	ctg Leu 255	gcc Ala	768
												cac His				816
												gcg Ala 285				864
												ctc Leu				912
gac Asp 305	agc Ser	ggc Gly	ccc Pro	gag Glu	gcc Ala 310	ccg Pro	ggc Gly	ggc Gly	gtc Val	ggc Gly 315	ccg Pro	acg Thr	cgg Arg	gcg Ala	gat Asp 320	960
					gac Asp											999

<210> 204 <211> 333 <212> PRT <213> Micromonospora carbonacea

<220> <223> ORF11

<400> 204

Val Leu Ala Ala Leu Ala Asp Arg Ala Val Thr Val Arg Ala Val Ala 1 5 10 15

Arg Arg Ala Ala Val Leu Pro Ala Ala Pro Gly Arg Ala Ala Phe Glu 20 25 30

Val Val Arg Ala Asp Leu Thr Asp Arg Gly Ala Leu Ala Ala Val 35 40 45

Arg Asp Ala Thr Ala Val Val Asn Leu Thr Leu Asp Ser Ser Gly Trp 50 60

Arg Gly Ala Asp Asp Asp Arg Ser Ala Arg Val Asn Val Glu Leu Thr 65 70 75 80

Arg Glu Leu Val Gly Met Leu Arg Pro Gly Pro Gly Gly Thr Pro Thr 85 90 95

Thr Leu Val Phe Ala Gly Ser Ala Ser Gln Val Gly Arg Pro Pro Arg 100 105 110

Ile Pro Ile Asp Gly Thr Glu Pro Asp His Pro Ala Thr Pro Tyr Asp 115 120 125

Arg Gln Lys Gln Ala Ala Glu Ser Leu Val Val Ala Ala Thr Gly Ala 130 135 140

Gly Val Val Asn Gly Val Ser Leu Arg Leu Pro Thr Val Phe Gly Pro 145 150 155 160

Val Pro Pro Gly Ala Gly Pro Asp Arg Gly Val Val Ser Thr Met Ile 165 170 175

Arg Arg Ala Leu Ser Gly Ala Pro Leu Thr Met Trp His Asp Gly Arg 180 185 190

Val Gln Arg Gln Leu Leu Tyr Val Ala Asp Ala Ala Ala Ala Phe Val 195 200 205

Ala Ala Leu Asp His Pro Gly Ala Leu Thr Gly Arg His Trp Pro Leu 210 215 220

Gly Asp Gly Arg Gly Glu Arg Leu Gly Asp Leu Phe Arg Ala Ile Ala 225 230 235 240

Ala Leu Val Ala Glu Arg Thr Gly Arg Pro Pro Val Pro Val Leu Ala
245 250 255

Val Pro Pro Pro Asp Glu Ala Arg Val Ser Asp Phe His Asp Met Val 260 265 270

Val Asp Ala Ser Ala Phe Gln Ala Val Thr Gly Trp Ala Pro Arg Val 275 280 285

Pro Leu Arg Leu Ala Leu Asp Arg Thr Val Ala Ala Leu Ala Arg Asp 290 295 300

Asp Ser Gly Pro Glu Ala Pro Gly Gly Val Gly Pro Thr Arg Ala Asp 305 310 315 320

Gln Ala Arg Lys Pro Asp Ser Ile Ser Arg Gln Val Arg

340

325 330